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OM protein - protein search, using sw model

Run on: September 21, 2005, 14:52:13 ; Search time 81.9233 Seconds
(without alignments)
618.452 Million cell updates/sec

Title: US-10-807-204-1

Perfect score: 753

Sequence: 1 MGLSGLPLVFPFILLGDIQ.....GNNNFQTEAICLVTCRKYH 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	131	7	ADA19800
2	753	100.0	131	7	ADA19811
3	731	97.1	131	7	ADA19814
4	625	83.0	106	7	ADA19801
5	551	73.2	98	7	ADA19808
6	492	65.3	136	7	ADA19815
7	467	62.0	133	2	AAW75219
8	467	62.0	133	5	AAE26982
9	467	62.0	133	5	AAE27120
10	467	62.0	133	6	ABU64993
11	467	62.0	133	7	ADA19812
12	467	62.0	133	8	ADG89802
13	467	62.0	164	3	AAV70010
14	467	62.0	179	8	ABW85103
15	404	53.7	86	5	ABP69809
16	404	53.7	86	6	ABJ26667
17	404	53.7	101	4	ABBI2236
18	401.5	53.3	117	5	AAE27094
19	401.5	53.3	117	5	AAE27165
20	401.5	53.3	117	6	ABU65038
21	401.5	53.3	117	8	ADG89847
22	400	53.1	102	5	AAE27095
23	400	53.1	102	5	AAE28009
24	400	53.1	102	6	ABU65039
25	400	53.1	102	8	ADG89848

26	398	52.9	134	7	ADA19813	Ada19813 Mouse BPP
27	248.5	33.0	101	8	ADQ66734	Adq66734 Novel hum
28	246	32.7	43	7	ADA19804	Ada19804 Engineere
29	242	32.1	64	4	AAE13093	Aae13093 Human ser
30	236	31.3	58	4	AAE13084	Aae13084 Human ser
31	236	31.3	58	4	AAE13084	Aae13084 Human ser
32	236	31.3	58	7	ADP41997	Adp41997 Human CAB
33	236	31.3	58	8	ADL16838	Adl16838 Human Kun
34	236	31.3	58	8	ADR89980	Adr89980 Human CAB
35	219	29.1	51	2	AAW75257	Aaw75257 Fragment
36	219	29.1	51	5	AAE27025	Aae27025 Human gen
37	219	29.1	51	5	AAE27163	Aae27163 Human gen
38	219	29.1	51	8	ADG89845	Adg89845 Human sec
39	187	24.8	560	2	AAE62523	Aae62523 Hookworm
40	187	24.8	2858	4	ABB71150	Abb71150 Drosophil
41	187	24.8	3060	4	ABB58064	Abb58064 Drosophil
42	182.5	24.2	571	7	AAE39498	Aae39498 Cloned mo
43	182.5	24.2	571	7	AAE39459	Aae39459 Mouse GDF
44	182.5	24.2	571	7	ADP3670	Adp3670 Mouse GDF
45	180	23.9	33	7	ADA19806	Ada19806 Engineere
46	180	23.9	33	7	ADA19809	Ada19809 Engineere
47	177	23.5	58	2	AAE99146	Aae99146 Aprotinin
48	175	23.2	43	4	AAE13096	Aae13096 Human ser
49	175	23.2	54	4	AAE13092	Aae13092 Trypsin i
50	173.5	23.0	503	5	ABJ01150	Abj01150 Ovary cel

ALIGNMENTS

RESULT 1
ADA19800
ID ADA19800 standard; protein; 131 AA.

AC ADA19800;

DT 20-NOV-2003 (first entry)

DE Engineered human DJ11 protein SEQ ID NO:1.

KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
antibacterial; immunosuppressive; antirheumatic; antiarthritis;
KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

OS Synthetic.

OS Homo sapiens.

Key	Location/Qualifiers
Misc-difference	1..131
Peptide	/note= "eppin-like precursor"
Protein	/label= signal
Disulfide-bond	26..131
Disulfide-bond	/note= "mature DJ11 protein"
Disulfide-bond	33..61
Disulfide-bond	/note = predicted disulfide bond
Disulfide-bond	40..65
Disulfide-bond	/note = predicted disulfide bond
Disulfide-bond	48..60
Disulfide-bond	/note = predicted disulfide bond
Disulfide-bond	54..69
Disulfide-bond	/note = predicted disulfide bond
Domain	77..127
Disulfide-bond	/note = Kunitz domain predicted by pfscan
Disulfide-bond	77..127
Disulfide-bond	/note = predicted disulfide bond
Disulfide-bond	85..110

FT Disulfide-bond 102. .123 /note = predicted disulfide bond
 FT Disulfide-bond 102. .123 /note = predicted disulfide bond

PN WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

PI Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

DR N-PSDB; ADA19810.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Claim 5; Page 69-70; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

XX Sequence 131 AA;

SQ Query Match 100.0%; Score 753; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Db 1 MGLSGLLPILVPFILLGDIQEPGHAGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Qy 61 CPFSGKKCLDFRDXICSMPOEAGPCLASIPHWYNNKTKICSEFFIYGGCGGNNNFQTE 120

Db 61 CPFSGKKCLDFRDXICSMPOEAGPCLASIPHWYNNKTKICSEFFIYGGCGGNNNFQTE 120

Qy 121 AICLVTCCKYH 131

Db 121 AICLVTCCKYH 131

RESULT 2

ADA19811

ID ADA19811 standard; protein; 131 AA.

XX

AC ADA19811;
 XX 20-NOV-2003 (first entry)
 XX Engineered human DJ11 protein SEQ ID NO:12.
 DE DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 OS WO2003070770-A2.
 FN 28-AUG-2003.
 PD 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 PR (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX Disclosure; Page 84; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

SQ Sequence 131 AA;

Query Match 100.0%; Score 753; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Db 1 MGLSGLLPILVPFILLGDIQEPGHAGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

XX PI Bougueleret L, Bairoch A, Niknejad A;
XX DR WPI; 2003-663849/62.
XX PF New engineered human Kunitz-type protease inhibitor for diagnosing,
XX PT preventing or treating conditions associated with excessive proteinase
XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX PT hemorrhage.
XX PS Claim 5; Page 71; 87pp; English.
XX CC The present invention describes an isolated, purified or recombinant DJ11
XX CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX CC biologically active portion. The polypeptide comprises at least 98 %
XX CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX CC anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
XX CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX CC activities, and can be used as a protease inhibitor and in gene therapy.
XX CC Composition and methods from the present invention can be used in
XX CC diagnosing, preventing or treating conditions associated with excessive
XX CC proteinase activity, such as acute pancreatitis, pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, myocardial
XX CC infarction, shock (including septic shock), hyperfibrinolytic
XX CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX CC be used in preserving platelet function, organ preservation or in wound
XX CC healing. The polynucleotide sequence encoding DJ11 may be used as
XX CC hybridisation probes, in chromosome and gene mapping, in the generation
XX CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX CC The present sequence represents the mature form of an engineered human
XX CC DJ11 protein from the present invention.
XX SQ Sequence 106 AA;
Query Match 83.0%; Score 625; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.2e-46; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 0;
Qy 26 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFCGKCKLDFRDKICSMFQAGP 85
Db 1 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFCGKCKLDFRDKICSMFQAGP 60
Qy 86 CLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTCCKYH 131
Db 61 CLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTCCKYH 106
RESULT 5
ADA19808
ID ADA19808 standard; protein; 98 AA.
AC ADA19808;
XX XX
XX DT 20-NOV-2003 (first entry)
XX DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:9.
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX KW antiallergic; thrombolytic; anticoagulant; cardiatic; vasotropic;
XX KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
XX KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX KW deep vein thrombosis; myocardial infarction; shock; septic shock;
XX KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX KW chronic inflammatory bowel disease; psoriasis.
OS Synthetic.
OS Homo sapiens.

XX WO2003070770-A2.
XX PD 28-AUG-2003.
XX PF 18-FEB-2003; 2003WO-EP001629.
XX PR 21-FEB-2002; 2002US-0358683P.
XX PA (GENE-) GENEPROT INC.
XX PI Bougueleret L, Bairoch A, Niknejad A;
XX PT WPI; 2003-663849/62.
XX PT New engineered human Kunitz-type protease inhibitor for diagnosing,
XX PT preventing or treating conditions associated with excessive proteinase
XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX PT hemorrhage.
XX PS Disclosure; Page 82; 87pp; English.
XX CC The present invention describes an isolated, purified or recombinant DJ11
XX CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX CC biologically active portion. The polypeptide comprises at least 98 %
XX CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX CC anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
XX CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX CC activities, and can be used as a protease inhibitor and in gene therapy.
XX CC Composition and methods from the present invention can be used in
XX CC diagnosing, preventing or treating conditions associated with excessive
XX CC proteinase activity, such as acute pancreatitis, pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, myocardial
XX CC infarction, shock (including septic shock), hyperfibrinolytic
XX CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX CC be used in preserving platelet function, organ preservation or in wound
XX CC healing. The polynucleotide sequence encoding DJ11 may be used as
XX CC hybridisation probes, in chromosome and gene mapping, in the generation
XX CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX CC The present sequence represents a partial engineered human DJ11 protein
XX CC amino acid sequence from the present invention.
XX SQ Sequence 98 AA;
Query Match 73.2%; Score 551; DB 7; Length 98;
Best Local Similarity 99.0%; Pred. No. 1.6e-39;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKCPKIKVEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKCPKIKVEVEEIDQCTKPRDCPENMKC 60
Qy 61 CPFCGKCKLDFRDKICSMFQAGPCLASIPHWYNNK 98
Db 61 CPFCGKCKLDFRDKICSMFQAGPCLASIPHWYNNK 98
RESULT 6
ADA19815
ID ADA19815 standard; protein; 136 AA.
XX AC ADA19815;
XX XX
XX DT 20-NOV-2003 (first entry)
XX DE Mouse DJ11 protein SEQ ID NO:16.
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX KW antiallergic; thrombolytic; anticoagulant; cardiatic; vasotropic;

antibacterial; immunosuppressive; antirheumatic; antiarthritic; nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy; acute pancreatitis; pulmonary injury; allergy-induced protease release; deep vein thrombosis; myocardial infarction; shock; septic shock; hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema; idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis; chronic inflammatory bowel disease; psoriasis.

Mus musculus.

WO2003070770-A2.

28-AUG-2003.

18-FEB-2003; 2003WO-EP001629.

21-FEB-2002; 2002US-0358683P.

(GENE-) GENEPROT INC.

Bougueleret L, Bairoch A, Niknejad A;

WPI; 2003-663849/62.

New engineered human Kunitz-type protease inhibitor for diagnosing, preventing or treating conditions associated with excessive proteinase activity, e.g. inflammation, pulmonary injuries, myocardial infarction or hemorrhage.

Disclosure: Fig 1; 87pp; English.

The present invention describes an isolated, purified or recombinant Djl1 polypeptide comprising a Kunitz-type protease inhibitor domain or its biologically active portion. The polypeptide comprises at least 98 % identity to residues 77-127 of a 131 amino acid sequence (S1, see ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see ADA19801). Djl1 has antiinflammatory, anti-allergic, thrombolytic, anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive, antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery activities, and can be used as a protease inhibitor and in gene therapy. Composition and methods from the present invention can be used in diagnosing, preventing or treating conditions associated with excessive proteinase activity, such as acute pancreatitis, pulmonary injury, allergy-induced protease release, deep vein thrombosis, myocardial infarction, shock (including septic shock), hyperfibrinolytic haemorrhage, and especially, inflammatory disorders (e.g. emphysema, idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis, chronic inflammatory bowel disease or psoriasis). The Djl1 proteins may be used in preserving platelet function, organ preservation or in wound healing. The polynucleotide sequence encoding Djl1 may be used as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and as targets for pharmaceutical intervention. The present sequence represents a mouse Djl1 protein given in comparison with Djl1 proteins in the exemplification of the present invention.

Sequence 136 AA;

Query Match 65.3%; Score 492; DB 7; Length 136;
Best Local Similarity 62.8%; Pred. No. 2,3e-34;
Matches 81; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGLSGLPLTVFLLGDTQPGHARGILGKPCIKVCEVEEIDQCTKPCDENMKC 60
DB 1 MRLMGLLPLFVFPILLWSIQBELAGFFIRTCPRVRKCEVERNECTRHQCCKKRC 60

QY 61 CFFSCGKKCLDFRKCISMPQAGPCLASIPHWYNNKTKICSEFYGCQCGNNNFPE 120
DB 61 CLFSCGKKCMLDRQDVCSLPQDPGCLAYLPRWYNNQETDLCTEFYGCQCGNNNFPE 120

QY 121 AICLVTCCK 129
DB 121 GICTVVCCK 129

RESULT 7
AAW75219
ID AAW75219 standard; protein; 133 AA.
XX AAW75219;
AC AAW75219;
XX
DT 29-JAN-1999 (first entry)
XX
DE Human secreted protein encoded by gene 24 clone HTEBY11.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9840483-A2.
XX
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US004858.
XX
PR 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068366P.
XX
(HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 1998-520811/44.
XX N-PSDB; AAV34309.
XX
XX Isolated human polynucleotide(s) encoding secretory peptide(s) - used to
XX develop products for the diagnosis and treatment of e.g. inflammation,
XX cancers, CNS disorders or immune system disorders.
XX
XX Claim 1; Page 167-168; 201pp; English.
XX
XX This sequence represents a secreted human protein encoded by the gene
XX clone detailed in the descriptor line. The gene can be used to generate
XX fusion proteins by linking to the gene to a human immunoglobulin Fc
XX portion (e.g. AAV34277) for increasing the stability of the fused protein
XX as compared to the human protein only. The invention relates to 28 novel
XX genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino
XX acid sequences AAW75196-W75235) which are useful for preventing, treating
XX or ameliorating medical conditions e.g. by protein or gene therapy. Also,
XX new polypeptides in a sample or by determining the amount of the
XX pathological conditions can be diagnosed by determining the presence of mutations
XX in the new polynucleotides. Specific uses are described for each of the
XX 28 polynucleotides, based on which tissues they are most highly expressed
XX in (see AAV34286 for described uses)
XX
SQ Sequence 133 AA;

Query Match 62.0%; Score 467; DB 2; Length 133;
Best Local Similarity 60.9%; Pred. No. 3,1e-32;
Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

tissue regeneration; immunosuppressive; antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; vulnary.

Best Local Similarity 60.9%; Pred. No. 3.le-32; Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0; Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60 Db 1 MGSSGLLSLLVLFVLLANVQPGGLTDLWLFPRCPKIRECECFQERDVCTKDRQCQDNKCC 60 Qy 61 CPTSCGKKCLDFRDKDICSMPOEAGPCLASTPHWYNYKTKICSEFIYGGCGGNNNFQTE 120 Db 61 CVFSCGKKCLDLKQDVCEMPKETGTCPLAYFLHMYDKDKNTCSMFVYGGCGGNNNFQSK 120 Qy 121 AICLVTCCK 128 Db 121 ANCLNTCK 128

RESULT 10

ABU64993 ID ABU64993 standard; protein; 133 AA.

XX AC ABU64993;

XX AC 15-MAY-2003 (first entry)

XX DE Human secreted protein gene 24, protein #1.

XX KW Secreted protein; immunodeficiency; multiple sclerosis; severe combined immunodeficiency; autoimmune disorder; cancer; rheumatoid arthritis; diabetes mellitus; haematopoietic disorder; inflammatory condition; septic shock; inflammatory bowel disease; Crohn's disease; respiratory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; ischaemic brain injury; neurodegenerative disorder; atherosclerosis; Alzheimer's disease; cardiovascular disorder; Parkinson's disease; blood-related disorder; thrombosis; acute glomerulonephritis; Addison's disease; hyperproliferative disorder; liver disease; reproductive system disorder; endocrine disorder; infectious disease; pancreatic disorder; vaccine; endometriosis; angiogenesis; lymphatic disorder; hair loss; body weight; body height; hair colour; human.

XX OS Homo sapiens.

XX PN US2002172994-A1.

XX PD 21-NOV-2002.

XX PF 11-MAY-2001; 2001US-00852797.

XX PR 14-MAR-1997; 97US-0040710P.

XX PR 14-MAR-1997; 97US-0040762P.

XX PR 30-MAY-1997; 97US-0048100P.

XX PR 30-MAY-1997; 97US-0048189P.

XX PR 30-MAY-1997; 97US-0048357P.

XX PR 30-MAY-1997; 97US-0050934P.

XX PR 06-JUN-1997; 97US-0048970P.

XX PR 05-SEP-1997; 97US-0057765P.

XX PR 19-DEC-1997; 97US-0068368P.

XX PR 12-MAR-1998; 98WO-US004858.

XX PR 11-SEP-1998; 98US-00152060.

XX PR 02-FEB-2001; 2001US-0265583P.

XX PA (RUBE/) RUBEN S M.

XX PA (ROSE/) ROSEN C A.

XX PA (LIYY/) LI Y.

Key Location/Qualifiers
Peptide 1..21 /label= Signal_peptide
Protein 22..133 /note= "Mature human secreted protein"

US2002076756-A1.

20-JUN-2002.

11-MAY-2001; 2001US-00853161.

02-FEB-2001; 2001US-0265583P.

(RUBE/) RUBEN S M.

(ROSE/) ROSEN C A.

(LIYY/) LI Y.

(ZENG/) ZENG Z.

(KYAW/) KYAW H.

(FISC/) FISCHER C L.

(LIHH/) LI H.

(SOPP/) SOPPET D R.

(GENT/) GENTZ R L.

(WEIY/) WEI Y.

(MOOR/) MOORE P A.

(YOUN/) YOUNG P E.

(GREEN/) GREENE J M.

(FERR/) FERRIE A M.

Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

Ferrie AM;

WPI; 2002-574454/61.

N-PSDB; AAD44877.

New nucleic acid molecules encoding 28 human secreted proteins, useful for diagnosing, preventing, treating or ameliorating medical conditions and as food additives or preservatives.

Claim 11; Page 185-186; 209pp; English.

Query Match 62.0%; Score 467; DB 5; Length 133;

Sequence 133 AA;

Query Match 62.0%; Score 467; DB 8; Length 179;
 Best Local Similarity 60.9%; Pred. No. 4.1e-32;
 Matches 78; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVFPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQTKPRDCPENMKC 60
 Db 1 MGSGLLSLVLLVFNANVQFGLTDLWLFPRCPKIRECECFQERDVCTKDRQCQDNKKC 60

Qy 61 CPFGCGKKCLDFRKIDCSMPQEAAGPCLASIPHWYNNKTKICSEFIYGGCCGNNNNFOTE 120
 Db 61 CVFSGCKKCLDLKQDVCEMPKETGTGCLAYFLHWYDKDKNTCSMFYGGCCGNNNNFQSK 120

Qy 121 AICLVTK 128
 Db 121 ANCLNTCK 128

RESULT 15
 ABP69809
 ID ABP69809 standard; protein; 86 AA.
 XX AC ABP69809;
 XX DT 20-JAN-2003 (first entry)
 XX DE Human polypeptide SEQ ID NO 1856.
 XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; neurotropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
 KW antiarthritic.
 XX OS Homo sapiens.
 XX FN WO200270539-A2.
 XX PD 12-SEP-2002.
 XX PF 05-MAR-2002; 2002WO-US005095.
 XX PR 05-MAR-2001; 2001US-00799451.
 XX PA (HYSE-) HYSEQ INC.
 XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX WPI; 2002-759812/82.
 DR N-PSDB; AB212026.
 XX New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.
 XX Claim 9; SEQ ID NO 1856; 1012pp + Sequence Listing; English.
 XX The invention relates to an isolated polynucleotide (1) comprising a
 CC nucleotide sequence selected from any of 948 sequences (AB21119-
 CC AB212066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,

CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 86 AA;
 SQ

Query Match 53.7%; Score 404; DB 5; Length 86;
 Best Local Similarity 98.6%; Pred. No. 4.9e-27;
 Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVFPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQTKPRDCPENMKC 60
 Db 1 MGLSGLLPILVFPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQTKPRDCPENMKC 60

Qy 61 CPFGCGKKCLDFRK 74
 Db 61 CPFGCGKKCLDFRK 74

RESULT 16
 ABJ26667
 ID ABJ26667 standard; protein; 86 AA.
 XX AC ABJ26667;
 XX DT 01-MAY-2003 (first entry)
 XX DE Human protein modification + maintenance molecule protein SEQ ID NO 21.
 KW Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
 KW cerebroprotective; antiparkinsonian; neurotropic; antiinflammatory;
 KW anticulcer; hepatotropic; gynaecological; antibacterial; virucide;
 KW protozoacide; antiparasitic; cell proliferative disease; PMOD;
 KW protein modification and maintenance molecule; immunogenic fragment;
 KW cancer; autoimmune; inflammatory disease; neurological disorder;
 KW gastrointestinal; developmental; vesicle trafficking disorder; infection;
 KW protein-protein interaction; drug-target interaction;
 KW gene expression profile; human.
 XX OS Homo sapiens.
 XX FN WO2003000844-A2.
 XX PD 03-JAN-2003.
 XX PF 18-JUN-2002; 2002WO-US019360.
 XX PR 22-JUN-2001; 2001US-0300508P.
 PR 06-JUL-2001; 2001US-0303445P.
 PR 13-JUL-2001; 2001US-0305405P.
 PR 09-AUG-2001; 2001US-0311442P.
 PR 24-AUG-2001; 2001US-0314821P.
 PR 29-AUG-2001; 2001US-0315992P.
 PR 03-MAY-2002; 2002US-0378205P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Gandhi AR, Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggan BM;
 PI Warren BA, Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Yue H;
 PI Forsythe TJ, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang J;
 PI Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG;
 PI Walla NK, Mason PM, Gururajan R, Lee S, Becha SD, Lee SY, Tran UK;
 PI Elliott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zebbarjadian Y;
 XX WPI; 2003-184039/18.
 DR N-PSDB; AB23220.
 XX New isolated human PMOD polypeptide and polynucleotide, useful for
 PT diagnosing, treating and preventing diseases or conditions associated
 PT with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis and

PT infections.

PS Claim 76; Page 196; 225pp; English.

XX The invention relates to an isolated polypeptide comprising: any of 28

XX sequences of 48-1256 amino acids; a natural amino acid sequence at least

XX 90% identical to the 28 amino acid sequences, 94% identical to a sequence

CC of 703 or 267 amino acids, 96% identical to a sequence of 414 amino

CC acids, or 97% identical to a sequence of 242 amino acids, all given in

CC the specification; or a biologically active or immunogenic fragment of

CC the isolated polypeptide. The polypeptides and polynucleotides are useful

CC in diagnosing, treating and preventing diseases or conditions associated

CC with the decreased expression of protein modification and maintenance

CC molecules (PMOD), such as cell proliferative diseases (e.g. cancer,

CC atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS,

CC allergies), neurological disorders (e.g. stroke, Parkinson's disease,

CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g.

CC endometriosis), developmental, vesicle trafficking disorders, and

CC infections (e.g. bacterial, viral, parasitic, protozoal). These are also

CC useful in assessing the effects of exogenous compounds on the expression

CC of nucleic acid and amino acid sequences of PMOD. The PMOD or its

CC fragments are useful in screening compounds for effectiveness as agonist

CC or antagonist of the polypeptides, or in altering the expression of the

CC target polynucleotide and compounds that specifically bind to or modulate

CC the activity of the polypeptide. The microarray is useful in monitoring

CC or measuring protein-protein interactions, drug-target interactions, and

CC gene expression profiles. This sequence represents a human PMOD protein

CC of the invention

XX

SQ Sequence 86 AA;

Query Match 53.7%; Score 404; DB 6; Length 86;

Best Local Similarity 98.6%; Pred. No. 4.9e-27;

Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Qy 61 CPFSGKCKLDFRK 74

Db 61 CPFSRGRKCKLDFRK 74

RESULT 17

ABB12236

ID ABB12236 standard; peptide; 101 AA.

AC ABB12236;

XX

DT 11-JAN-2002 (first entry)

XX

DE Human eppin-1 homologue, SEQ ID NO:2606.

XX

KW Human; cytokine; cell proliferation; cell differentiation; growth factor;

KW haematopoiesis regulation; tissue growth; immunomodulator; activin;

KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;

KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;

KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

KW chronic inflammatory condition; proliferative retinopathy;

KW atherosclerosis; coronary heart disease; arterial ischaemia;

KW bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;

KW cell culture; drug screening; gene therapy; antiinflammatory;

KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;

KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;

KW antifungal; vulnuary; antiulcer.

XX

OS Homo sapiens.

XX

FN WO200157188-A2.

XX

PD 09-AUG-2001.

XX

05-FEB-2001; 2001WO-US003800.

XX

03-FEB-2000; 2000US-00496914.

PR

27-APR-2000; 2000US-00560875.

XX

(HYSE-) HYSEQ INC.

PA

XX

Tang YT, Liu C, Drmanac RT;

PI

WPI; 2001-457740/49.

XX

N-PSDB; ABA09480.

DR

XX

Human proteins and DNA encoding sequences useful for preventing, treating

PT or ameliorating a medical condition in a mammalian subject e.g. arthritis

PT and cancer.

XX

Claim 20; Page 318; 1963pp; English.

XX

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and

CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The

CC invention also relates to vectors and recombinant host cells comprising a

CC nucleotide of the invention, methods of producing the novel polypeptides,

CC antibodies against the polypeptides, methods of detecting the nucleotides

CC or polypeptides in a sample, and methods of identifying compounds which

CC bind to polypeptides of the invention. Although novel, many of the

CC polypeptides of the invention have homology to known proteins, thereby

CC giving an insight into their probable biological activities, and hence

CC potential therapeutic applications. The polypeptides of the invention may

CC have various activities, including cytokine, cell proliferation or cell

CC differentiation activities; stem cell growth factor activity;

CC haematopoiesis regulatory activity; tissue growth activity;

CC immunomodulatory activity; activin- or inhibin-related activities;

CC chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC the invention are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug

CC screening techniques. The present sequence represents a novel human

CC polypeptide of the invention

XX

SQ Sequence 101 AA;

Query Match 53.7%; Score 404; DB 4; Length 101;

Best Local Similarity 98.6%; Pred. No. 5.7e-27;

Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Db 16 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 75

Qy 61 CPFSGKCKLDFRK 74

Db 76 CPFSRGRKCKLDFRK 89

RESULT 18

AAE27094
ID AAE27094 standard; protein; 117 AA.
XX
AC AAE27094;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human secreted protein #1.
XX
KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotrophic; vulnery; cystostatic; nontropic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.
XX
OS Homo sapiens.
XX
QY US200207287-A1.
XX
PD 20-JUN-2002.
XX
PF 11-MAY-2001; 2001US-00852659.
XX
PR 11-SEP-1998; 98US-00152060.
XX
PA (RUBE//) RUBEN S M.
PA (ROSE//) ROSEN C A.
PA (LIY//) LI Y.
PA (ZENG//) ZENG Z.
PA (KYAW//) KYAW H.
PA (FISC//) FISCHER C L.
PA (LITH//) LI H.
PA (SOPP//) SOPPET D R.
PA (GENT//) GENTZ R L.
PA (WEI//) WEI Y.
PA (MOOR//) MOORE P A.
PA (YOUN//) YOUNG P E.
PA (GREE//) GREENE J M.
PA (FERR//) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
DR WPI; 2002-598780/64.
XX
KW Novel human secreted polypeptides and polynucleotides for diagnosing,
KW preventing, treating immune, hyperproliferative, cardiovascular,
KW neurological, reproductive disorders and identifying modulators of
KW therapeutic use.
XX
PS Disclosure; Page 16; 209pp; English.
XX
CC AAD4636-AA44676 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
CC AAE27000-AAE27025 represent human secreted protein fragments or their
CC variants. The secreted proteins and genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Specific uses are described for each of the 28 genes, based on
CC the tissues in which they are most highly expressed and include
CC developing products for the diagnosis or treatment of immunodeficiencies,
CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions

disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related dementia, and prion disease), cardiovascular disorders (e.g. atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary bypass complications), inflammation (e.g. hepatitis, gout, trauma, pancreatitis, sarcoidosis, dermatitis, allergic transplant rejection), blood-related disorders (thrombosis, arterial thrombosis), hyperproliferative disorders, renal disorders (e.g. acute glomerulonephritis), endocrine disorders (e.g. Addison's disease, hyperthyroidism, hyperpituitarism), liver diseases and disorders, reproductive system disorders (e.g. endometriosis), infectious diseases, and pancreatic disorders. Many other diseases and disorders are listed in the specification. They also useful as a vaccine adjuvant. Further they are useful to enhance or inhibit complement mediated cell lysis, for stimulating wound and tissue repair, angiogenesis, and the repair of vascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreted protein of the invention

XX Sequence 117 AA;

Query Match 53.3%; Score 401.5; DB 6; Length 117;

Best Local Similarity 66.0%; Pred. No. 1.1e-26;

Matches 66; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

QY 29 LKPCPKIKVECEVEIEIOCTKPRCPENMKCCPSGCKKCLDFKIDCSMPQAGPCLA 88

DB 14 LGR-CPKIRECEFOEDVCTKROQDNKKCCVFCGCKKCLDLKQDCEMPKGTGPCLA 72

QY 89 SIPHWYNNKTKICSEFTYGGCGQNNNNFQTEAICLVTK 128

DB 73 YPLHWYDKKONTCSMFYGGCGQNNNNFQSKANCLNTCK 112

RESULT 21

ADG89847

ID ADG89847 standard; protein; 117 AA.

AC ADG89847;

XX 11-MAR-2004 (first entry)

DE Human secreted protein gene 24 protein #5.

Secreted protein; gene therapy; neural disorder; immune system disorders; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; cancer; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia; Grave's disease; diabetes; hepatitis; aschma; allergy; nephritis; Parkinson's disease; Alzheimer's disease; atherosclerosis; myocardial infarction; AIDS; infection; human.

XX Homo sapiens.

OS US2003225009-A1.

PN 04-DEC-2003.

XX 30-JAN-2002; 2002US-00058993.

XX 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.

PR 30-MAY-1997; 97US-0050934P.

PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.

PR 19-DEC-1997; 97US-0068368P.

PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
PR 11-MAY-2001; 2001US-00852659.
PR 11-MAY-2001; 2001US-00852797.
PR 11-MAY-2001; 2001US-00853161.

XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.

XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX WPI; 2004-042167/04.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

XX Disclosure; SEQ ID NO 120; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from

CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.

XX Sequence 117 AA;

Query Match 53.3%; Score 401.5; DB 8; Length 117;

Best Local Similarity 66.0%; Pred. No. 1.1e-26;

Matches 66; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

Qy 29 LGKPCPKIKVCEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKCISMPQAGPCLA 88

Db 14 LGR-CPKIRECEFEQERDVCTKDRQCQDNKKCCVFCGKCKLDLQDVCEMPKETGPCLA 72

Qy 89 SIPHWYNTKTKICSEFIYGGCGQNNNNFQTEATCLVTCK 128

Db 73 YFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTCK 112

RESULT 22

ID AAE27095 standard; protein; 102 AA.

XX AAE27095;

AC AAE27095;

XX 13-DEC-2002 (first entry)

DT Human secreted protein #2.

DE Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;

KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotropic; vulnary; cytostatic; nootropic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.

XX Homo sapiens.

XX OS

XX US2002077287-A1.

XX PN

XX 20-JUN-2002.

XX PD

XX 11-MAY-2001; 2001US-00852659.

XX PF

XX 11-SEP-1998; 98US-00152060.

XX PR

XX (RUBE/) RUBEN S M.

XX (ROSE/) ROSEN C A.

XX (LIY/) LI Y.

XX (ZENG/) ZENG Z.

XX (KYAW/) KYAW H.

XX (FISC/) FISCHER C L.

XX (LIH/) LI H.

XX (SOPP/) SOPPET D R.

XX (GENT/) GENTZ R L.

XX (WEI/) WEI Y.

XX (MOOR/) MOORE P A.

XX (YOUN/) YOUNG P E.

XX (GREE/) GREENE J M.

XX (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

XX Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

XX Ferrie AM;

XX WPI; 2002-598780/64.

XX DR

XX XX

PT Novel human secreted polypeptides and polynucleotides for diagnosing,
PT preventing, treating immune, hyperproliferative, cardiovascular,
PT neurological, reproductive disorders and identifying modulators of
PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

PS AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
XX protein genes, and AAE26959-AAE26999 represent the proteins they encode.
CC AAE27000-AAE27025 represent human secreted protein fragments or their
CC variants. The secreted proteins and genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Specific uses are described for each of the 28 genes, based on
CC the tissues in which they are most highly expressed and include
CC developing products for the diagnosis or treatment of immunodeficiencies,
CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
CC sarcoidosis and allogenic transplant rejection, blood-related disorder
CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
CC lung cancer, allergic disorders, pneumonitis, renal disorders, endocrine
CC glomerulonephritis, neurological diseases, liver disorders, endocrine
CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
CC infectious diseases and reproductive system disorders e.g. endometriosis.

CC The present sequence represents a human secreted protein of the invention

XX SQ Sequence 102 AA;

Query Match 53.1%; Score 400; DB 5; Length 102;

Best Local Similarity 66.7%; Pred. No. 1.3e-26;

Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 33 CPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKCISMPQAGPCLASIPH 92

Db 2 CPKIRECEFEQERDVCTKDRQCQDNKKCCVFCGKCKLDLQDVCEMPKETGPCLAYFLH 61

Qy 93 WYNNKTKICSEFIYGGCGQNNNNFQTEATCLVTCK 128

Db 62 WYDCKDNTCSMFYGGCGQNNNNFQSKANCLNTCK 97

RESULT 23

AAE28009

ID AAE28009 standard; protein; 102 AA.

XX AAE28009;

XX 13-DEC-2002 (first entry)

DT Human gene 24 encoded secreted protein fragment #2.

DE Human; secreted protein; autoimmune disease; hyperproliferative disorder;

XX rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;

XX cerebral ischaemia; cardiovascular disorder; nervous system disorder;

XX cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;

XX infection; corneal infection; skin aging; food additive; preservative;

XX tissue regeneration; immunosuppressive; antiproliferative; cytostatic;

XX cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;

XX antibacterial; virucide; fungicide; ophthalmological; gene therapy;

XX vulnary.

XX XX

XX The invention relates to an isolated polypeptide comprising an amino acid
CC sequence at least 95% identical to sequence of 28 human secreted
CC proteins, their fragment, polypeptide domain, epitope, secreted form,
CC variant, allelic variant, or species homologue, or the encoded sequence
CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
CC acids, recombinant vectors, host cells, antibodies, and genes. The
CC proteins and nucleic acids are useful for diagnosing, preventing,
CC treating, prognosing or ameliorating a medical condition e.g.
CC immunodeficiencies (e.g. X-linked agammaglobulinemia, B cell
CC immunodeficiencies, severe combined immunodeficiencies), autoimmune
CC disorders (e.g. systemic erythematosis, rheumatoid arthritis, multiple
CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,
CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
CC injury and/or stroke, traumatic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
CC dementia, and prion disease), cardiovascular disorders (e.g.
CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
CC pancreatitis, sarcoidosis, dermatitis, allogenic transplant rejection),
CC blood-related disorders (thrombosis, arterial thrombosis),
CC hyperproliferative disorders, renal disorders (e.g. acute
CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
CC hyperthyroidism, hypoparathyroidism), liver diseases and disorders,
CC reproductive system disorders (e.g. endometriosis), infectious diseases,
CC and pancreatic disorders. Many other diseases and disorders are listed in
CC the specification. They also useful as a vaccine adjuvant. Further they
CC are useful to enhance or inhibit complement mediated cell lysis, for
CC stimulating wound and tissue repair, angiogenesis, and the repair of
CC vascular or lymphatic diseases or disorders. They are also useful to
CC prevent hair loss, to modulate mammalian characteristics such as body
CC height, weight, hair colour, and to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors or other nutritional components. The proteins are
CC also useful for identifying binding partners. The present sequence
CC represents a secreted protein of the invention

Sequence 102 AA;

Query Match 53.1%; Score 400; DB 6; Length 102;
Best Local Similarity 66.7%; Pred. NO. 1.3e-26;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Oy 33 CPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKKCLDFKDCMFPQEAQPCLASIPH 92
Db 2 CPKIRECEFERDVCTKQRCQDNKKCCVFCGKKCLDLKQDVCEMPKETGPCLAYFLH 61
Oy 93 WYNNKTKICSEFYGGCGGNNNFQTEAICLVTK 128
Db 62 WYDKDKNTCSMFVYGGCGGNNNFQSKANCLNTCK 97

RESULT 25
ADG9848
ID ADG89848 standard; protein; 102 AA.

XX AC ADG89848;

XX DT 11-MAR-2004 (first entry)

DE DE Human secreted protein gene 24 protein #6.

XX Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;

KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
XX myocardial infarction; AIDS; infection; human.

XX OS Homo sapiens.

XX FN US2003225009-A1.

XX PD 04-DEC-2003.

XX PF 30-JAN-2002; 2002US-00058993.

XX PR 14-MAR-1997; 97US-0040710P.

XX PR 14-MAR-1997; 97US-0040762P.

XX PR 30-MAY-1997; 97US-0048100P.

XX PR 30-MAY-1997; 97US-0048189P.

XX PR 30-MAY-1997; 97US-0048357P.

XX PR 30-MAY-1997; 97US-0050934P.

XX PR 06-JUN-1997; 97US-0048970P.

XX PR 05-SEP-1997; 97US-0057765P.

XX PR 19-DEC-1997; 97US-0068388P.

XX PR 12-MAR-1998; 98WO-US0004858.

XX PR 11-SEP-1998; 98US-00152060.

XX PR 02-FEB-2001; 2001US-0265583P.

XX PR 11-MAY-2001; 2001US-00852659.

XX PR 11-MAY-2001; 2001US-00852797.

XX PR 11-MAY-2001; 2001US-00853161.

XX (ROSE/) ROSEN C A.

XX (RUBE/) RUBEN S M.

XX (LIYY/) LI Y.

XX (ZENG/) ZENG Z.

XX (KYAW/) KYAW H.

XX (FISC/) FISCHER C L.

XX (LIHH/) LI H.

XX (SOPP/) SOPPET D R.

XX (GENT/) GENTZ R L.

XX (WEIY/) WEI Y.

XX (MOOR/) MOORE P A.

XX (YOUN/) YOUNG P E.

XX (GREE/) GREENE J M.

XX (FERR/) FERRIE A M.

XX (HAST/) HASTINGS G A.

XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

XX Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

XX Ferrie AM, Hastings GA;

XX WPI; 2004-042167/04.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
XX treating diseases associated with aberrant expression or activity of the
XX polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX Disclosure; SEQ ID NO 121; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a
XX secreted protein that is at least 95% identical to a polynucleotide
XX fragment of any of the nucleotide sequences listed in table 1A of the
XX specification, which is hybridisable to the nucleotide sequences, a
XX polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
XX or epitope of any of the amino acid sequences) listed in table 1A of the
XX specification, a polynucleotide which is an (allelic) variant of the
XX nucleotide sequences listed in the specification, a polynucleotide which
XX encodes a species homologue of the above amino acid sequences, a
XX polynucleotide capable of hybridising under stringent conditions to any
XX of the above polynucleotides, where the polynucleotide does not hybridise
XX under stringent conditions to a nucleic acid molecule having a nucleotide
XX sequence of only A or T residues. Also included are a recombinant vector
XX comprising the above nucleic acid molecule, making a recombinant host
XX cell comprising the above nucleic acid molecule, an isolated polypeptide
XX comprising a sequence that is at least 95% identical to the polypeptide
XX (or its fragment, domain, epitope, secreted form, (allelic) variant or
XX homologue) encoded by the above nucleic acid molecule, an isolated

PF 20-JUL-1999; 99US-00358569.
 XX
 PR 20-JUL-1999; 99US-00358569.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Delaria K, Rocznik S, Davies C;
 XX
 DR WPI; 2001-662224/76.
 XX
 XX New isolated protein for inhibiting human serine protease activity in the
 PT treatment of e.g. emphysema and adult respiratory distress syndrome.
 XX
 PS Disclosure; Col 6; 16pp; English.
 XX
 CC The invention relates to human BTL.009 protein, a serine proteinase
 CC inhibitor of the Kunitz family that exhibits greater potency towards
 CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
 CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
 CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
 CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
 CC and diseases involving lung and vascular injury. BTL.009 is also useful
 CC for preventing neutrophil and monocyte activation and formation of active
 CC oxygen species during the oxidative burst of stimulated granulocytes.
 CC BTL.009 is useful for reducing platelet activation and blood coagulation
 CC and for the prophylactic or therapeutic treatment of patients undergoing
 CC angioplasty. The present sequence is human serine proteinase inhibitor
 CC BTL.009 C-terminal peptide containing Kunitz domain which is used in the
 CC exemplification of the invention
 XX
 SQ Sequence 64 AA;
 Query Match 32.1%; Score 242; DB 4; Length 64;
 Best Local Similarity 65.5%; Pred. No. 2.5e-13;
 Matches 38; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 QY 71 DPKDICSMPQAGPCLASIPHWYKTKICSEFYGGCGQNNNNFQTEAICLVTK 128
 DB 1 DLKQDVCMPKETGPGCLAYFLHWYDKDNTCSMFVYGGCGQNNNNFQSKANCLNTCK 58
 RESULT 30
 AAEL13084
 ID AAEL13084 standard; peptide; 58 AA.
 XX
 AC AAEL13084;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Human serine proteinase inhibitor BTL.009 peptide.
 XX
 KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6294648-B1.
 XX
 PD 25-SEP-2001.
 XX
 PF 20-JUL-1999; 99US-00358569.
 XX
 PR 20-JUL-1999; 99US-00358569.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Delaria K, Rocznik S, Davies C;

XX WPI; 2001-662224/76.
 DR
 XX New isolated protein for inhibiting human serine protease activity in the
 XX treatment of e.g. emphysema and adult respiratory distress syndrome.
 PT
 XX Claim 1; Col 15-16; 16pp; English.
 PS
 XX The invention relates to human BTL.009 protein, a serine proteinase
 CC inhibitor of the Kunitz family that exhibits greater potency towards
 CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
 CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
 CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
 CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
 CC and diseases involving lung and vascular injury. BTL.009 is also useful
 CC for preventing neutrophil and monocyte activation and formation of active
 CC oxygen species during the oxidative burst of stimulated granulocytes.
 CC BTL.009 is useful for reducing platelet activation and blood coagulation
 CC and for the prophylactic or therapeutic treatment of patients undergoing
 CC angioplasty. The present sequence is human serine proteinase inhibitor
 CC BTL.009 peptide corresponding to Kunitz domain used in the
 CC exemplification of the invention. Note: The present sequence shown in
 CC column 14 and sequence listing of the specification lacks 3 amino acid
 CC residues at the C-terminal end
 XX
 SQ Sequence 58 AA;
 Query Match 31.3%; Score 236; DB 4; Length 58;
 Best Local Similarity 66.1%; Pred. No. 7.4e-13;
 Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 73 RKDICSMPQAGPCLASIPHWYKTKICSEFYGGCGQNNNNFQTEAICLVTK 128
 DB 1 KQDVCMPKETGPGCLAYFLHWYDKDNTCSMFVYGGCGQNNNNFQSKANCLNTCK 56
 RESULT 31
 AAAB60630
 ID AAAB60630 standard; protein; 58 AA.
 XX
 AC AAAB60630;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Kunitz domain, SEQ ID NO:8, used to identify BTL.010 protein.
 XX
 KW Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;
 KW proteinase-3 inhibitor; Kunitz domain; emphysema;
 KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 KW platelet activation; blood coagulation; neutrophil activation;
 KW monocyte activation; angioplasty; inflammatory disease; lung injury;
 KW vascular injury; nephrotropic; antirheumatic; antiarthritic.
 XX
 OS Unidentified.
 XX
 PN US6180607-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 05-AUG-1999; 99US-00369494.
 XX
 PR 05-AUG-1999; 99US-00369494.
 XX
 PA (DAVI/) DAVIES C.
 PA (CHEN/) CHEN D.
 PA (ROCZ/) ROCZNIK S.
 XX
 PI Davies C, Chen D, Rocznik S;
 XX
 DR WPI; 2001-190860/19.
 XX

CC sequences of the invention are useful for treating diseases, e.g.
CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
CC glomerulonephritis or inflammatory diseases. The BFL010 protein is also
CC useful for preventing neutrophil and monocyte activation and formation of
CC active oxygen species during the oxidative burst of stimulated
CC granulocytes. It is also useful for reducing platelet activation and
CC blood coagulation. BFL010 DNA is useful in gene therapy. The present
CC sequence is human Kunitz domain (KD) peptide.

XX Sequence 58 AA;

Query Match 31.3%; Score 236; DB 8; Length 58;
Best Local Similarity 66.1%; Pred. No. 7.4e-13;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDTCMPQZAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEATCLVTCK 128
Db 1 KQDVCEMPKETGTCFLAYFLHWWYDKDKNTCSMFYGGCGNNNFQSKANCLATCK 56

RESULT 34

ADR89980
ID ADR89980 standard; peptide; 58 AA.

XX ADR89980;

XX AC

XX DT 18-NOV-2004 (first entry)

XX DE Human CAB37 protein kunitz domain peptide.

XX KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;
XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
XX cytotatic; haemostatic; CAB37 protein; human.

XX OS Homo sapiens.

XX PN US2004171794-A1.

XX PD 02-SEP-2004.

XX PF 07-FEB-2003; 2003US-00361997.

XX PR 07-FEB-2003; 2003US-00361997.

XX PA (LADN/) LADNER R C.

XX PI (LEYA/) LEY A C.

XX PI Ladner RC, Ley AC;

XX DR WPI; 2004-625120/60.

XX PT New kunitz domain peptide useful as human neutrophil elastase inhibitor
XX for the treatment of e.g. cystic fibrosis and related disease.

XX PS Disclosure; SEQ ID NO 5; 123pp; English.

XX CC The invention relates to proteins comprising kunitz domain peptide,
XX designated DPI-14 for inhibiting human neutrophil elastase, fused to
XX albumin. The invention is useful for treating cystic fibrosis and related
XX diseases, hereditary angioedema, cancer and related diseases including
XX chronic obstructive pulmonary disease, asthma, bronchitis, acute
XX respiratory syndrome, pneumonia and bleeding. The invention acts as a
XX cytotatic and haemostatic agent. The present sequence is the human CAB37
XX protein (A4) kunitz domain peptide. This sequence is used in the
XX invention.

XX SQ Sequence 58 AA;

Query Match 31.3%; Score 236; DB 8; Length 58;
Best Local Similarity 66.1%; Pred. No. 7.4e-13;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDTCMPQZAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEATCLVTCK 128
Db 1 KQDVCEMPKETGTCFLAYFLHWWYDKDKNTCSMFYGGCGNNNFQSKANCLATCK 56

RESULT 35

AAW75257

ID AAW75257 standard; protein; 51 AA.

XX AC AAW75257;

XX DT 29-JAN-1999 (first entry)

XX DE Fragment of human secreted protein encoded by gene 24.

XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX OS Homo sapiens.

XX PN WO9840483-A2.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US004858.

XX PR 14-MAR-1997; 97US-0040710P.

XX PR 14-MAR-1997; 97US-0040762P.

XX PR 30-MAY-1997; 97US-0048100P.

XX PR 30-MAY-1997; 97US-0048189P.

XX PR 30-MAY-1997; 97US-0048357P.

XX PR 30-MAY-1997; 97US-0050934P.

XX PR 06-JUN-1997; 97US-0048970P.

XX PR 05-SEP-1997; 97US-0057765P.

XX PR 19-DEC-1997; 97US-0068368P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

XX PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;

XX PI Ferrie AM;

XX DR WPI; 1998-520811/44.

XX DR N-PSDB; AAV34309.

XX PT Isolated human polynucleotide(s) encoding secretory peptide(s) - used to
XX develop products for the diagnosis and treatment of e.g. inflammation,
XX cancers, CNS disorders or immune system disorders.

XX PS Disclosure; Page 24; 201pp; English.

XX CC This sequence represents a fragment of a secreted human protein encoded
XX by the nucleic acid molecule designated Gene 24 (AAV34309). The gene can
XX be used to generate fusion proteins by linking to the gene to a human
XX immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of
XX the fused protein as compared to the human protein only. The invention
XX relates to 28 novel genes and their fragments (nucleic acid sequences:
XX AAV34286-V34325; amino acid sequences AAW75196-W75235) which are useful
XX for preventing, treating or ameliorating medical conditions e.g. by
XX protein or gene therapy. Also, pathological conditions can be diagnosed
XX by determining the amount of the new polypeptides in a sample or by
XX determining the presence of mutations in the new polynucleotides.
XX Specific uses are described for each of the 28 polynucleotides, based on
XX which tissues they are most highly expressed in (see AAV34286 for
XX described uses)

SQ Sequence 51 AA;
 Query Match 29.1%; Score 219; DB 2; Length 51;
 Best Local Similarity 68.6%; Pred. No. 1.9e-11;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 Qy 77 CSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 127
 Db 1 CEMPKEGTGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTC 51
 RESULT 36
 AAE27025 ID AAE27025 standard; protein; 51 AA.
 XX AC AAE27025;
 XX DT 13-DEC-2002 (first entry)
 XX DE Human gene 24 encoded secreted protein variant, SEQ ID NO:118.
 XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotrophic; vulnery; cytotatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.
 XX OS Homo sapiens.
 XX FN US2002077287-A1.
 XX PD 20-JUN-2002.
 XX PF 11-MAY-2001; 2001US-00852659.
 XX PR 11-SEP-1998; 98US-00152060.
 XX PA (RUBE/) RUBEN S M.
 XX PA (ROSE/) ROSEN C A.
 XX PA (LIYY/) LI Y.
 XX PA (ZENG/) ZENG Z.
 XX PA (KYAW/) KYAW H.
 XX PA (FISC/) FISCHER C L.
 XX PA (LIHH/) LI H.
 XX PA (SOPP/) SOPPET D R.
 XX PA (GENT/) GENTZ R L.
 XX PA (WEIY/) WEI Y.
 XX PA (MOOR/) MOORE P A.
 XX PA (YOUN/) YOUNG P E.
 XX PA (GREE/) GREENE J M.
 XX PA (FERR/) FERRIE A M.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX WPI; 2002-598780/64.
 XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 XX Disclosure; Page 16; 209pp; English.
 PS AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 XX

protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 AAE27000-AAE27025 represent human secreted protein fragments or their
 variants. The secreted proteins and genes are useful for preventing,
 treating or ameliorating medical conditions, e.g., by protein or gene
 therapy. Specific uses are described for each of the 28 genes, based on
 the tissues in which they are most highly expressed and include
 developing products for the diagnosis or treatment of immunodeficiencies,
 e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 Grave's disease, diabetes mellitus, dermatitis, inflammatory bowel
 disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 breast), central nervous system (CNS) disorders e.g., ischaemic brain
 injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 sarcoidosis and allogenic transplant rejection, blood-related disorder
 (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 lung cancer, allergic disorders, pneumonitis, renal disorders, e.g. acute
 glomerulonephritis, neurological diseases, liver disorders, endocrine
 disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein variant of the
 CC invention
 XX Sequence 51 AA;
 SQ

Query Match 29.1%; Score 219; DB 5; Length 51;
 Best Local Similarity 68.6%; Pred. No. 1.9e-11;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 Qy 77 CSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 127
 Db 1 CEMPKEGTGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTC 51
 RESULT 37
 AAE27163 ID AAE27163 standard; protein; 51 AA.
 XX AC AAE27163;
 XX DT 13-DEC-2002 (first entry)
 XX DE Human gene 24 encoded secreted protein fragment kunitz-type domain.
 XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiodysplasia;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytotatic;
 KW cardiant; vasotrophic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 KW vulnery.
 XX OS Homo sapiens.
 XX FN US2002076756-A1.
 XX PD 20-JUN-2002.
 XX PF 11-MAY-2001; 2001US-00853161.
 XX PR 02-FEB-2001; 2001US-0265583P.
 XX PA (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.
PA (LIYU/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEI/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2002-574454/61.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
XX Disclosure; Page 16; 209pp; English.
XX
XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment kunitz-type domain referred to in the
CC disclosure of the invention
XX
XX Sequence 51 AA;
XX
XX Query Match 29.1%; Score 219; DB 5; Length 51;
XX Best Local Similarity 68.8%; Pred. No. 1.9e-11;
XX Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 77 CSMQBPAGCLASIPHWYNNKTKIGSEFIYGGCGNNNNFQTEAICLVTC 127
XX 1 CEMPKEGTGCLAFVFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 51
XX
XX RESULT 38
XX ADG89845
XX ID ADG89845 standard; protein; 51 AA.
XX
XX AC ADG89845;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human secreted protein gene 24 protein #3.
XX
XX Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;

KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.
XX
XX Homo sapiens.
XX
XX US2003225009-A1.
XX
XX 04-DEC-2003.
XX
XX 30-JAN-2002; 2002US-00058993.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057765P.
XX 19-DEC-1997; 97US-0068368P.
XX 12-MAR-1998; 98MO-US004858.
XX 11-SEP-1998; 98US-00152060.
XX 02-FEB-2001; 2001US-0285583P.
XX 11-MAY-2001; 2001US-0085265P.
XX 11-MAY-2001; 2001US-00852797.
XX 11-MAY-2001; 2001US-00853161.
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (LIYU/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIHH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEI/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX (HAST/) HASTINGS G A.
XX
XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
XX WPI; 2004-042167/04.
XX
XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
XX Disclosure; SEQ ID NO 118; 320pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide


```
SQ Sequence 2858 AA;
Query Match 24.8%; Score 187; DB 4; Length 2858;
Best Local Similarity 33.3%; Pred. No. 4.7e-07;
Matches 38; Conservative 13; Mismatches 33; Indels 30; Gaps 5;

QY 46 DOCTKPR---DCPENM-----KCCPF---SCG-----KKCLD-----FRKD 75
Db 1748 DRCLPKQTGDCSEKLAHWFSESEKRCVPFYSGCGGNKNFPPTLESCEHCPQVAKD 1807

QY 76 ICSMPQAGPCLASIPHHWYKTKICSEFYGGCGGNNNNFQTEAICLVTCCK 129
Db 1808 ICEIPAEVGECAVYTSWYDQACRQFYGGCGGNENRFPPTESCLARCDR 1861

RESULT 41
ID ABB58064 standard; protein; 3060 AA.
XX
AC ABB58064;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 984.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
DR N-PSDB; ABL02167.
XX
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 984; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16178-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3060 AA;
Query Match 24.8%; Score 187; DB 4; Length 3060;
Best Local Similarity 33.3%; Pred. No. 5e-07;
Matches 38; Conservative 13; Mismatches 33; Indels 30; Gaps 5;

QY 46 DOCTKPR---DCPENM-----KCCPF---SCG-----KKCLD-----FRKD 75
Db 1748 DRCLPKQTGDCSEKLAHWFSESEKRCVPFYSGCGGNKNFPPTLESCEHCPQVAKD 1807

RESULT 42
ID AAE39498 standard; protein; 571 AA.
XX
AC AAE39498;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cloned mouse GDF-associated serum protein (GASP) 1.
XX
KW Mouse; GDF-associated serum protein; GASP; myotrophic lateral sclerosis;
KW growth and differentiation factor; GDF; chronic glucocorticoid therapy;
KW familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
KW progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
KW bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
KW muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
KW carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
KW nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;
KW androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;
KW metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
KW myotonia; neuroprotective; obesity; immunomodulator; diabetes.
XX
OS Mus sp.
XX
PN US2003162714-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003US-00369736.
XX
PR 21-FEB-2002; 2002US-0357845P.
XX
PR 20-DEC-2002; 2002US-0434644P.
XX
XX
PA (AMHP ) WYETH.
XX
PI Hill JJ, Wolfman NM;
XX
DR WPI; 2003-756055/71.
XX
DR N-PSDB; AAD59931.
XX
XX
PT Composition containing growth and differentiation factor-associated serum
PT protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
PT for diagnosis.
XX
PS Example 9; Fig 13; Opp; English.
XX
CC The present invention relates to the use of a protein GDF (growth and
CC differentiation factor)-associated serum protein (GASP) 1 comprising
CC at least one follistatin domain to modulate the level or activity of
CC growth and differentiation factor (GDF) -8. Administration of GASP1 is
CC used to modulate GDF-8 for treatment of muscular disorders such as
CC muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
CC myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
CC progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
CC congestive obstructive pulmonary disease, congenital myopathy (myotonia),
CC familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
CC Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
CC carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
CC and other muscle wasting syndromes such as traumatic or chronic injury to
CC muscle, metabolic disorders such as diabetes types 1 or 2, impaired
CC glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
CC induced by trauma and obesity, adipose tissue disorder such as obesity,
CC and bone degenerative conditions such as osteoporosis, osteopaenia,
CC osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
CC premature gonadal failure, vitamin D deficiency, androgen suppression,
CC secondary hyperparathyroidism, nutritional deficiencies and anorexia
CC nervosa. The present sequence is cloned mouse GDF (growth and
CC differentiation factor)-associated serum protein (GASP)
```



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XX SQ Sequence 571 AA;
Query Match 24.2%; Score 182.5; DB 7; Length 571;
Best Local Similarity 31.8%; Pred. No. 2.4e-07;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
Db 322 ECLKPPDSEDCGEGQTRWHFDAQANNCLTFTFGCHHNLNHFYEAACMLACMSGPLATC 381

Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGCQCGNNNNFQTEAICLVTC 127
Db 382 SLPALQGFCKAYVPRWAYNSQTGLCQSPFYGCGEGNGNPFESREACEESC 431

RESULT 43
AAE39459
ID AAE39459 standard; protein; 571 AA.
AC AAE39459;
DT 18-DEC-2003 (first entry)
DE Mouse GDF-associated serum protein (GASP)1 protein.
KW Mouse; GDF-associated serum protein; GASP; amyotrophic lateral sclerosis;
KW growth and differentiation factor; GDF; chronic glucocorticoid therapy;
KW familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
KW progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
KW bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
KW muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
KW carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
KW nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;
KW androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;
KW metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
KW myotonia; neuroprotective; obesity; immunomodulator; diabetes.
OS Mus sp.
XX
XX Key Location/Qualifiers
XX Domain 105..170
XX /note= "Follistatin domain"
XX
XX US2003162714-A1.
XX
XX 28-AUG-2003.
XX
XX 21-FEB-2003; 2003US-00369736.
XX
XX 21-FEB-2002; 2002US-0357845P.
XX 20-DEC-2002; 2002US-0434644P.
XX
XX (AMHP ) WYETH.
XX
XX Hill JJ, Wolfman NM;
XX WPI; 2003-756055/71.
XX DR N-PSDB; AAD59923.
XX
XX Composition containing growth and differentiation factor-associated serum
XX protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
XX for diagnosis.
XX
XX Disclosure; Fig 6C; Opp; English.
XX
XX The present invention relates to the use of a protein GDF (growth and
XX differentiation factor)-associated serum protein (GASP) 1 comprising
XX at least one follistatin domain to modulate the level or activity of
XX growth and differentiation factor (GDF) -8. Administration of GASPI is
XX used to modulate GDF-8 for treatment of muscular disorders such as
XX muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
XX myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),

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CC progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
CC congestive obstructive pulmonary disease, congenital myopathy (myotonia),
CC familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
CC Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
CC carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
CC and other muscle wasting syndromes such as traumatic or chronic injury to
CC muscle, metabolic disorders such as diabetes types 1 or 2, impaired
CC glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
CC induced by trauma and obesity, adipose tissue disorder such as obesity,
CC and bone degenerative conditions such as osteoporosis, osteopaenia,
CC osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
CC premature gonadal failure, vitamin D deficiency, androgen suppression,
CC secondary hyperparathyroidism, nutritional deficiencies and anorexia
CC nervosa. The present sequence is mouse GDF (growth and differentiation
CC factor)-associated serum protein (GASP)
XX
XX SQ Sequence 571 AA;
Query Match 24.2%; Score 182.5; DB 7; Length 571;
Best Local Similarity 31.8%; Pred. No. 2.4e-07;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
Db 322 ECLKPPDSEDCGEGQTRWHFDAQANNCLTFTFGCHHNLNHFYEAACMLACMSGPLATC 381

Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGCQCGNNNNFQTEAICLVTC 127
Db 382 SLPALQGFCKAYVPRWAYNSQTGLCQSPFYGCGEGNGNPFESREACEESC 431

RESULT 44
ADD93670
ID ADD93670 standard; protein; 571 AA.
XX
XX ADD93670;
XX AC
XX 29-JAN-2004 (first entry)
XX
XX Mouse GDF-associated serum protein 1 (GASPl).
XX
XX Mouse; GDF-associated serum protein 1; GASPl; antidiabetic; anorectic;
XX osteopathic; gene therapy.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Peptide 1..29
XX /note= "Signal peptide"
XX Protein 30..571
XX /note= "Mature protein"
XX Domain 105..170
XX /note= Follistatin domain
XX Modified-site 313
XX /note= "potential N-glycosylation site"
XX Modified-site 514
XX /note= "potential N-glycosylation site"
XX
XX WO2003072714-A2.
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US0005150.
XX
XX 21-FEB-2002; 2002US-0357846P.
XX 20-DEC-2002; 2002US-0434645P.
XX
XX (AMHP ) WYETH.
XX
XX Hill JJ, Wolfman NM;
XX WPI; 2003-812402/76.
XX DR N-PSDB; ADD93719, ADD93720.

```


XX New compositions comprising a protein containing at least one follistatin
PT domain, useful for treating muscular dystrophy (e.g. sarcopenia, and
PT cachexia), metabolic disease (e.g. diabetes or obesity), or bone
PT degenerative diseases.
XX
XX
XX Example 9; Fig 6C; 113pp; English.
XX
XX The present sequence is the protein sequence for mouse GDF-associated
CC serum protein 1 (GASPI), a protein which includes a follistatin domain
CC and which binds to growth and differentiation factor-8 (GDF-8 or
CC myostatin). The invention provides methods for modulating the effects of
CC GDF-8 on cells. These methods involve administering a protein comprising
CC at least one follistatin domain, or a nucleic acid encoding such a
CC protein. The methods are used to treat disorders relating to the level or
CC activity of GDF-8. These include a muscular disorder such as muscular
CC dystrophy (e.g. severe or benign X-linked muscular dystrophy, limb-girdle
CC dystrophy, facioscapulohumeral dystrophy, myotonic dystrophy, distal
CC muscular dystrophy, progressive dystrophic ophthalmoplegia,
CC oculopharyngeal dystrophy, Fukuyama-type congenital muscular dystrophy,
CC congenital myopathy, myotonia congenita, familial periodic paralysis,
CC paroxysmal myoglobinuria, myasthenia gravis, Eaton-Lambert syndrome,
CC secondary myasthenia, denervation atrophy, paroxysmal muscle atrophy,
CC muscle wasting syndrome, sarcopenia, and cachexia), traumatic or chronic
CC injury to muscle tissue, metabolic disease or disorder (e.g. type 2
CC diabetes, non-insulin-dependent diabetes mellitus, hyperglycaemia, or
CC obesity), adipose tissue disorder (e.g. obesity), and bone degenerative
CC disease (e.g. osteoporosis) (all claimed).

XX Sequence 571 AA;
SQ
Query Match 24.2%; Score 182.5; DB 7; Length 571;
Best Local Similarity 31.8%; Pred. No. 2.4e-07;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SGCKCLDFRKDIC 77
DB 322 ECLKPPDSDCGEQTRHFDQAANNCLTFTFGCHHNLNHPETYEACMLACMSGPLATC 381
QY 78 SMOEAGCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
DB 382 SLFALQGPCKAYVRWAYNSQTLGCSFYGGCGGNFRESACEESC 431

RESULT 45
ADAL19806
ID ADAL19806 standard; peptide; 33 AA.
XX
XX ADAL19806;
XX
XX 20-NOV-2003 (first entry)
XX
XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:7.
XX
XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiatheric; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2003070770-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-BP001629.

PR 21-FEB-2002; 2002US-0358683P.
XX (GENE-) GENEPROT INC.
PA Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Disclosure; Page 80; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.
XX
XX Sequence 33 AA;
SQ
Query Match 23.9%; Score 180; DB 7; Length 33;
Best Local Similarity 97.0%; Pred. No. 2.6e-08;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 99 TKICSEFYGGCGQNNNFQTEAICLVTCCKYH 131
DB 1 TKICSEFYGGCGQNNNFQTEAICLVTCCKYH 33
RESULT 46
ADAL19809
ID ADAL19809 standard; peptide; 33 AA.
XX
XX ADAL19809;
XX
XX 20-NOV-2003 (first entry)
XX
XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:10.
XX
XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiatheric; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX

PN WO2003070770-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Disclosure; Page 82-83; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnerary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.
XX
XX Sequence 33 AA;
SQ
Query Match 23.9%; Score 180; DB 7; Length 33;
Best Local Similarity 97.0%; Pred. No. 2.6e-08;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 99 TKICSEFYGGCGQNNNNFQTEAICLVTKCKYH 131
Db 1 TKICSEFYGGCGQNNNNFQTEAICLVTKCKYH 33
RESULT 47
AAR99146
ID AAR99146 standard; protein; 58 AA.
XX
XX AAR99146;
XX
XX
XX 12-FEB-1997 (first entry)
XX
XX Aprotinin-like Kunitz domain.
XX
XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha 1 antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX
XX Synthetic.
OS
XX

PN WO9620278-A2.
XX
XX 04-JUL-1996.
XX
XX 15-DEC-1995; 95WO-US016349.
XX
XX 16-DEC-1994; 94US-00358160.
XX
XX (PROT-) PROTEIN ENG CORP.
XX
XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX WPI; 1996-321851/32.
XX
XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX
XX Example 23; Page 47; 105pp; English.
XX
XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211
XX
XX Sequence 58 AA;
SQ
Query Match 23.5%; Score 177; DB 2; Length 58;
Best Local Similarity 56.4%; Pred. No. 8.1e-08;
Matches 31; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
Qy 73 RKDICSMPQAGCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 127
Db 1 RPDFCLLPAETGPRAMIPRFYNNAKSGKCEPFYGGCGGNANNNFKTEECRRTC 55
RESULT 48
AAR913096
ID AAR913096 standard; peptide; 43 AA.
XX
XX AAR913096;
XX
XX 28-JAN-2002 (first entry)
XX
XX Human serine proteinase inhibitor BTL.009 peptide fragment #2.
DE
XX Human; BTL.009 protein; serine proteinase inhibitor; cytosstatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
XX Homo sapiens.
OS
XX US6294648-B1.
XX
XX 25-SEP-2001.
XX
XX 20-JUL-1999; 99US-00358569.
XX
XX 20-JUL-1999; 99US-00358569.
XX
XX (FARB) BAYER CORP.
XX

PI Delaria K, Rocznik S, Davies C;
XX WPI; 2001-662224/76.
XX New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX Disclosure; Col 5-6; 16pp; English.
XX The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL.009 peptide fragment related to the invention
XX Sequence 43 AA;
SQ
Query Match 23.2%; Score 175; DB 4; Length 43;
Best Local Similarity 69.0%; Pred. No. 9e-08; Indels 0; Gaps 0;
Matches 29; Conservative 4; Mismatches 9;
QY 87 LASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 128
DB 1 LAYFLHWYDKDNTCSFVYGGCGGNNNNFQSKANCLNTCK 42
RESULT 49
AAE13092
ID AAE13092 standard; peptide; 54 AA.
XX AAE13092;
XX 28-JAN-2002 (first entry)
XX Trypsin inhibitor peptide.
XX BTL.009 protein; serine proteinase inhibitor; cytostatic; therapeutic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW trypsin inhibitor.
XX Unidentified.
XX US6294648-B1.
XX 25-SEP-2001.
XX 20-JUL-1999; 99US-00358569.
XX 20-JUL-1999; 99US-00358569.
XX (FARB) BAYER CORP.
XX Delaria K, Rocznik S, Davies C;
XX WPI; 2001-662224/76.
XX New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX Disclosure; Col 5-6; 16pp; English.

XX The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is trypsin inhibitor peptide related to
CC the invention
XX Sequence 54 AA;
SQ
Query Match 23.2%; Score 175; DB 4; Length 54;
Best Local Similarity 50.0%; Pred. No. 1.1e-07;
Matches 27; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
QY 75 DICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 128
DB 1 DLCLPQARGPCKAALLRYFNSTSNACEPFTYGGCGGNNNNFETENCLEICE 54
RESULT 50
ABJ01150
ID ABJ01150 standard; protein; 503 AA.
XX ABJ01150;
XX 28-NOV-2002 (first entry)
XX Ovary cell-specific amino acid sequence 96.
XX Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
KW ovary specific protein; ovarian cancer; breast cancer; vaccine;
KW gene therapy.
XX Homo sapiens.
XX WO200238606-A2.
XX 16-MAY-2002.
XX 07-NOV-2001; 2001WO-US046459.
XX 08-NOV-2000; 2000US-0246640P.
XX (DIAD-) DIADEXUS INC.
XX Sun Y, Recipon H, Salceda S, Liu C;
XX WPI; 2002-519297/55.
XX Polypeptide and polynucleotides present in normal and neoplastic ovary
PT cells, useful for identifying, monitoring, staging, diagnosing,
PT preventing and treating ovarian cancer, and non-cancerous disease states
PT in the ovary.
XX Claim 11; Page 244-245; 247pp; English.
XX The invention comprises amino acid and DNA sequences which are present in
CC normal and neoplastic ovary cells. The DNA and protein sequences of the
CC invention are useful for determining the presence of an ovary specific
CC nucleic acid or an ovary specific protein in a sample. The DNA and
CC protein sequences of the invention are useful for diagnosing and
CC monitoring the presence and metastasis of ovarian cancer and breast
CC cancer. Amino acids ABJ01055 - ABJ01155 represent the ovary cell specific
CC protein sequences of the invention
XX

SQ Sequence 503 AA;

Query Match 23.0%; Score 173.5; DB 5; Length 503;
Best Local Similarity 31.8%; Fred. No. 1.3e-06;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;
Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
Db 258 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHFETYEACMLACMSGPLAAC 317
Qy 78 SMPQAGGCLASIPHHWYNKTKICSEFIYGGCGNNNNNFQTEAICLVTC 127
Db 318 SLPALQGCKAYAPRWAYNSQTGCQSFYGGCEGNGNPFESREACEESC 367

Search completed: September 21, 2005, 16:36:48
Job time : 87.9233 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:27:13 ; Search time 23.9587 Seconds
(without alignments)
408.162 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 753
Sequence: 1 MGLSGLLPILVFFILLGDIQ.....GNNNFQTEAICLVTCCKYH 131

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PTCUS-COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	62.0	133	4	US-09-152-060-75
2	242	32.1	64	3	US-09-358-569D-10
3	236	31.3	58	3	US-09-369-494-8
4	236	31.3	58	4	US-09-569-670-8
5	233	30.9	54	3	US-09-358-569D-8
6	231	30.7	55	3	US-09-358-569D-1
7	186	24.7	66	1	US-08-358-160-113
8	186	24.7	79	6	5466783-7
9	186	24.7	79	6	5466783-7
10	177	23.5	58	1	US-08-358-160-71
11	175	23.2	43	3	US-09-358-569D-13
12	175	23.2	54	3	US-09-358-569D-9
13	175	23.2	67	1	US-08-358-160-123
14	173	23.0	58	1	US-08-358-160-17
15	173	23.0	58	1	US-08-358-160-18
16	169	22.4	77	6	5466783-4
17	169	22.4	77	6	5466783-4
18	168	22.3	86	4	US-09-910-430-8
19	167	22.2	58	1	US-08-358-160-10
20	167	22.2	58	1	US-08-358-160-11
21	166	22.0	58	1	US-07-664-989B-48
22	166	22.0	58	1	US-07-664-989B-51
23	166	22.0	58	1	US-08-358-160-1
24	166	22.0	58	1	US-08-358-160-15
25	166	22.0	58	1	US-08-358-160-26
26	166	22.0	62	1	US-08-358-160-27
27	166	22.0	107	4	US-09-270-767-46540

28	165	21.9	58	1	US-07-664-989B-49
29	165	21.9	58	1	US-08-358-160-24
30	164	21.8	58	1	US-08-358-160-9
31	164	21.8	61	2	US-08-829-876-211
32	164	21.8	61	2	US-08-829-876-214
33	164	21.8	61	3	US-09-234-874A-211
34	164	21.8	61	3	US-09-234-874A-214
35	164	21.8	61	4	US-09-234-873A-211
36	164	21.8	61	4	US-09-234-873A-214
37	163	21.6	58	1	US-07-664-989B-84
38	163	21.6	58	1	US-08-358-160-12
39	163	21.6	58	1	US-08-358-160-61
40	163	21.6	58	1	US-08-463-155A-56
41	163	21.6	58	1	US-08-463-152B-56
42	163	21.6	58	3	US-08-676-124-69
43	163	21.6	58	3	US-09-414-878-69
44	163	21.6	58	3	US-09-240-136-69
45	163	21.6	58	4	US-09-638-770A-69
46	163	21.6	61	2	US-08-829-876-180
47	163	21.6	61	2	US-08-829-876-218
48	163	21.6	61	3	US-09-234-874A-180
49	163	21.6	61	3	US-09-234-874A-218
50	163	21.6	61	4	US-09-234-873A-180

ALIGNMENTS

RESULT 1
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003PL US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match 62.0%; Score 467; DB 4; Length 133;
Best Local Similarity 60.9%; Pred. No. 6e-39;
Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
QY 1 MGLSGLLPILVFFILLGDIQEPGHAEGILGKPCPKIVEEEDQCTKPPDCPENMKC 60
DB 1 MGSSGLLSLLVLLVLLANVQPGGLTWLPPRCPKIRECECFQERDVTCTKQCCQDNKCC 60

Qy 61 CPFSGKKCLDFRDKCSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTE 120
Db 61 CVFSGKKCLDLKQDVCEMPKETGCLAYFLHWYDKDNTCSMFVYGGCGGNNNFQSK 120
Qy 121 AICLVTK 128
Db 121 ANCLNTCK 128

RESULT 2

US-09-358-569D-10
; Sequence 10, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Extension of
; OTHER INFORMATION: Seq id 1
US-09-358-569D-10

Query Match 32.1%; Score 242; DB 3; Length 64;
Best Local Similarity 65.5%; Pred. No. 5.5e-17;
Matches 38; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 71 DFRDKCSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTK 128
Db 1 DLKQDVCEMPKETGCLAYFLHWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 58

RESULT 3

US-09-369-494-8
; Sequence 8, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-8

Query Match 31.3%; Score 236; DB 3; Length 58;
Best Local Similarity 66.1%; Pred. No. 1.9e-16;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTK 128
Db 1 KQDVCEMPKETGCLAYFLHWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 56

RESULT 4

US-09-569-670-8
; Sequence 8, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8

Query Match 31.3%; Score 236; DB 4; Length 58;
Best Local Similarity 66.1%; Pred. No. 1.9e-16;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTK 128
Db 1 KQDVCEMPKETGCLAYFLHWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 56

RESULT 5

US-09-358-569D-8
; Sequence 8, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-8

Query Match 30.9%; Score 233; DB 3; Length 54;
Best Local Similarity 68.5%; Pred. No. 3.6e-16;
Matches 37; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 75 DICSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTK 128
Db 1 DVCMPKETGCLAYFLHWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 54

RESULT 6

US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher

;; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
;; FILE REFERENCE: MSB-7259
;; CURRENT APPLICATION NUMBER: US/09/358.569D
;; CURRENT FILING DATE: 1999-07-20
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1
;; LENGTH: 55
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: derived from
;; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match 30.7%; Score 231; DB 3; Length 55;
Best Local Similarity 65.5%; Pred. No. 5.7e-16;
Matches 36; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
Qy 73 RKDICSMPQEGAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 127
Db 1 KQDVCMPKGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 7
US-08-358-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 113:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 66 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-358-160-113
Query Match 24.7%; Score 186; DB 1; Length 66;
Best Local Similarity 50.0%; Pred. No. 2e-11;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
Qy 73 RKDICSMPQEGAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 128
Db 4 KRDICRLPPEQGPGCKGRIPRYFYNPASRMCSFYGGCKGNKNNFKTKAECVCRACR 59
RESULT 8
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain; Kretzmer, Kuniko K.; Broze, George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 7;
; LENGTH: 79
5466783-7
Query Match 24.7%; Score 186; DB 6; Length 79;
Best Local Similarity 50.0%; Pred. No. 2.4e-11;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
Qy 73 RKDICSMPQEGAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 128
Db 4 KRDICRLPPEQGPGCKGRIPRYFYNPASRMCSFYGGCKGNKNNFKTKAECVCRACR 59
RESULT 9
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain; Kretzmer, Kuniko K.; Broze, George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 7;
; LENGTH: 79
5466783-7

Query Match 24.7%; Score 186; DB 6; Length 79;
Best Local Similarity 50.0%; Pred. No. 2.4e-11;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 73 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 128
Db 4 KRDICRPPGQCKGRIPRYFYNPASRMCSFYGGCKGNKNNFKTKAECVCRAC 59

RESULT 10

US-08-358-160-71
; Sequence 71, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358.160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133.031
; FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009.319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664.989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487.063
; FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240.160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-358-160-71
Query Match 23.5%; Score 177; DB 1; Length 58;
Best Local Similarity 56.4%; Pred. No. 1.4e-10;

Matches 31; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
Qy 73 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 127
Db 1 RPDICLLPAETGPRAMIPRYFYNNAKSGKCEPFYGGCGGNANNNFKTEECRRTC 55

RESULT 11

US-09-358-569D-13
; Sequence 13, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: sequence derived from EST database
US-09-358-569D-13

Query Match 23.2%; Score 175; DB 3; Length 43;
Best Local Similarity 69.0%; Pred. No. 1.6e-10;
Matches 25; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 87 LASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 128
Db 1 LAVFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTCK 42

RESULT 12

US-09-358-569D-9
; Sequence 9, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-9

Query Match 23.2%; Score 175; DB 3; Length 54;
Best Local Similarity 50.0%; Pred. No. 2e-10;
Matches 27; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 75 DICSMPOAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 128
Db 1 DLCLPQARGPCAKALLRYFNSTSNACEPFTYGGCGQNNNNFETTEMCLRICE 54

RESULT 13

US-08-358-160-123

Query Match 22.2%; Score 167; DB 1; Length 58;
 Best Local Similarity 50.0%; Pred. No. 1.3e-09;
 Matches 28; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Qy 73 RKDICSMPQEAGPCIASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 128
 Db 1 RPDFCQLGYSAGPCVAMFPFRFYNGTSMACETFOYGGCGMGNFVTEKDCQLQTCR 56

RESULT 21

US-07-664-989B-48
 ; Sequence 48, Application US/07664989B
 ; Patent No. 5223409
 ; GENERAL INFORMATION:
 ; APPLICANT: Ladner, Robert Charles
 ; APPLICANT: Guterma, Sonia Kosow
 ; APPLICANT: Roberts, Bruce Lindsay
 ; APPLICANT: Markland, William
 ; APPLICANT: Ley, Arthur Charles
 ; APPLICANT: Kent, Rachel Baribault
 ; TITLE OF INVENTION: Directed Evolution of No. 5223409el
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street, N.W.
 ; STREET: Suite 300
 ; CITY: Washington,
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 4.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/664,989B
 FILING DATE: 19910301
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US89/03731
 FILING DATE: 01-SEP-1989

APPLICATION NUMBER: 07/487,063
 FILING DATE: 02-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/240,160
 FILING DATE: 02-SEP-1988
 NAME: Cooper, Iver P.
 REGISTRATION NUMBER: 28005
 REFERENCE/DOCKET NUMBER: LADNER 7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-664-989B-48

Query Match 22.0%; Score 166; DB 1; Length 58;
 Best Local Similarity 47.3%; Pred. No. 1.7e-09;
 Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQEAGPCIASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 127
 Db 1 RPDFCQLGYSAGPCVAMFPFRFYNGTSMACETFOYGGCGMGNFVTEKDCQLQTCR 55

RESULT 22
 US-07-664-989B-51
 ; Sequence 51, Application US/07664989B
 ; Patent No. 5223409
 ; GENERAL INFORMATION:
 ; APPLICANT: Ladner, Robert Charles
 ; APPLICANT: Guterma, Sonia Kosow
 ; APPLICANT: Roberts, Bruce Lindsay
 ; APPLICANT: Markland, William
 ; APPLICANT: Ley, Arthur Charles
 ; APPLICANT: Kent, Rachel Baribault
 ; TITLE OF INVENTION: Directed Evolution of No. 5223409el
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street, N.W.
 ; STREET: Suite 300
 ; CITY: Washington,
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 4.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/664,989B
 FILING DATE: 19910301
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US89/03731
 FILING DATE: 01-SEP-1989

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/487,063
 FILING DATE: 02-MAR-1990
 APPLICATION NUMBER: 07/240,160
 FILING DATE: 02-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Cooper, Iver P.
 REGISTRATION NUMBER: 28005
 REFERENCE/DOCKET NUMBER: LADNER 7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 51:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-664-989B-51

Query Match 22.0%; Score 166; DB 1; Length 58;
 Best Local Similarity 47.3%; Pred. No. 1.7e-09;
 Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQEAGPCIASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 127
 Db 1 RPDFCQLGYSAGPCVAMFPFRFYNGTSMACETFOYGGCGMGNFVTEKDCQLQTCR 55

RESULT 23

US-08-358-160-1
 ; Sequence 1, Application US/08358160
 ; Patent No. 5663143
 ; GENERAL INFORMATION:
 ; APPLICANT: LEY, Arthur C.
 ; APPLICANT: LADNER, Robert C.
 ; APPLICANT: GUTERMAN, Sonia K.

APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-1

Query Match 22.0%; Score 166; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 1.7e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 73 RKDSCMPQEGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 127
DB 1 RPDCLPEPYTGPCVAMPFRFYNAKAGLCQTFVYGGCGGNGNFKSABDCMRTC 55

RESULT 24
US-08-358-160-15
Sequence 15, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William

APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-15

Query Match 22.0%; Score 166; DB 1; Length 58;
Best Local Similarity 48.2%; Pred. No. 1.7e-09;
Matches 27; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 73 RKDSCMPQEGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 128
DB 1 KEDFCQLGYSAGPCVAMPFRFYNGTSMACETFOYGGCGGNGNFTVKDCLQTCR 56

RESULT 25
US-08-358-160-26
Sequence 26, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ


```
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-26

Query Match 22.0%; Score 166; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 1.7e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 127
Db 1 RPDFCLEPPYTGPCIAFFPRFYNAKAGLCQTFVYGGCMGNGNFKSAEDCMRTC 55

RESULT 26
US-08-358-160-27
; Sequence 27, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-27

Query Match 22.0%; Score 166; DB 1; Length 62;
Best Local Similarity 47.3%; Pred. No. 1.8e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 127
Db 5 RPDFCLEPPYTGPCIAFFPRFYNAKAGLCQTFVYGGCMGNGNFKSAEDCMRTC 59

RESULT 27
US-09-270-767-46540
; Sequence 46540, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46540
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
```


US-09-270-767-46540

Query Match 22.0%; Score 166; DB 4; Length 107;
Best Local Similarity 39.1%; Pred. No. 3.1e-09;
Matches 27; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

QY 61 CPFGCKCLDFRDKICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTE 120
DB 36 CNYNCRQGVLKAKDICBPAEVBGCANYVTISWYDQDACVQFYGGCGGNNRFPTE 95
QY 121 AICLVCKK 129
DB 96 ESCLARCDR 104

RESULT 28
US-07-664-989B-49
; Sequence 49, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Lev, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Suite 300
; STATE: Washington,
; COUNTRY: DC
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-49

Query Match 21.9%; Score 165; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 2.1e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 127
DB 1 RPFDCLEPPYTPGCVAIFFRYFYNAKAGLCQTFYVGGCMGNGNFKSAEDCMRTC 55

RESULT 29
US-08-358-160-24
; Sequence 24, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-24

Query Match 21.9%; Score 165; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 2.1e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 127


```

; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE: 11-Jun-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-08-829-876-214

Query Match 21.8%; Score 164; DB 2; Length 61;
Best Local Similarity 46.3%; Pred. No. 2.8e-09;
Matches 25; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 74 KDICSMPEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 127
Db 4 REVCEQATGTCRALIPRYFDVTGKCAPFFYGGCGGNNNNFDEEYCMAVC 57

RESULT 33
US-09-234-874A-211
; Sequence 211, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-234-874A-211

Query Match 21.8%; Score 164; DB 3; Length 61;
Best Local Similarity 46.3%; Pred. No. 2.8e-09;
Matches 25; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 74 KDICSMPEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 127
Db 4 REVCEQATGTCRALIPRYFDVTGKCAPFFYGGCGGNNNNFDEEYCMAVC 57

RESULT 34
US-09-234-874A-214
; Sequence 214, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-234-874A-211
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STREET: Suite 300
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 4.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/664,989B
FILING DATE: 19910301
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-664-989B-84

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 73 RKDTCMPQAGPCLASIPHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
DB 1 RPDFCLEPPTGCVAMPFRFYNAKAGLCQTFMYGGCGKGNFKSAEDCMRTC 55

RESULT 38
US-08-358-160-12
Sequence 12, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-12

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 48.2%; Pred. No. 3.3e-09;
Matches 27; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 73 RKDTCMPQAGPCLASIPHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 128
DB 1 RPDFCQLGYSTGCVAMPFRFYNGTSMACETFOYGGCMGNGNFVTEKDCLOICR 56

RESULT 39
US-08-358-160-61
Sequence 61, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160

; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEV=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-61

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDTCSPQEAAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFOTEAIICLVTC 127
Db 1 RPDFCLEPPYTGPCVAMPFRIFYNAKAGLCQTFMYGGCGGKNNFKSAEDCMRTC 55

RESULT 40
US-08-463-155A-56
; Sequence 56, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-432B-56

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 74 KDICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFOTEAIICLVTC 127
Db 2 REVCEQAEDGPCRAAIPRWYFDVTGKCAFFIYGGCGGNNRNFDTIEYCAAVC 55

RESULT 42
US-08-676-124-69
; Sequence 69, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:

; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-155A-56

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 74 KDICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFOTEAIICLVTC 127
Db 2 REVCEQAEDGPCRAAIPRWYFDVTGKCAFFIYGGCGGNNRNFDTIEYCAAVC 55

RESULT 41
US-08-463-432B-56
; Sequence 56, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,432B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-432B-56

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 74 KDICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFOTEAIICLVTC 127
Db 2 REVCEQAEDGPCRAAIPRWYFDVTGKCAFFIYGGCGGNNRNFDTIEYCAAVC 55

RESULT 42
US-08-676-124-69
; Sequence 69, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:

APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND=3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-676-124-69

Query Match 21.6%; Score 163; DB 3; Length 58;
Best Local Similarity 47.2%; Pred. No. 3.3e-09;
Matches 25; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 75 DICSMPQAGPCLASIPHWYNNKTKICSEFYGGCGNNNNFQTEAICLVTC 127
Db 3 DICKLPKDTGPCRAFDKWKYDPTKSCFEFVYGGCGNENKFGSQKEKVC 55

RESULT 43
US-09-414-878-69
Sequence 69, Application US/09414878
Patent No. 6071723
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-414-878-69

Query Match 21.6%; Score 163; DB 3; Length 58;
Best Local Similarity 47.2%; Pred. No. 3.3e-09;
Matches 25; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 75 DICSMPQAGPCLASIPHWYNNKTKICSEFYGGCGNNNNFQTEAICLVTC 127
Db 3 DICKLPKDTGPCRAFDKWKYDPTKSCFEFVYGGCGNENKFGSQKEKVC 55

RESULT 44
US-09-240-136-69
Sequence 69, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98


```

; FILING DATE: 07-JAN-1997
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-638-770A-69

Query Match 21.6%; Score 163; DB 4; Length.58;
Best Local Similarity 47.2%; Pred.No.3.3e-09;
Matches 25; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 75 DTCSMPQEGAGCLASIPHWYKTKICSEFYGGCGGNNNFTQAICLVTC 127
DB 3 DICKLPDGTGRCARDKRWYDPTKSCSEFYVYGGCGGNNKFGSKCEKVC 55
||||:||||:||||:||||:||||:||||:||||:||||:||||:|
||||:||||:||||:||||:||||:||||:||||:||||:|

RESULT 46
US-08-829-876-180
; Sequence 180, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:

```



```

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,874A
FILING DATE: 11-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/436,555
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 056324/0106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-874A-218

Query Match      21.6%; Score 163; DB 3; Length 61;
Best Local Similarity 46.3%; Pred. No. 3.5e-09;
Matches 25; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Qy    74 KDISEMQEAGPCLASIPHWNKTKICSEFFYGGCGNNNFTQAICLVTC 127
      :::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    4 REVCSQEASGCPCAAHYHFVDTGKCAFFYGGCGNNNFDTTEYCNAVC 57
      ::|||::|||::|||::|||::|||::|||::|||::|||::

RESULT 50
US-09-234-873A-180
Sequence 180, Application US/09234873A
Patent No. 6613890
GENERAL INFORMATION:
APPLICANT: White, Tyler R.
           Damm, Deborah
           Lesikar, David D.
           McFadden, Kathleen
           Garrick, Brett L.
TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,873A
FILING DATE: 21-Jan-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,876
FILING DATE: 02-APR-1997
APPLICATION NUMBER: 08/436,555

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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:33:14 ; Search time 81.9233 Seconds
(without alignments)
650.835 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 753
Sequence: 1 MGLSGLPILVFFILGDIQ.....GNNNFQTEAICLVTKCKYH 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 50 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdb.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pdb.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pdb.*
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19: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pdb.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pdb.*
21: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pdb.*
22: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*
23: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753	100.0	131	16	US-10-807-204-1
2	753	100.0	131	16	US-10-807-204-12
3	731	97.1	131	16	US-10-807-204-15
4	625	83.0	106	16	US-10-807-204-2
5	551	73.2	98	16	US-10-807-204-9
6	492	65.3	136	16	US-10-807-204-16
7	467	62.0	133	9	US-09-853-161-75
8	467	62.0	133	9	US-09-852-659A-75
9	467	62.0	133	9	US-09-852-797-75
10	467	62.0	133	15	US-10-058-993-75
11	467	62.0	133	16	US-10-807-204-13

12	404	53.7	86	17	US-10-480-988-21	Sequence 21, Appl
13	404	53.7	101	15	US-10-276-774-2606	Sequence 2606, Ap
14	401.5	53.3	117	9	US-09-852-659A-119	Sequence 119, App
15	401.5	53.3	117	15	US-10-058-993-120	Sequence 120, App
16	400	53.1	102	9	US-09-852-659A-120	Sequence 120, App
17	400	53.1	102	15	US-10-058-993-121	Sequence 121, App
18	398	52.9	134	16	US-10-807-204-14	Sequence 14, Appl
19	358	52.9	134	16	US-10-807-204-5	Sequence 5, Appl
20	236	31.3	58	16	US-10-361-997-5	Sequence 5, Appl
21	236	31.3	58	17	US-10-931-153-21	Sequence 21, Appl
22	197	29.1	51	15	US-10-058-993-118	Sequence 118, App
23	197	26.2	759	17	US-10-825-692-48	Sequence 48, Appl
24	184	24.4	64	10	US-09-896-095-160	Sequence 160, App
25	184	24.4	64	14	US-10-038-722-103	Sequence 103, App
26	184	24.4	64	14	US-10-115-134-17	Sequence 17, App
27	182.5	24.2	571	14	US-10-369-736-3	Sequence 3, Appl
28	182.5	24.2	571	14	US-10-369-738-49	Sequence 49, Appl
29	182.5	24.2	571	14	US-10-369-738-3	Sequence 3, Appl
30	182.5	24.2	571	14	US-10-369-738-49	Sequence 49, Appl
31	182.5	24.2	571	19	US-11-028-058-3	Sequence 3, Appl
32	182.5	24.2	571	19	US-11-028-058-49	Sequence 49, Appl
33	180	23.9	33	16	US-10-807-204-7	Sequence 7, Appl
34	180	23.9	33	16	US-10-807-204-10	Sequence 10, Appl
35	177	23.5	58	14	US-10-038-722-5	Sequence 5, Appl
36	175	23.2	67	10	US-09-896-095-147	Sequence 147, App
37	175	23.2	67	14	US-10-038-722-90	Sequence 90, Appl
38	175	23.2	67	15	US-10-115-134-4	Sequence 4, Appl
39	173.5	23.0	503	14	US-10-007-280A-233	Sequence 233, App
40	173.5	23.0	576	9	US-09-794-589-2	Sequence 2, Appl
41	173.5	23.0	576	14	US-10-315-380-2	Sequence 2, Appl
42	173.5	23.0	576	14	US-10-369-736-7	Sequence 7, Appl
43	173.5	23.0	576	14	US-10-369-738-7	Sequence 7, Appl
44	173.5	23.0	576	19	US-11-028-058-7	Sequence 7, Appl
45	173.5	23.0	640	14	US-10-369-736-5	Sequence 5, Appl
46	173.5	23.0	640	14	US-10-369-738-5	Sequence 5, Appl
47	173.5	23.0	640	19	US-11-028-058-5	Sequence 5, Appl
48	173	23.0	58	14	US-10-038-722-17	Sequence 17, Appl
49	173	23.0	58	14	US-10-038-722-18	Sequence 18, Appl
50	173	23.0	58	14	US-10-038-722-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:
; NAME/KEY: SIGNAL


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; LOCATION: (1)...(25)
; OTHER INFORMATION: predicted by SignalP 2.0
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (48)...(60)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (54)...(69)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(127)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (86)...(110)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (102)...(123)
; OTHER INFORMATION: predicted disulfide bond
; OTHER INFORMATION: predicted disulfide bond
; US-10-807-204-1

Query Match      100.0%; Score 753; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.8e-65;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Qy 61 CPFGCGKKCLDFRKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTE 120
Db 61 CPFGCGKKCLDFRKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTE 120

Qy 121 AICLVTCCKYH 131
Db 121 AICLVTCCKYH 131

RESULT 3
US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Baïroch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015 US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-807-204-15

Query Match      97.1%; Score 731; DB 16; Length 131;
Best Local Similarity 98.5%; Pred. No. 6.5e-63;
Matches 129; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Qy 61 CPFGCGKKCLDFRKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTE 120
Db 61 CPFGCGKKCLDFRKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTE 120

Qy 121 AICLVTCCKYH 131
Db 121 AICLVTCCKYH 131

RESULT 4
US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Baïroch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015 US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
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; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
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; NAME/KEY: DISULFID
; LOCATION: (23)...(35)
; OTHER INFORMATION: predicted disulfide bond
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; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
;
US-10-807-204-2
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Query Match 83.0%; Score 625; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 9.6e-53;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGCCLDFRDKDICSMPQEAGP 85
Db 1 EGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGCCLDFRDKDICSMPQEAGP 60
QY 86 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTKKXH 131
Db 61 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTKKXH 106
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RESULT 5
US-10-807-204-9
; Sequence 9, Application US/10807204
; Publication No. US20040229312A1
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; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-807-204-9

Query Match 73.2%; Score 551; DB 16; Length 98;
Best Local Similarity 99.0%; Pred. No. 1.3e-45;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
QY 61 CPFGCGKKCLDFRDKDICSMPQEAGPCLASIPHHWYNNK 98
Db 61 CPFGCGKKCLDFRDKDICSMPQEAGPCLASIPHHWYNNK 98
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RESULT 6
US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
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US-10-807-204-16

Query Match 65.3%; Score 492; DB 16; Length 136;
Best Local Similarity 62.8%; Pred. No. 9.4e-40;
Matches 81; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
QY 61 CPFGCGKKCLDFRDKDICSMPQEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTE 120
Db 61 CLFGCGKKCMDLRQDVCSLPQDPGCLAYLPRWYNNQETDLCTEFIYGGCGQNNNNFQTE 120
QY 121 AICLVTKK 129
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Db 121 GICTVVCKK 129

RESULT 7

US-09-853-161-75

Sequence 75, Application US/09853161

Patent No. US20020076756A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins

FILE REFERENCE: P2003P3

CURRENT APPLICATION NUMBER: US/09/853,161

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/152,060

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: PCT/US98/04858

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/040,762

PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/040,710

PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/050,934

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,100

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,357

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,189

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/057,765

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,970

PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/068,368

PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 75

LENGTH: 133

TYPE: PRT

ORGANISM: Homo sapiens

US-09-853-161-75

Query Match 62.0%; Score 467; DB 9; Length 133;

Best Local Similarity 60.9%; Pred. No. 2.4e-37;

Mismatches 18; Mismatches 32; Indels 0; Gaps 0;

Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

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Db 1 MGSSGLLSLLVFLVLANVQGLTDLWLPFRCPKIRECECFQERDVCTKDRQCQDNKKC 60

Qy 61 CPFSCGKKCLDFRKDCISMPQEAQPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTE 120

Db 61 CVFSCGKKCLDLKQDVCEMPKETGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSK 120

Qy 121 AICLVTCCK 128

Db 121 ANCLNTCK 128

RESULT 8

US-09-852-659A-75

Sequence 75, Application US/09852659A

Patent No. US20020077287A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins

FILE REFERENCE: P2003P4

CURRENT APPLICATION NUMBER: US/09/852,659A

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,357

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,100

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/050,934

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,189

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/057,765

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,970

PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/068,368

PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 75

LENGTH: 133

TYPE: PRT

ORGANISM: Homo sapiens

US-09-853-161-75

Query Match 62.0%; Score 467; DB 9; Length 133;

Best Local Similarity 60.9%; Pred. No. 2.4e-37;

Mismatches 18; Mismatches 32; Indels 0; Gaps 0;

Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFLLGDIQEPHAGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Db 1 MGSSGLLSLLVFLVLANVQGLTDLWLPFRCPKIRECECFQERDVCTKDRQCQDNKKC 60

Qy 61 CPFSCGKKCLDFRKDCISMPQEAQPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTE 120

Db 61 CVFSCGKKCLDLKQDVCEMPKETGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSK 120

Qy 121 AICLVTCCK 128

Db 121 ANCLNTCK 128

APPLICANT: GANDHI, Ameena R.; KABLE, Amy E.;
APPLICANT: SWARNAKAR, Anita; HAFALIA, April J.A.;
APPLICANT: TRAN, Bao; DUGGAN, Brendan M.;
APPLICANT: WARREN, Bridget A.; ISON, Craig H.;
APPLICANT: HONCHELL, Cynthia D.; NGUYEN, Dannel B.;
APPLICANT: LU, Dyung Aina M.; LEE, Ernestine A.;
APPLICANT: YUE, Henry; FORSYTHE, Ian J.;
APPLICANT: BARROSO, Ines; RAMKUMAR, Jayalaxmi;
APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
APPLICANT: YANG, Junning; THANGAVELU, Kavitha;
APPLICANT: GIETZEN, Kimberly J.; DING, Li;
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
APPLICANT: YAO, Monique G.; CHAWLA, Narinder K.;
APPLICANT: MASON, Patricia M.; GURURAJAN, Rajagopal;
APPLICANT: LEE, Sally; BECHA, Shanya D.;
APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
APPLICANT: ELLIOTT, Vicki S.; LUO, Wen;
APPLICANT: SPRAGUE, William W.; TANG, Y. Tom;
APPLICANT: LU, Yan; ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
FILE REFERENCE: PF-1040 USN
CURRENT APPLICATION NUMBER: US/10/480,988
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PCT/US02/19360
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/300,508
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/311,442
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: US 60/314,821
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/315,992
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 60/378,205
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL Program
SEQ ID NO 21
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7675588CD1
US-10-480-988-21

Query Match 53.7%; Score 404; DB 17; Length 86;
Best Local Similarity 98.6%; Pred. No. 2e-31;
Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVFFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVFFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Qy 61 CPFSCKGKCLDFRK 74
Db 61 CPFSRGKKCLDFRK 74

RESULT 13
US-10-276-774-2606
Sequence 2606, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 2606
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-276-774-2606

Query Match 53.7%; Score 404; DB 15; Length 101;
Best Local Similarity 98.6%; Pred. No. 2.3e-31;
Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVFFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 16 MGLSGLLPILVFFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 75

Qy 61 CPFSCKGKCLDFRK 74
Db 76 CPFSRGKKCLDFRK 89

RESULT 14
US-09-852-659A-119
Sequence 119, Application US/09852659A
Patent No. US20020077287A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 119
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-659A-119

Query Match 53.3%; Score 401.5; DB 9; Length 117;
Best Local Similarity 66.0%; Pred. No. 4.7e-31;
Matches 66; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

Qy 29 LGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKCKLDFRKIDCSMPQAGPCLA 88


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; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-121

Query Match      53.1%; Score 400; DB 15; Length 102;
Best Local Similarity 66.7%; Pred. No. 5.7e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 33 CPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMFQEAQPCIASIPH 92
Db 2 CPKIRECECFQERDVCTKRDQCQDNKKCCVFCGKKCLDLKQDVCEMFKETGTPCLAYFLH 61

Qy 93 WYWNKTKICSEFYGGCGNNNNFQTEAICLVTK 128
Db 62 WYDCKONTCSMFYVGGCGNNNNFQSKANCLNTCK 97

RESULT 18
US-10-807-204-14
; Sequence 14, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-14

Query Match      52.9%; Score 398; DB 16; Length 134;
Best Local Similarity 51.9%; Pred. No. 1.2e-30;
Matches 67; Conservative 25; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MGLSLLPILVPFLLGDIQSPGHAEGTLGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MKLSGFSVILVFLGLARVQGPSLADLFPFRCCFRFEECHQERDLCTDRDCPKKEKC 60

Qy 61 CPFSCGKKCLDFRDKICSMFQEAQPCIASIPHWYNNKTKICSEFYGGCGNNNNFQTE 120
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Db 61 CVFNCGKKCLNPQDICSLEPKDSYCMAYFRRWFMFKENSTCQVFIYGGCGNNNNFQSQ 120
Qy 121 AICLVTKCK 129
Db 121 SICQNAECK 129

RESULT 19
US-10-807-204-5
; Sequence 5, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-5

Query Match      34.3%; Score 258; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 PCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 74
Db 1 PCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 43

RESULT 20
US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US2004017194A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5

Query Match      31.3%; Score 236; DB 16; Length 58;
Best Local Similarity 66.1%; Pred. No. 2.4e-15;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDTCSPQBAQPCIASIPHWYNNKTKICSEFYGGCGNNNNFQTEAICLVTK 128
Db 1 KQDVCEMFKETGTPCLAYFLHWYDKKONTCSMFYVGGCGNNNNFQSKANCLNTCK 56

RESULT 21
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US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-PEGYLATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match 31.3%; Score 236; DB 17; Length 58;
Best Local Similarity 66.1%; Pred. No. 2.4e-15;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 73 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 128
Db 1 KQDVCEMPKETGCLAYFLHMYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 56

RESULT 22
US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003PS
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
```

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; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-118

Query Match 29.1%; Score 219; DB 15; Length 51;
Best Local Similarity 68.6%; Pred. No. 9.4e-14;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 77 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
Db 1 CEMPKETGCLAYFLHMYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 51

RESULT 23
US-10-825-692-48
; Sequence 48, Application US/10825692
; Publication No. US2005004232A1
; GENERAL INFORMATION:
; APPLICANT: Hotez, Peter
; APPLICANT: Ashcom, James
; APPLICANT: Bdamchian, Mannaz
; APPLICANT: Zhan, Bin
; APPLICANT: Wang, Yan
; APPLICANT: Hawdon, John
; APPLICANT: Loukas, Alexander
; APPLICANT: Williamson, Angela
; APPLICANT: Jones, Brian
; APPLICANT: Bethony, Jeffrey
; APPLICANT: Goud, Gaddam
; APPLICANT: Botazzi, Maria E.
; APPLICANT: Mendez, Susana
; TITLE OF INVENTION: Hookworm Vaccine
; FILE REFERENCE: 03740007aa
; CURRENT APPLICATION NUMBER: US/10/825,692
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/329,533
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 60/332,007
; PRIOR FILING DATE: 2001-11-23
; PRIOR APPLICATION NUMBER: US 60/375,404
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: PCT US02/33106
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Ancylostoma caninum
US-10-825-692-48

Query Match 26.2%; Score 197; DB 17; Length 759;
Best Local Similarity 46.1%; Pred. No. 2e-10;
Matches 35; Conservative 13; Mismatches 26; Indels 2; Gaps 1;

QY 56 ENMKCCPFSCGKKCL--DFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCG 113
Db 560 ETMEDCTFTCEQRKAPLEKDVCSQPITAGPCRASIPRYGYDSKKRCKVKFTYGGCKGN 619

QY 114 NNNFQTEAICLVTCCK 129
Db 620 GNRFPKNECEKTKR 635

RESULT 24
US-09-896-095-160
; Sequence 160, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
```


Thu Sep 22 07:16:43 2005

; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-736-49

Query Match 24.2%; Score 182.5; DB 14; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
DB 322 ECLKPPDSEDCEEQTRWHFDAQANNCLTFTFGCHHNLNHPETYEACMLACMSGPLATC 381
QY 78 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 127
DB 382 SLPALQGPCKAYVPRWAYNSQTGLCQSFYGGCEGNGNPFESREACEESC 431

RESULT 29
US-10-369-738-3
; Sequence 3, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-738-3

Query Match 24.2%; Score 182.5; DB 14; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
DB 322 ECLKPPDSEDCEEQTRWHFDAQANNCLTFTFGCHHNLNHPETYEACMLACMSGPLATC 381
QY 78 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 127
DB 382 SLPALQGPCKAYVPRWAYNSQTGLCQSFYGGCEGNGNPFESREACEESC 431

RESULT 30
US-10-369-738-49
; Sequence 49, Application US/10369738
; Publication No. US20030180306A1

; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-738-49

Query Match 24.2%; Score 182.5; DB 14; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
DB 322 ECLKPPDSEDCEEQTRWHFDAQANNCLTFTFGCHHNLNHPETYEACMLACMSGPLATC 381
QY 78 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 127
DB 382 SLPALQGPCKAYVPRWAYNSQTGLCQSFYGGCEGNGNPFESREACEESC 431

RESULT 31
US-11-028-058-3
; Sequence 3, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-3

Query Match 24.2%; Score 182.5; DB 19; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
DB 322 ECLKPPDSEDCEEQTRWHFDAQANNCLTFTFGCHHNLNHPETYEACMLACMSGPLATC 381
QY 78 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 127
DB 382 SLPALQGPCKAYVPRWAYNSQTGLCQSFYGGCEGNGNPFESREACEESC 431

RESULT 32
US-11-028-058-49
; Sequence 49, Application US/11028058


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; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-49

Query Match      24.2%; Score 182.5; DB 19; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 47 OCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDLC 77
Db 322 ECLKPPDSDCGEQTRWHFDAQANCLTFTFGHCHHNLNHFYEAACMLACNSGLATC 381

Qy 78 SMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
Db 382 SLPALQGPCKAYVFRWAYNSQTGLCQSFYGGCGEGNNGNFSREACBESC 431

RESULT 33
US-10-807-204-7
; Sequence 7, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-7

Query Match      23.9%; Score 180; DB 16; Length 33;
Best Local Similarity 97.0%; Pred. No. 3.6e-10;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 99 TKICSEFIYGGCGGNNNNFQTEAICLVTCCKKYH 131
Db 1 TKICSEFIYGGCGGNNNNFQTEAICLVTCCKKYH 33

RESULT 34
US-10-807-204-10
; Sequence 10, Application US/10807204
; Publication No. US20040229312A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-10

Query Match      23.9%; Score 180; DB 16; Length 33;
Best Local Similarity 97.0%; Pred. No. 3.6e-10;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 99 TKICSEFIYGGCGGNNNNFQTEAICLVTCCKKYH 131
Db 1 TKICSEFIYGGCGGNNNNFQTEAICLVTCCKKYH 33

RESULT 35
US-10-038-722-5
; Sequence 5, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5

Query Match      23.5%; Score 177; DB 14; Length 58;
Best Local Similarity 56.4%; Pred. No. 1.2e-09;
Matches 31; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 73 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
Db 1 RPDFFLLPAETGPCRAMIPRFYNAKSGKCEPIYGGCGGNANFNKTEECRRTC 55

RESULT 36
US-09-896-095-147
; Sequence 147, Application US/09896095
```



```

; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-038-722-17

Query Match      23.0%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 3e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 128
Db 1 RPDFCQLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCMGNGNMFVTEKDCLOT 56

RESULT 49
US-10-038-722-18
; Sequence 18, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      23.0%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 3e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 128
Db 1 RPDFCQLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCMGNGNMFVTEKDCLOT 56
```

```

RESULT 50
US-10-038-722-19
; Sequence 19, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-038-722-19

Query Match      23.0%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 3e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 128
Db 1 RPDFCQLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCMGNGNMFVTEKDCLOT 56

Search completed: September 21, 2005, 16:45:51
Job time : 83.9233 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:21:48 ; Search time 18.9351 Seconds
(without alignments)
665.663 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 753
Sequence: 1 MGLSGLPILVPFILLGDIQ.....GNNNFQTEAICLVTCCKYH 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	24.7	110	1 TITTOR	basic proteinase i
2	184.5	24.5	1522	2 H88380	protein T22F7.3 [i
3	172.5	22.9	1599	2 T18210	hypothetical prote
4	172	22.8	67	1 TIBOC	trypsin inhibitor,
5	171	22.7	1416	2 E88550	protein ZC84.1 [im
6	171	22.7	2844	2 S28291	hypothetical prote
7	169.5	22.5	922	2 T23573	hypothetical prote
8	167.5	22.2	1474	2 D88550	protein ZC84.6 [im
9	161	21.4	62	2 A44180	taicatoxin serine
10	161	21.4	747	2 JH0773	Alzheimer's diseas
11	160	21.2	57	2 A59204	basic proteinase i
12	160	21.2	252	2 JG0185	hepatocyte growth
13	160	21.2	1743	2 T26859	hypothetical prote
14	157	20.8	58	1 TIRABK	isoinhibitor K (BP
15	157	20.8	111	2 S41082	amyloid precursor
16	157	20.8	337	1 TIFGBI	alpha-1-microglobu
17	157	20.8	751	2 A49974	beta-amyloid precu
18	157	20.8	763	2 A49321	amyloid beta (A4)
19	157	20.8	765	2 S42880	amyloid precursor-
20	155.5	20.7	2150	2 T32497	hypothetical prote
21	154	20.5	484	4 Q32761	hypothetical Alzhe
22	154	20.5	770	1 QRHUA4	Alzheimer's diseas
23	153	20.3	62	2 S19327	venom basic protei
24	152	20.2	62	2 S07451	proteinase inhibit
25	152	20.2	76	2 S06678	Alzheimer's diseas
26	152	20.2	76	2 S03607	Alzheimer's diseas
27	152	20.2	352	1 HCHU	alpha-1-microglobu
28	152	20.2	352	1 TIBOBI	alpha-1-microglobu
29	151	20.1	65	1 TIVIVC	venom basic protei

30	151	20.1	100	2 A32282	Alzheimer's diseas
31	149.5	19.9	62	2 S01802	chymotrypsin inhib
32	149.5	19.9	249	2 T32060	hypothetical prote
33	149.5	19.9	300	2 S12143	lipoprotein-associ
34	149.5	19.9	372	2 JC2556	alpha-1-microglobu
35	149	19.8	57	1 TIFHBP	proteinase inhibit
36	149	19.8	76	2 S04855	Alzheimer's diseas
37	149	19.8	123	2 A29652	inter-alpha-trypsi
38	148.5	19.7	62	2 S01803	chymotrypsin inhib
39	148	19.7	299	2 I46937	tissue factor path
40	147	19.5	125	1 TIBOBI	alpha-1-microglobu
41	146	19.4	100	1 TIBO	basic proteinase i
42	146	19.4	805	2 T34212	hypothetical prote
43	146	19.4	1558	2 C89114	hypothetical prote
44	146	19.4	2167	2 T34395	hypothetical prote
45	145.5	19.3	1043	2 T19734	uterine plasmin/tr
46	145	19.3	122	1 A55115	short epsilon-dend
47	144	19.1	57	2 B59399	venom basic protei
48	144	19.1	59	1 TIEPED	isoelectrophoretic
49	144	19.1	59	2 S00371	isoelectrophoretic
50	144	19.1	59	2 A59399	Long epsilon-dendr

ALIGNMENTS

RESULT 1

TITTOR

basic proteinase inhibitor - loggerhead

C:Species: Caretta caretta (loggerhead)

C>Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A01224

R:Kato, I.; Tominaga, N.

Fed. Proc. 38, 832, 1979

A:Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tand

A:Reference number: A01224

A:Accession: A01224

A:Molecule type: protein

A:Residues: 1-110 <KAT>

A:Cross-references: UNIPROT:P00993

C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inh

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:63-105/Domain: antileukoproteinase repeat homology <ALP>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8-58,17-41,33-54,67-93,76-97,80-92,86-101/disulfide bonds: #status predicted

F:18/inhibitory site: Lys (trypsin) #status predicted

Query Match 24.7%; Score 186; DB 1; Length 110;

Best Local Similarity 50.0%; Pred. No. 2.1e-09;

Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 73 RKDICSMPQEQAGPCPLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 128

Db 4 KRDCRLPEQGPCKGRIPRYFYNPASRMCSFIYGGCKGNKNFKTAECVRACR 59

RESULT 2

H88380

protein T22F7.3 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: H88380

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biologi

A:Reference number: A75000; MUID:99069613; PMID:9851916

A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg

A:Accession: H88380

A:Status: preliminary

A:Molecule type: DNA

493/1; 2555/1; 2720/1; 2739/3; 2819/1
F:220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>
F:343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F:442-495/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>
F:546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPI4>
F:654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI5>
F:1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BPI6>
F:1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BPI7>
F:1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BPI8>
F:1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>
F:2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BPI0>

Query Match 22.7%; Score 171; DB 2; Length 2844;
Best Local Similarity 30.4%; Pred. No. 5.8e-07;
Matches 35; Conservative 14; Mismatches 34; Indels 32; Gaps 3;

QY 37 KVECEV-----EEDQCTKPRDCPENMK-----CCPFCGKKCLDPR 73
DB 388 RHECEMYCARLQCEGSPURIGEEAQRCONNAQCPSSECKADQGVCCP-----RK 438

QY 74 KDICSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 128
DB 439 QTICAQPLRIGDCTENVKHYWYNARTQCOMFEYTGCGQGNNDNFDSDMCQNFCK 493

RESULT 7
T23573
hypothetical protein K10D3.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23573
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z15762
A:Accession: T23573
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-922 <WIL>
A:Cross-references: UNIPROT:Q21418; EMBL:Z75545; PIDN:CAA99886.1; GSPDB:GN00019; CESP:K1
A:Experimental source: clone K10D3
C:Genetics:
A:Gene: CESP:K10D3.4
A:Map position: 1
A:Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 22.5%; Score 169.5; DB 2; Length 922;
Best Local Similarity 31.9%; Pred. No. 3.1e-07;
Matches 45; Conservative 14; Mismatches 53; Indels 29; Gaps 7;

QY 11 VPFILGDIQEPGHARGILGKPCPKIKVCEV-----EEDQCTKPRDCPENMK----- 60
DB 328 IQFSYLG---QCGNFNFLSQDHCEKFCRILCSAGE---PLKSSGGRNMECSPTGSCA 381

QY 61 --CP--FSC-----GKKCLDFKDTCSMPQEGAGPCLASIPHWYNNKTKICSEFIY 107
DB 382 NSCPSTHSCSTSGSTTFGVCPCPRQYVCKLPREQNGCTYSNRWFWNAKTGNCBEFIY 441

QY 108 GCGCGNNNNFQTEAICLVTK 128
DB 442 SGCQGNANNFETYKCODEYCR 462

RESULT 8
D88550
protein ZC84.6 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D88550
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D88550
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1474 <STO>
A:Cross-references: UNIPROT:O62504; GB:chr_III; PIDN:CAA79570.1; PID:g3881447; GSPDB:GNO
C:Genetics:
A:Gene: ZC84.6
A:Map position: 3

Query Match 22.2%; Score 167.5; DB 2; Length 1474;
Best Local Similarity 27.1%; Pred. No. 6.8e-07;
Matches 38; Conservative 17; Mismatches 44; Indels 41; Gaps 5;

QY 12 PFILGDIQEPGHARGILGKPCPKIKVCEV-----EEDQCTKPRDCP 55
DB 369 PFTYLG---AGGNYNNFLS-----RIDCELYCARLQCDRGNPLRIGDVTQSCASNNDCP 419

QY 56 ENMK-----CCPFCGKKCLDFKDTCSMPQEGAGPCLASIPHWYNNKTKICSEFIY 108
DB 420 SSHECKMDQAVCCP-----RMQTICTQPLRVGNCDRSVRRYWYSAATRCOSFEYT 470

QY 109 GCGQGNNNFQTEAICLVTK 128
DB 471 GCGQGNNNFETLVDCQTECR 490

RESULT 9
A44180
taicotoxin serine proteinase inhibitor component - Australian taipan
C:Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44180
R:Possani, L.D.; Martin, B.M.; Yatani, A.; Mochca-Morales, J.; Zamudio, F.Z.; Gurrola, G
Toxicon 30, 1343-1364, 1992
A:Title: Isolation and physiological characterization of taicotoxin, a complex toxin wit
A:Reference number: A44180; MUID:93134601; PMID:1485334
A:Accession: A44180
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-62 <POS>
A:Cross-references: UNIPROT:Q7LZE4
A:Experimental source: subsp. scutellatus, venom
A:Note: sequence extracted from NCBI backbone (NCBIP:122482)
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 21.4%; Score 161; DB 2; Length 62;
Best Local Similarity 49.1%; Pred. No. 1.9e-07;
Matches 27; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 73 RKDICSMPQEGAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 127
DB 3 RPKFCHLPKPGFCRAAIPRFYFNPHSKQCEKFIYGGCHGNANKFTPDCENYTC 57

RESULT 10
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity
A;Reference number: A33260; MUID:8932030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M23270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Pirelli, F.; Levy, E.; van Duinen, S.G.; Bote, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PREL>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-770 <YOSI>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-530, 'QWLMPVAPFAWEAKVGR' <YOS>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 689-716, 'F', 718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijesman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
araki, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692, 'G', 694-718 <KAMI>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: Familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)

A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288, 'V', 365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756, 'S', 758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TANI>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Mulchaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponté, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Dr
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtot

Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.
Query Match 20.5%; Score 154; DB 1; Length 770;
Best Local Similarity 44.4%; Pred. No. 6e-06;
Matches 24; Conservative 8; Mismatches 22; Indels 0; Gaps 0;
Qy 74 KDICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
Db 288 REVCSQAETGFCRAMISRWFVDVTEGKCAFFYGGCGGNRRNFDTEYCMAVC 341
RESULT 23
S19327
venom basic proteinase inhibitor - leaf-nosed viper
N:Alternate names: trypsin inhibitor (kunitz-type)
C:Species: Eristocophis macmahoni (leaf-nosed viper)
C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S19327
R:Sididi, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A:Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf-
A:Reference number: S19327; MUID:92077130; PMID:1743283
A:Accession: S19327
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62 <SID>
A:Cross-references: UNIPROT:P24541
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor; venom
F:2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 20.3%; Score 153; DB 2; Length 62;
Best Local Similarity 51.0%; Pred. No. 9.5e-07;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
Qy 77 CSMPQEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
Db 2 CYLDDPQVCXKHIPFRFYNNPASNKCKNFIYGGCGGNANFETRAECRHTC 52
RESULT 24
S07451
Proteinase inhibitor 5.II - snake-locks sea anemone
C:Species: Anemonia sulcata (snake-locks sea anemone)
C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S07451; B27222
R:Wunderer, G.; Machleidt, W.; Fritz, H.

Meth. Enzymol. 80, 816-820, 1981
A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia su
A:Reference number: S07451
A:Accession: S07451
A:Molecule type: protein
A:Residues: 1-59 <WUN>
A:Cross-references: UNIPROT:P10280
A:Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R:Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A:Title: Isolierung und strukturaufklaerung eines haemolytisch aktiven peptide aus der se
A:Reference number: A94700
A:Accession: B27222
A:Molecule type: protein
A:Residues: 1-38, 'R', 40, 'BB', 45-48, 'ZZ', 51, 'Z', 53-62 <KRE>
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 20.2%; Score 152; DB 2; Length 62;
Best Local Similarity 49.0%; Pred. No. 1.2e-06;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
Qy 77 CSMPQEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
Db 5 CELPKVVGPCRARPPRYNNSSKRCBKFIYGGCGGNANFHTLECEKVC 55
RESULT 25
S06678
Alzheimer's disease amyloid beta protein - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S06678
R:Koo, E.H.; Sisodia, S.S.; Price, D.L.
submitted to the EMBL Data Library, July 1989
A:Reference number: S06678
A:Accession: S06678
A:Molecule type: mRNA
A:Residues: 1-76 <KOO>
A:Cross-references: UNIPROT:P29216; EMBL:X15985; NID:g38080; PIDN:CAA34116.1; PID:g93013;
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase in
C:Keywords: alternative splicing; serine proteinase inhibitor
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 20.2%; Score 152; DB 2; Length 76;
Best Local Similarity 45.3%; Pred. No. 1.4e-06;
Matches 24; Conservative 7; Mismatches 22; Indels 0; Gaps 0;
Qy 75 DICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
Db 1 EVCSEQAETGFCRAMISRWFVDVTEGKCAFFYGGCGGNRRNFDTEYCMAVC 53
RESULT 26
S03607
Alzheimer's disease amyloid A4 protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S03607
R:Kang, J.; Mueller-Hill, B.
Nucleic Acids Res. 17, 2130, 1989
A:Title: The sequence of the two extra exons in rat preA4.
A:Reference number: S03607; MUID:89183625; PMID:2648331
A:Accession: S03607
A:Molecule type: mRNA
A:Residues: 1-76 <KAN>
A:Cross-references: UNIPROT:P08592; EMBL:X14066; NID:g56957; PIDN:CAA32229.1; PID:g93026;
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase in
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 20.2%; Score 152; DB 2; Length 76;

Best Local Similarity 45.3%; Pred. No. 1.4e-06;
Matches 24; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 75 DICSMPOAGCLASIPHWYKTKICSBIYGCQGNNNFOTEAICLVTC 127
DQ 1 EVCSEQAGTGPCRAMISRWYFDVTGKCAPFFYGCQGNRNNFDTTEYCHAVC 53

RESULT 27
HCHU
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human
rich protein
A:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) pI
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; P90450; B39079; A61580; B253217
R:Vetr, H.; Gebhard, W.
Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
A:Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
A:Reference number: S13433; MUID:91214554; PMID:1708673
A:Accession: S13433
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <VET1>
A:Cross-references: UNIPROT:P02760; EMBL:X54816; NID:G24475; PIDN:CAA38585.1; PID:G82561
R:Diarras-Mehrpour, M.; Bourguignon, J.; Sesboue, R.; Salier, J.P.; Leveillard, T.; Mart
Eur. J. Biochem. 191, 131-139, 1990
A:Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene
A:Reference number: S10778; MUID:90336621; PMID:1696200
A:Accession: S10778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <DIA>
R:Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
Nucleic Acids Res. 14, 7839-7850, 1986
A:Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-
A:Reference number: A93642; MUID:87040757; PMID:2430261
A:Accession: A93642
A:Molecule type: mRNA
A:Residues: 1-352 <KAU>
A:Cross-references: GB:X04494; NID:G24478; PIDN:CAA28182.1; PID:G24479
R:Lopez Otin, C.; Grubb, A.O.; Mendez, E.
Arch. Biochem. Biophys. 228, 544-554, 1984
A:Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge
A:Reference number: A90074; MUID:84126849; PMID:6198962
A:Accession: A90074
A:Molecule type: protein
A:Residues: 20-56,58-202 <LOP>
A:Experimental source: individual with tubular proteinuria
A>Note: no evidence of sequence heterogeneity could be found, in spite of persistent het
R:Iakagi, T.; Iakagi, K.; Kawai, T.
Biochem. Biophys. Res. Commun. 98, 997-1001, 1981
A:Title: Complete amino acid sequence of human alpha--1-microglobulin.
A:Reference number: A90225; MUID:81184038; PMID:6164372
A:Accession: A90225
A:Molecule type: protein
A:Residues: 20-47;58-136,138-141,'T',143-144,146-198 <TAK>
A:Experimental source: pooled urine of patients with tubular proteinuria
R:Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempart, K.; Salier, J.P.
Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
A:Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in
A:Reference number: A90686; MUID:85225968; PMID:2408638
A:Accession: A90686
A:Molecule type: protein
A:Residues: 206-290,'Vt',293-342,'E',344-350 <REI>
R:Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueske, T.; Daudon, M.
Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
A:Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ca
A:Reference number: P90450; MUID:93221481; PMID:8466493
A:Accession: P90450
A:Molecule type: protein

A:Residues: 206-214,'X' <ATW1>
R:Englind, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.
J. Biol. Chem. 266, 747-751, 1991
A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot
A:Reference number: A39079; MUID:91093267; PMID:1898736
A:Accession: B39079
A:Molecule type: protein
A:Residues: 206-225 <ENGL>
R:Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
Int. J. Biochem. 23, 1201-1203, 1991
A:Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inhi:
A:Reference number: A61580; MUID:92175157; PMID:1794445
A:Accession: A61580
A:Molecule type: protein
A:Residues: 214,'X',216-222,'X' <CHI>
R:McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.
J. Biol. Chem. 261, 5378-5383, 1986
A:Title: Two apparent human endothelial cell growth factors from human hepatoma cells ar
A:Reference number: A92583; MUID:86168278; PMID:3007499
A:Accession: B25604
A:Molecule type: protein
A:Residues: 206-214,'X',216-230,'X',232-239,'X',241-248,'XX',251-252,'X',254 <MCK>
R:Englind, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
A:Reference number: A92736; MUID:89380192; PMID:2476436
A:Accession: C34245
A:Molecule type: protein
A:Residues: 206-225 <ENG2>
R:Traboni, C.; Cortese, R.
Nucleic Acids Res. 14, 6340, 1986
A:Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobul
A:Reference number: A25303; MUID:86312901; PMID:2428011
A:Accession: A25303
A:Molecule type: mRNA
A:Residues: 1-218,'HW' <TRA>
A>Note: this mRNA sequence appears to contain errors after residue 218
R:Calero, M.; Escribano, J.; Grubb, A.; Mendez, E.
J. Biol. Chem. 269, 384-389, 1994
A:Title: Location of a novel type of interpolyptide chain linkage in the human protein
A:Reference number: A53110; MUID:94103241; PMID:7506257
A:Accession: A53110
A:Molecule type: protein
A:Residues: 45-57 <CALI>
R:Vetr, H.; Koegler, M.; Gebhard, W.
FEBS Lett. 245, 137-140, 1989
A:Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inhi
A:Reference number: S03552; MUID:89171290; PMID:2466696
A:Accession: S03552
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 206-352 <VET2>
R:Malik, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fourne
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A:Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation
A:Reference number: S28928; MUID:93039735; PMID:1384548
A:Accession: S28930
A:Status: preliminary
A:Molecule type: protein
A:Residues: 206-215 <NAL>
R:Morelle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalek, C.; Fournet
Eur. J. Biochem. 221, 881-888, 1994
A:Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of int
A:Reference number: S43466; MUID:94229087; PMID:7513643
A:Accession: S43466
A:Status: preliminary
A:Molecule type: protein
A:Residues: 206-221 <MOR>
R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
Biochemistry 33, 7423-7429, 1994
A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable compl
A:Reference number: A53642; MUID:94271799; PMID:7516184
A:Accession: A53642

A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-217 <WIS>
R;Calero, M.; Mendez, E.; Garcia, E.
Biochim. Biophys. Acta 1249, 91-99, 1995
A;Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)
A;Reference number: S55688; MUID:95284116; PMID:7539295
A;Accession: S55688
A;Molecule type: protein
A;Residues: 20-24 <CHU2>
R;Bourguignon, J.; Diarra-Mehrpor, M.; Sesboue, R.; Frain, M.; Sala-Trepat, J.M.; Marti
Biochim. Biophys. Res. Commun. 131, 1146-1153, 1985
A;Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide se
A;Reference number: 152208; MUID:86025577; PMID:2413856
A;Accession: 152208
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 302-352 <BOU>
R;Cross-references: GB:M11562; NID:G186587; PIDN:AAA59194.1; PID:G307077
R;Wojcik, E.G.C.; van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Berti
Biochem. J. 311, 753-759, 1995
A;Title: Factor IX zuchphen: a Cys(18) -> Arg mutation results in formation of a heterodi
A;Reference number: S59509; MUID:96067589; PMID:7487929
A;Accession: S59509
A;Molecule type: protein
A;Residues: 27-35, 'Y', 37 <WOJ>
R;Atmani, F.; Mizon, J.; Khan, S.R.
Eur. J. Biochem. 236, 984-990, 1996
A;Title: Identification of uronic-acid-rich protein as urinary bikunin, the light chain
A;Reference number: S66434; MUID:96270753; PMID:8665922
A;Accession: S66434
A;Molecule type: protein
A;Residues: 206-214, 'X', 216-230 <ATW2>
R;Akerstroem, B.; Bratt, T.; Enghild, J.J.
FEBS Lett. 362, 50-54, 1995
A;Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect cel
A;Reference number: S68728; MUID:95212582; PMID:7535251
A;Accession: S68728
A;Molecule type: protein
A;Residues: 89-100 <AKE>
R;Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A;Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a no
A;Reference number: S02431; MUID:88167187; PMID:2450785
A;Accession: S02431
A;Molecule type: protein
A;Residues: 206-214, 'X', 216-217 <JES>
R;Lopez, C.; Grubb, A.; Mendez, E.
FEBS Lett. 144, 349-353, 1982
A;Title: Human protein HC displays variability in its carboxyl-terminal amino acid seque
A;Reference number: A91304
A;Contents: annotation; variant of alpha-1-microglobulin
A;Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys an
R;Hochstrasser, K.; Schonberger, O.L.; Rossmannith, I.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
by affinity chromatography.
A;Reference number: A91698; MUID:82074265; PMID:6171497
A;Contents: annotation; carbohydrate binding sites
R;Morii, M.; Travis, J.
Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
A;Title: The reactive site of human inter-alpha-trypsin inhibitor is in the amino-termi
A;Reference number: A90682; MUID:85225940; PMID:3890890
A;Contents: annotation; inhibitory site
A;Note: in vitro, the first twelve residues of the amino end of the inhibitor appear to
wn
C;Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolytically p
C;Comment: Alpha-1-microglobulin occurs in many physiological fluids including plasma, u
. It contains at least one brown-yellow chromophore.

Query Match 20.2%; Score 152; DB 1; Length 352;
Best Local Similarity 44.6%; Pred. No. 4.8e-06;
Matches 25; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

Qy 73 RKDICSMPQBPAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTK 128
Db 227 KEDSCQLGYSGPOMGNTSYFYNGTSMACETQYGGCGNGNNFVTEKSLQTCR 282

RESULT 28

TIBOBI

alpha-1-microglobulin / inter-alpha-trypsin inhibitor precursor [validated] - bovine
N;Alternate names: BI-14 (inhibitory fragment of ITI); bikunin; ITI
C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Feb-1995 #sequence revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: S68149; A91717; A90685; S31219; A01209
R;Lindqvist, A.; Akerstroem, B.
Biochim. Biophys. Acta 1306, 98-106, 1996
A;Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver c
A;Reference number: S68149; MUID:96201710; PMID:8611630
A;Accession: S68149
A;Molecule type: mRNA
A;Residues: 1-352 <LIN>
R;Cross-references: UNIPROT:P00978; EMBL:U35642; NID:G1016297; PIDN:AA807599.1; PID:G1016
Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A;Reference number: A91717; MUID:84133807; PMID:6199275
A;Accession: A91717
A;Molecule type: protein
A;Residues: 227-267, 'L', 269-273, 'Q', 275-297, 'AF', 300-329, 'Q', 331-345, 'R', 347-348 <HOC>
R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A;Reference number: A90685; MUID:85225967; PMID:2408637
A;Accession: A90685
A;Molecule type: protein
R;Residues: 347-349 <HOC2>
R;Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A;Reference number: A91718; MUID:84133808; PMID:6199276
A;Contents: annotation; reactive sites
R;Castillo, G.M.; Templeton, D.M.
FEBS Lett. 318, 292-296, 1993
A;Title: Subunit structure of bovine ESF (extracellular-matrix stabilizing factor(s)). A
A;Reference number: S31219; MUID:93178646; PMID:7680011
A;Accession: S31219
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-214, 'X', 216, 'X', 218-220 <CAS>
C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;35-188/Domain: lipocalin homology <LIP>
F;231-281/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;241/inhibitory site: Leu (chymotrypsin, elastase) #status experimental
F;250/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;297/inhibitory site: Arg (trypsin) #status experimental

Query Match 20.2%; Score 152; DB 1; Length 352;
Best Local Similarity 41.5%; Pred. No. 4.8e-06;
Matches 27; Conservative 9; Mismatches 27; Indels 2; Gaps 1;

Qy 66 GKXCLDFRK--DICSMPQBPAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAIC 123
Db 218 GQPVTFNFSKADSCQLDYSQGPCLGLFKRIFYNGTSMACETFLYGGCGNGNNFVTEKSLQTCR 277

Qy 124 LVTKC 128
Db 278 LQTCR 282

RESULT 29

TIVIVC

A.Accession: G13173
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-300 <WES>
A.Cross-references: EMBL:X54708; NID:G1612; PIDN:CAA38515.1; PID:G1613
R.Collabor: P.; Crabb, J.W.; Buonassisi, V.
J. Cell. Physiol. 148, 320-326, 1991
A.Title: Enhanced inhibition of tissue factor by the extended form of an endothelial-type proteinase inhibitor
A.Reference number: A61373; MUID:91349227; PMID:1880157
A.Accession: A61373
A.Molecule type: protein
A.Residues: 25-33, 'X', 35-46 <COL>
A.Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase
C.Keywords: anticoagulant; glycoprotein
F.50-100/Domain: animal Kunitz-type proteinase inhibitor homology <Bp1>
F.121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F.213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

C:Species: Bombyx mori (silkworm)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01803
R:Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3072972
A:Accession: S01803
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:CROSS-references: UNIPROT:P10832
C:Superfamily: basic proteinase inhibitor
C:Keywords: serine proteinase inhibitor
F:9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 19.7%; Score 148.5; DB 2; Length 62;
Best Local Similarity 52.6%; Pred. No. 2.3e-06;
Matches 30; Conservative 5; Mismatches 21; Indels 1; Gaps 1;
QY 74 KDICSM-PQ-AGPCLASIPHWYNNKTKICSEFYGGCGNNNFQTEAICLVTCCK 129
DB 6 KPICQAFGNSGPFAYIKLYNQTKKCEBFYGGCKGNDNRFTLAECQKCIK 62
RESULT 39
I46937
tissue factor pathway inhibitor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I46937
R:Belaouaj, A.; Kuppupswamy, M.N.; Birktoft, J.J.; Baja, S.P.
Thromb. Res. 69, 547-553, 1993
A:Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A:Reference number: I46937; MUID:93276427; PMID:8503123
A:Accession: I46937
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-239 <BEL>
C:CROSS-references: UNIPROT:P19761; GB:S61902; NID:G386015; PIDN:AAB26836.1; PID:G386016
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F:49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>
F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
Query Match 19.7%; Score 148; DB 2; Length 299;
Best Local Similarity 29.3%; Pred. No. 9.3e-06;
Matches 48; Conservative 21; Mismatches 51; Indels 44; Gaps 8;
QY 3 LSLGLPILV-----PFILLGDI-----QEPGHA-----EG-----ILGKP 32
DB 14 LLLGLVPAPVSSAAEDEFNTIDIKPLQKPTHTSFCAMKVDGPKRAVIKRPFFNLTQ 73
QY 33 CPK-IKVEE-----VEEDQCTK--PRDCPENMKCCPSCGKCKLDLFRKIDICSM-PQ-AG 84
DB 74 CBEFYGGCGENRNFESLECKEKCARDYPKMTKLTQKQK-----PDFCFLEEDPG 127
QY 85 PCLASIPHWYNNKTKICSEFYGGCGNNNFQTEAICLVTCCK 128
DB 128 ICRGYITRIFYNNQSKQCFERFYGGCLGLNLFESLECKNTCE 171
RESULT 40
TIHOBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
N:Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
C:Species: Equus caballus (domestic horse)
C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: A01210; A45653
R:Hochrassner, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A:Reference number: A90685; MUID:85225967; PMID:2408637
A:Accession: A01210

A:Molecule type: protein
A:Residues: 3-125 <HOC>
A:CROSS-references: UNIPROT:P04365
R:Veeraragavan, K.; Singh, K.; Wachter, E.; Hochrassner, K.
Biochem. Int. 26, 405-413, 1992
A:Title: Characterization of a trypsin inhibitor from equine urine.
A:Reference number: A45653; MUID:92328813; PMID:1627153
A:Accession: A45653
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12, 'E', 14-33 <VEE>
A:CROSS-references: PIDN:AAB22430.1; PID:G250858
A:Experimental source: urine
A:Note: sequence extracted from NCBI backbone (NCBI:P107966)
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis
first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
C:Comment: The amino acid at position P2' (19-Met) appears to determine the specificity
d elastase; those with leucine interact strongly.
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
F:17/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:73/Inhibitory site: Arg (trypsin) #status predicted
Query Match 19.5%; Score 147; DB 1; Length 125;
Best Local Similarity 42.9%; Pred. No. 5.6e-06;
Matches 24; Conservative 9; Mismatches 23; Indels 0; Gaps 0;
QY 73 RKDICSM-PQ-AGPCLASIPHWYNNKTKICSEFYGGCGNNNFQTEAICLVTCCK 128
DB 3 KEDSQDLHAQGPCLGMISRYFYNGTSMACETFYGGCLGNGNPNFASQKCLQTCR 58
RESULT 41
TIHO
basic proteinase inhibitor precursor - bovine
N:Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPTI; cationic kallik
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C:Accession: S00277; A30333; S10546; S02486; S28197; A90162; A92023; A90736; A90927; A34
R:Creighton, T.E.; Charles, I.G.
J. Mol. Biol. 194, 11-22, 1987
A:Title: Sequences of the genes and polypeptide precursors for two bovine protease inhib
A:Reference number: S00274; MUID:87283904; PMID:2441071
A:Accession: S00277
A:Molecule type: DNA; mRNA
A:Residues: 1-100 <CR2>
A:CROSS-references: UNIPROT:P00974; GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1;
R:Creighton, T.E.; Charles, I.G.
Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987
A:Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor
A:Reference number: A90926; MUID:88295740; PMID:2456884
A:Accession: A30333
A:Molecule type: DNA
A:Residues: 1-100 <CR3>
A:CROSS-references: GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1; PID:G162769
R:Kingston, I.B.; Anderson, S.
Biochem. J. 233, 443-450, 1986
A:Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic
A:Reference number: S10546; MUID:86158754; PMID:2420326
A:Accession: S10546
A:Molecule type: DNA
A:Residues: 34-37 <KIN>
R:Fioretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
Biol. Chem. Hoppe-Seyler 369(suppl.), 37-42, 1988
A:Title: Aprotinin-like isoinhibitors in bovine organs.
A:Reference number: S02485; MUID:89076531; PMID:2462435
A:Accession: S02486
A:Molecule type: protein
A:Residues: 36-93 <PIO>

Db 1446 VCDEAKDGPCTNFVTKYNNKADGTCNRFHYGGCGTNNRFDNEQCKAAACQNH 1500

RESULT 44

T34395

hypothetical protein C37C3.6b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T34395; T34394

R:Geisels, C.; Bradshaw, H. 1996

A:Submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid C37C3.

A:Reference number: Z21518

A:Accession: T34395

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-2167 <GBI>

A:Cross-references: UNIPROT:O76840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN000023; CESP:C37C3.6a

A:Experimental source: strain Bristol N2; clone C37C3

A:Accession: T34394

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-1555, 'SKF' <GE2>

A:Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN000023; CESP:C37C3.6a

A:Experimental source: strain Bristol N2; clone C37C3

C:Genetics:

A:Gene: CESP:C37C3.6b; CESP:C37C3.6a

A:Map position: 5

A:Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/

Query Match 19.4%; Score 146; DB 2; Length 2167;

Best Local Similarity 40.0%; Pred. No. 6.9e-05;

Matches 22; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

Qy 76 ICSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTKKY 130

Db 1446 VCDEAKDGPCTNFVTKYNNKADGTCNRFHYGGCGTNNRFDNEQCKAAACQNH 1500

RESULT 45

T19734

hypothetical protein C34F6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T19734

R:White, S.

A:Submitted to the EMBL Data Library, November 1996

A:Reference number: Z19171

A:Accession: T19734

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-1043 <WIL>

A:Cross-references: UNIPROT:O17644; EMBL:Z81479; PIDN:CAB03944.1; GSPDB:GN000028; CESP:C34F6

A:Experimental source: clone C34F6

C:Genetics:

A:Gene: CESP:C34F6.1

A:Map position: X

A:Introns: 17/3; 62/1; 129/3; 181/1; 292/1; 348/1; 404/1; 665/1; 769/1; 876/1; 977/3

Query Match 19.3%; Score 145.5; DB 2; Length 1043;

Best Local Similarity 25.6%; Pred. No. 4.2e-05;

Matches 34; Conservative 20; Mismatches 46; Indels 33; Gaps 4;

Qy 21 EPGHAEGL-----GKPCPKIKVECEVE-----IDCTKPRDC-----PE 56

Db 702 QKGNANNFLTEDCGLVCPVLPNCPCLSGEPILLSLQKEPVICGGEDTCRNGYCHVGGAPE 761

Qy 57 NNMCCPFSCGCKCLDFRKCICSNPQAGCLASIPHWYNNKTKICSEFIYGGCGNNNN 116

Db 762 TTNCCPGT-----RRPCDLPLEVGGQGVKLERWFFDGGIQMCRPFVYGMKGNNSN 812

Qy 117 FQTEAICLVTKCK 129

Db 813 FLTKQSCRQCKE 825

RESULT 46

A55115

uterine plasmin/trypsin inhibitor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A55115

R:Stallings-Mann, M.L.; Burke, M.G.; Trout, W.E.; Roberts, R.M.

J. Biol. Chem. 269, 24090-24094, 1994

A:Title: Purification, characterization, and cDNA cloning of a Kunitz-type proteinase in

A:Reference number: A55115; MUID:95014140; PMID:7929061

A:Accession: A55115

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-122 <STA>

A:Cross-references: UNIPROT:Q29100; GB:L14282; NID:G682652; PIDN:AAA62425.1; PID:G682653

A:Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Ar

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor

F:38-88/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 19.3%; Score 145; DB 1; Length 122;

Best Local Similarity 47.1%; Pred. No. 8.2e-06;

Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

Qy 77 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 127

Db 38 CREPPTGPCSAHFVRFYNNATGLCQSFYVGGCGKQNNFMDKECLHTC 88

RESULT 47

B59399

short epsilon-dendrotoxin His55, subunit - Dendroaspis angusticeps

C:Species: Dendroaspis angusticeps

C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004

C:Accession: B59399

R:Sigle, R.; Hackett, M.; Aird, S.D.

Toxicon 40, 297-308, 2002

A:Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis

A:Reference number: A59399

A:Accession: B59399

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-57 <AIR>

A:Cross-references: UNIPROT:Q7LZE3

A:Note: trypsin inhibitor; K+ channel antagonist

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

F:5-55/Disulfide bonds: #status experimental

F:14-38/Disulfide bonds: #status experimental

F:30-51/Disulfide bonds: #status experimental

Query Match 19.1%; Score 144; DB 2; Length 57;

Best Local Similarity 48.1%; Pred. No. 5.4e-06;

Matches 26; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

Qy 74 KDICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 127

Db 2 RTFKCLPAEPGPGKASIPAFYNNAAKKCQLFHYGGCKGNANRFSTIEKCRHAC 55

RESULT 48

TIEPED

venom basic proteinase inhibitor E - black mamba

C:Species: Dendroaspis polylepsis polylepsis (black mamba)

C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004

C:Accession: A01215

R:Joubert, F.J.; Strydom, D.J.

Eur. J. Biochem. 87, 191-198, 1978

A:Title: Snake venoms. The amino-acid sequence of trypsin inhibitor E of Dendroaspis pol

A:Reference number: A01215; MUID:78214615; PMID:668688

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OM protein - protein search, using sw model

Run on: September 21, 2005, 15:41:33 ; Search time 72.2625 Seconds
(without alignments)
928.315 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 753
Sequence: 1 MGLSGLPILVPFILLDIQ.....GNNNFQTEALVTCCKYH 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 50 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574	76.2	131	1 WFD6 HUMAN	Q9bgy6 homo sapien
2	526	69.9	137	2 Q9BDL0	Q9bd10 oryctolagus
3	467	62.0	133	1 EPII HUMAN	Q95925 homo sapien
4	467	62.0	143	2 O86TE9	Q86tp9 homo sapien
5	462	61.4	182	2 Q6IE19	Q6ie19 rattus norv
6	461	61.2	133	2 Q8HZ45	Q8nz45 papio papio
7	453	60.2	133	1 EPII MACMU	Q9bd11 macaca mula
8	398	52.9	134	1 EPII MOUSE	Q9da01 mus musculu
9	231	30.7	77	2 Q8HZ44	Q8hz44 papio hamad
10	217	28.8	241	1 WFD8 HUMAN	Q8tuo0 homo sapien
11	197	26.2	759	2 Q8IT91	Q8it91 ancylostoma
12	187	24.8	2772	2 Q9VAV4	Q9vav4 drosophila
13	187	24.8	2776	2 Q869A0	Q869a0 drosophila
14	187	24.8	2894	2 Q7KRX2	Q7krx2 drosophila
15	187	24.8	2898	2 Q868Z9	Q868z9 drosophila
16	186	24.7	110	1 IBP CARCR	P00993 caretta car
17	184.5	24.5	588	2 Q22685	Q22685 caenorhabdi
18	182.5	24.2	571	2 Q7TQN3	Q7tqn3 mus musculu
19	182	24.2	2419	2 Q7PXZ1	Q7pxz1 anopheles g
20	175	23.2	3198	2 Q9U8G8	Q9u8g8 manduca sex
21	174	23.1	515	2 Q6DRJ1	Q6drj1 brachydanio
22	173.5	23.0	576	2 Q8TEU8	Q8teu8 homo sapien
23	173.5	23.0	576	2 Q6UXZ9	Q6uxz9 homo sapien
24	173	23.0	587	2 Q6AX20	Q6ax20 xenopus lae
25	173	23.0	751	2 Q708Z0	Q708z0 xenopus lae
26	172.5	22.9	1599	2 Q00983	Q00983 caenorhabdi
27	172	22.8	67	1 IBPC BOVIN	P00976 bos taurus
28	172	22.8	516	2 Q7R363	Q7r363 brachydanio
29	172	22.8	750	2 Q6DUB6	Q6dub6 xenopus tro
30	171	22.7	1416	1 YN81 CAEEL	Q03610 caenorhabdi
31	170.5	22.6	122	1 BTIA_BOOMI	P83609 boophilus m

32	170	22.6	83	2 Q6ITB9	Q6itb9 pseudechia
33	169.5	22.5	342	2 Q7SZ46	Q7sz46 xenopus lae
34	169.5	22.5	922	2 Q21418	Q21418 caenorhabdi
35	169	22.4	83	2 Q6ITB5	Q6itb5 oxyuranus m
36	169	22.4	169	2 Q9N0X7	Q9n0x7 bos taurus
37	168	22.3	86	2 Q9GP15	Q9gp15 ixodes rici
38	167.5	22.2	1297	2 Q9N343	Q9n343 caenorhabdi
39	167.5	22.2	1474	2 Q62504	Q62504 caenorhabdi
40	167	22.2	80	2 Q8T387	Q8t387 araneus ven
41	167	22.2	83	2 Q6ITB4	Q6itb4 oxyuranus m
42	167	22.2	83	2 Q6ITB6	Q6itb6 oxyuranus s
43	167	22.2	90	2 Q6T6S5	Q6t6s5 bitis gabon
44	166.5	22.1	342	2 Q6P2V8	Q6p2v8 xenopus tro
45	166	22.0	83	2 Q90WAL	Q90wal pseudonaja
46	166	22.0	507	2 Q6I750	Q6i750 rattus norv
47	165.5	22.0	2174	2 Q9GQR0	Q9gqr0 drosophila
48	165	21.9	234	2 Q7YRQ8	Q7yrq8 bos taurus
49	165	21.9	283	2 Q6ZNI4	Q6zni4 homo sapien
50	165	21.9	507	1 SPT1_MOUSE	Q9r097 mus musculu

ALIGNMENTS

RESULT 1

ID	WFD6 HUMAN	STANDARD;	PRT;	131 AA.
AC	Q9BOY6; Q8NFV6;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	WAP four-disulfide core domain protein 6 precursor (Putative protease inhibitor WAP6).			
DE	Name=WPD6; Synonym=C20orf171, WAP6;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
EX	MEDLINE=2304654; PubMed=12206714; DOI=10.1042/BJ20020869;			
RA	Clauss A., Lilja H., Lundwall A.;			
RT	"A locus on human chromosome 20 contains several genes expressing protease inhibitor domains with homology to whey acidic protein.";			
RL	Biochem. J. 368:233-242(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
EX	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Begguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle E., Hunt A.R., Hunt S.E., Jekesch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvaesalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA	Marsh V.L., Martin S.L., McConachie L.J., McLaughlin K., McMurray A.A.,			
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,			
RA	Phillimore B.U.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,			
RA	Skuce C.D., Smith M.B., Soderlund C., Steward C.A., Sulston J.E.,			
RA	Swann R.M., Symamore N., Taylor M., Tee L., Thomas D.W., Thorpe A.,			
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,			
RA	Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,			
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			
RA	Rogers J.;			


```
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BQY6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9BOY6-2; Sequence=VSP_007550, VSP_007551;
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels
CC are found in epididymis, testis and trachea.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AF411861; AAN03684.1; -.
CC EMBL; AL031663; CAC36264.1; -.
CC HSSP; P02760; 1BIK.
CC Genew; HGNC:16164; WFDC6.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP_Inh_Kunz-BPTI; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 1.
CC PRINTS; PR00759; BASICTPASE.
CC PROSITE; PS00222; Prot_Inh_Kunz-m; 1.
CC PROSITE; PS00222; Prot_Inh_Kunz-m; 1.
CC SMART; SM00131; KU; 1.
CC SMART; SM00217; WAP; 1.
CC PROSITE; PS00317; 4_DISULFIDE_CORE; FALSE NEG.
CC PROSITE; PS00280; BPTI_KUNITZ_1; FALSE NEG.
CC PROSITE; PS0279; BPTI_KUNITZ_2; 1.
CC KW Alternative splicing; Serine protease inhibitor; Signal.
CC SIGNAL 1 25 Potential.
CC CHAIN 26 131 WAP four-disulfide core domain protein 6.
CC DOMAIN 31 69 WAP.
CC DOMAIN 70 128 BPTI/Kunitz inhibitor.
CC DISULFID 33 61 By similarity.
CC DISULFID 48 60 By similarity.
CC DISULFID 54 69 By similarity.
CC VARSPLIC 75 86 IYAVCHRRLLAPA -> VSLTYHKEELE (in isoform
CC 2).
CC FT FTID=VSP_007550.
CC FT Missing (in isoform 2).
CC FT /FTID=VSP_007551.
CC VARSPLIC 87 131
CC SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;

Query Match 76.2%; Score 574; DB 1; Length 131;
Best Local Similarity 82.4%; Pred. NO. 4.1e-47;
Matches 108; Conservative 1; Mismatches 22; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQPGHAEGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQPGHAEGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
QY 61 CPFGSGKKCLDFRKIDCSMPQEGAPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTE 120
Db 61 CPFGSGKKCLDFRKIDCSMPQEGAPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTE 120
QY 121 AICLVTCCKYH 131
Db 121 AICLVTCCKYH 131

RESULT 2
Q9BDL0 PRELIMINARY; PRT; 137 AA.
ID Q9BDL0
AC Q9BDL0;
```

```
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of mouse Eppin and a gene cluster of similar
RT protease inhibitors on mouse chromosome 2.";
RL Gene 312:125-134(2003).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF346415; AAK31337.1; -.
DR HSSP; Q16019; 1AAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICTPASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;

Query Match 69.9%; Score 526; DB 2; Length 137;
Best Local Similarity 71.1%; Pred. No. 1.6e-42;
Matches 91; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQPGHAEGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MRLSRLLPILLPILLGDIQPGHAEGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
QY 61 CPFGSGKKCLDFRKIDCSMPQEGAPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTE 120
Db 61 CLFNGCGKKCLDRKVCMPKETGPGCLAFIPRWYDKERICTEFYGGCGNNNNFQTE 120
QY 121 AICLVTCCK 128
Db 121 AICLVTCCK 128

RESULT 3
EPPI_HUMAN STANDARD; PRT; 133 AA.
ID EPPI_HUMAN
AC O95925; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Spididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
DE domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINLW1; Synonyms=WAP7, WFDC7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epididymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French F.S., O'Rand M.G.;
RT "Cloning and sequencing of human Eppin: a novel family of protease
```


RT inhibitors expressed in the epididymis and testis.";

RL Gene 270:93-102(2001).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RA Stavrides G.S., Huckle E.J., Deloukas P.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

RA Deloukas P., Matthews L.H., Aehurst J.L., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.R., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Koights A., Laird G.K., Lawlor S., Levaeslhalo M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;

RT "The DNA sequence and comparative analysis of human chromosome 20.";

RL Nature 414:865-871(2001).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullány S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=O95925-1; Sequence=Displayed;

CC Name=2;

CC IsoId=O95925-2; Sequence=VSP_006755;

CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -!- SIMILARITY: Contains 1 WAP-type domain.

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CC -----

CC EMBL; AF286370; AAC00548.1; -

CC EMBL; AF286369; AAC00547.1; -

CC EMBL; AF286368; AAC00546.1; -

CC EMBL; AL118493; CAB56343.1; -

CC EMBL; AL031663; CAB37635.1; -

CC EMBL; AL031663; CAB37635.1; -

CC EMBL; BC053369; AAC53389.1; -

CC HSSP; P00974; 1BPI.

CC Genew; HGNC:15932; SPINLW1.

CC InterPro; IPR002223; Prot_Inh_Kunz-m.

CC InterPro; IPR008197; WAP.

CC Pfam; PF00014; Kunitz_BPTI; 1.

CC Pfam; PF00095; WAP; 1.

CC PRINTS; PR00003; 4DISULPHORE.

CC PRINTS; PR00759; BASICPTASE.

CC ProDom; PD000222; Prot_Inh_Kunz-m; 1.

CC SMART; SM00131; KU; 1.

CC SMART; SM00217; WAP; 1.

CC PROSITE; PS00317; 4_DISULFIDE_CORE; 1.

CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.

CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.

CC KW Alternative splicing; Serine protease inhibitor; Signal.

CC SIGNAL 1 21 Potential.

CC CHAIN 22 133 Eppin.

CC DOMAIN 29 73 WAP.

CC DISULFID 33 61 BPTI/Kunitz inhibitor.

CC DISULFID 40 65 By similarity.

CC DISULFID 48 65 By similarity.

CC DISULFID 54 69 By similarity.

CC DISULFID 77 127 By similarity.

CC DISULFID 86 110 By similarity.

CC DISULFID 102 123 By similarity.

CC VARSPLIC 1 31

CC SEQUENCE 133 AA; 15284 MW; F7831B20336ED9DC CRC64;

CC /FTId=VSP_006755.

CC GCKTALSUG (in isoform 2).

CC MGSSGLLSLLVLLVLLANVQGPGLTDLWLPFR -> MLSKAH

CC -----

CC Query Match 62.0%; Score 467; DB 1; Length 133;

CC Best Local Similarity 60.9%; Pred. No. 6.8e-37;

CC Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

CC

CC QY 1 MGLSGLLPILVPPILLGDIQEPGHAEGILGKPCPKIYCEVEEIDQCTKPRDCPENMKC 60

CC Db 1 MGSSGLLSLLVLLVLLANVQGPGLTDLWLPFRRCCKIRECECFQERDVCTKQCCDNKKC 60

CC QY 61 CPFGCGKCLDPKDKICSMPOBAGCLASIPHWYNNKTKICSEFIYGCQCGNNNNFQTE 120

CC Db 61 CVFGCGKCLDQKQDVCEMPKGTGCLAYFLHWYDKDKONTCSMFYGGCGQNNNNFQSK 120

CC QY 121 AICLVTK 128

CC Db 121 ANCLNTCK 128

CC

CC RESULT 4

CC Q86TP9 PRELIMINARY; PRT; 143 AA.

CC AC Q86TP9;

CC DT 01-JUN-2003 (TrEMBLrel. 24, Created)

CC DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

CC DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

CC DE SPINLW1 protein (Fragment).

CC GN Name=SPINLW1;

CC OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Stachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strauberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH44829.1; -.
DR HSSP; P00974; IUUA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
FT NON-TER 1
SQ SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;

Query Match 62.0%; Score 467; DB 2; Length 143;
Best Local Similarity 60.9%; Pred. No. 7,3e-37;
Matches 78; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

Oy 1 MGLSGLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
Db 11 MGSSGLLSLVFLVLANVPGGLTDLFPRRCPIKEECFQSRDVCVKDQODNKKC 70

Oy 61 CPFGCGKCLDFKDCISMPQEGAGCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTE 120
Db 71 CVFSGCKKLDLQDVCSEMPKETGCLAYFLHWYDKDNTCSMFVYGGCGGNNNFQSK 130

Oy 121 AICLVTK 128
Db 131 ANCLNTCK 138

RESULT 5
O6IE19 PRELIMINARY; PRT; 182 AA.
AC O6IE19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

```
DE WAP four-disulfide core 6-like 1.
GN Name=wfdc61;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA PubMed=15060002; DOI=10.1101/gr.1946304;
RA Puente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors."
RL Genome Res. 14:609-622 (2004).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000374; CAB51900.1; -.
DR HSSP; P00974; 1K6U.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EB12D7BFF756707E CRC64;

Query Match 61.4%; Score 462; DB 2; Length 182;
Best Local Similarity 58.3%; Pred. No. 2.8e-36;
Matches 74; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

Oy 5 GLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKCPFS 64
Db 5 GLLPFLVPLIFLWSIQKPLQGLFKTCPKYIKCDFEERSQCSRHKQCKQRCMFA 64

Oy 65 CGKCKLDFKDCISMPQEGAGCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICL 124
Db 65 CGKCKLDELNEDICSLPQDAGFCLAYLPRWYNNKTNLCTQFIYGGCGGNTNNFLSKDICT 124

Oy 125 VTCKKYH 131
Db 125 SICTRKH 131

RESULT 6
O8HZ45 PRELIMINARY; PRT; 133 AA.
AC O8HZ45;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epididymal protease inhibitor 1.
GN Name=Eppin;
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sivashanmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY141973; AAN08507.1; -.
DR HSSP; P00974; IUUA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
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DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 133 AA; 15277 MW; B33AE57ECBBE84 CRC64;

Query Match 61.2%; Score 461; DB 2; Length 133;
Best Local Similarity 60.9%; Pred. No. 2.6e-36;
Matches 78; Conservative 15; Mismatches 35; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
DB 1 MGSSGLLSLLVLFILLVNVQFGLTDLWLPFRRCPTIRECEFRERDVCTRHRCQPDNKKC 60
QY 61 CFFSGCKKCLDPRKDCISMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTE 120
DB 61 CVFSGCKKCLDKQDVCENPNETGCLAFFIRWYDKNNYCTSTFYGGCGQNNNNFQSE 120
QY 121 AICLVTK 128
DB 121 ANCLNTCK 128

RESULT 7
EPPIN_MACMU
ID EPPIN_MACMU STANDARD; PRT; 133 AA.
AC Q9DA01;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epilidymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=SPINLW1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epilidymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epilidymis and testis."
CC -1- SUBCELLULAR LOCATION: Secreted (potential).
CC -1- TISSUE SPECIFICITY: Expressed in epilidymis and testis.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AF346414; AAK31336.1; -.
CC HSSP; P00974; 1BPI.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.

DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 133 AA; 15277 MW; 433AE946E39A35E9 CRC64;

Query Match 60.2%; Score 453; DB 1; Length 133;
Best Local Similarity 60.2%; Pred. No. 1.5e-35;
Matches 77; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
DB 1 MGSSGLLSLLVLFILLVNVQFGLTDLWLPFRRCPTIRECEFRERDVCTRHRCQPDNKKC 60
QY 61 CFFSGCKKCLDPRKDCISMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTE 120
DB 61 CVFSGCKKCLDKQDVCENPNETGCLAFFIRWYDKNNYCTSTFYGGCGQNNNNFQSE 120
QY 121 AICLVTK 128
DB 121 ANCLNTCK 128

RESULT 8
EPPIN_MOUSE
ID EPPIN_MOUSE STANDARD; PRT; 134 AA.
AC Q9DA01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epilidymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=Spinlwl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Epilidymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epilidymis and testis."
CC -1- SUBCELLULAR LOCATION: Secreted (potential).
CC -1- TISSUE SPECIFICITY: Expressed in epilidymis and testis.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AF346414; AAK31336.1; -.
CC HSSP; P00974; 1BPI.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
```


RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Saitana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vitaro D., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayaishizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Caeavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC -----
DR EMBL; AF346413; AAK31335.1; -;
DR EMBL; AK006296; BAK24514.1; -;
DR EMBL; BC048637; AAK48637.1; -;
DR HSSP; P31713; 1SHP.
DR MGP; MGI:1922776; Spin1w1.
DR GO; GO:0001669; C:acrosome; IDA.
DR GO; GO:0005737; C:cycloplasm; IDA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS02080; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.

FT CHAIN 22 134 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 134 AA; 15470 MW; DFFEB63D4D4C427F CRC64;
Query Match 52.9%; Score 398; DB 1; Length 134;
Best Local Similarity 51.9%; Pred. No. 2.7e-30;
Matches 67; Conservative 25; Mismatches 37; Indels 0; Gaps 0;
Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
Db 1 MKLSGFVSIILVFLGLLARVQGPSLADLLFPRCPRPREECEHQRDLCTDRDCPKKCKC 60
Qy 61 CPFSCGKCKLDPRKIDICSMQEOEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTE 120
Db 61 CVFNCGKKCLNPQODICSLPKDSGYCMAYFRWFWFNKENSTQVFIYGGCGNNNNFQSQ 120
Qy 121 AICLVTCCK 129
Db 121 SICVACEK 129
RESULT 9
ID Q8HZ44 PRELIMINARY; PRT; 77 AA.
AC Q8HZ44;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epididymal protease inhibitor 2.
GN Name=Eppin;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sivashanmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY141975; AAN08509.1; -;
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
KW Protease.
SQ SEQUENCE 77 AA; 8787 MW; B86E5868C57CEBD0 CRC64;
Query Match 30.7%; Score 231; DB 2; Length 77;
Best Local Similarity 55.4%; Pred. No. 1.4e-14;
Matches 41; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
Db 1 MGSSGLLSLIVFILLANVQGPSGLTDLWLFPRCPRTREECEFRDRVCTRHRQCNDKCK 60
Qy 61 CPFSCGKCKLDPRK 74
Db 61 CVFSCGKCKLDLQK 74
RESULT 10
WFD8 HUMAN
ID _WFD8_HUMAN STANDARD; PRT; 241 AA.

AC Q81UA0; Q96A34;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE WAP four-disulfide core domain protein 8 precursor (Putative protease
 DE inhibitor WAP8).
 GN Name=WAP8; Synonym=C20orf170, WAP8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
 RA Claus A., Lilja H., Lundwall A.;
 RT "A locus on human chromosome 20 contains several genes expressing
 RT protease inhibitor domains with homology to whey acidic protein.";
 RL Biochem. J. 368:233-242 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA Deloukas P., Matthews L.H., Aghvaret J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaeslano M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showken R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed ubiquitously, the highest levels are
 CC found in the epididymis followed by testis and trachea.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -1- SIMILARITY: Contains 3 WAP-type domains.
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 CC EMBL; AF492015; AN70997.1; -;
 CC EMBL; AF492016; AN70998.1; -;
 CC EMBL; AL031663; CAB37634.2; -;
 CC EMBL; AL591715; CAB39449.1; -;
 CC HSSP; P31713; 1SHP.
 CC Genew; HGNC:16163; WPC8.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR InterPro; IPR008197; WAP.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF00095; WAP; 3.
 DR PRINTS; PR00003; 4DISULPHORE.

DR PRINTS; PR00759; BASICPTASE.
 DR PRODOM; ED000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR SMART; SM00217; WAP; 3.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; 3.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Repeat; Serine protease inhibitor; Signal.
 FT SIGNAL 1 38 Potential.
 FT CHAIN 39 241 WAP four-disulfide core domain protein 8.
 FT DOMAIN 47 90 WAP 1.
 FT DOMAIN 95 145 BPTI/Kunitz inhibitor.
 FT DOMAIN 150 193 WAP 2.
 FT DOMAIN 197 239 WAP 3.
 FT DISULFID 51 79 By similarity.
 FT DISULFID 58 83 By similarity.
 FT DISULFID 66 78 By similarity.
 FT DISULFID 95 145 By similarity.
 FT DISULFID 104 128 By similarity.
 FT DISULFID 120 141 By similarity.
 FT DISULFID 72 87 By similarity.
 FT DISULFID 154 182 By similarity.
 FT DISULFID 165 186 By similarity.
 FT DISULFID 169 181 By similarity.
 FT DISULFID 175 190 By similarity.
 FT DISULFID 201 229 By similarity.
 FT DISULFID 208 232 By similarity.
 FT DISULFID 216 228 By similarity.
 FT DISULFID 222 236 By similarity.
 SQ SEQUENCE 241 AA; 27797 MW; 2566B54AF4BDC57B CRC64;
 Query Match 28.8%; Score 217; DB 1; Length 241;
 Best Local Similarity 38.5%; Pred. No. 9.3e-13;
 Matches 40; Conservative 13; Mismatches 47; Indels 4; Gaps 1;
 QY 24 HAEGTLGKPCPKIKVECEVEIIDCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPOEA 83
 DB 46 HKPGL-----CPKRLTCTTELPDSCNTDFDCKEYQKCCFFACQKCKMDPFQSPCLPVHR 101
 QY 84 GPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
 DB 102 GNCNHEAQRWHDFFQNYVCTPFKYRGCGGNANFLSEDACTAC 145
 RESULT 11
 Q81T91 PRELIMINARY; PRT; 759 AA.
 ID Q81T91
 AC Q81T91; 01-WAR-2003 (TREMBlrel. 23, Created)
 DT 01-WAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Kunitz-like protease inhibitor precursor.
 OS Ancylostoma caninum (Dog hookworm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Ancylostomatidae; Ancylostomatidae; Ancylostominae; Ancylostoma.
 OX NCBI_TaxID=29170;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Baltimore;
 RX MEDLINE=22645137; PubMed=12760667;
 RA Hawdon J.M., Datu B., Crowell M.;
 RT "Molecular cloning of a novel multidomain Kunitz-type proteinase
 RT inhibitor from the hookworm Ancylostoma caninum.";
 RL J. Parasitol. 89:402-407 (2003).
 CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
 CC EMBL; AF533590; AAN10061.1; -;
 CC HSSP; P31713; 1SHP.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 12.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00131; KU; 12.

DR PROSITE; PS50835; IG_Like; 3.
DR PROSITE; PS50900; PLAC; 1.

RN
[2]
Science 267:2185-2193 (2000).


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KW Matrix protein.
SQ SEQUENCE 2898 AA; 313250 MW; 2F992742F2D64A00 CRC64;

Query Match      24.8%; Score 187; DB 2; Length 2898;
Best Local Similarity 33.3%; Pred. No. 7.7e-09;
Matches 38; Conservative 13; Mismatches 33; Indels 30; Gaps 5;

QY 46 DOCTPR-----DCPENM-----KCCPF--SCG-----KKCLD-----FRKD 75
1788 DRCLPQKQDCEKSLAKWHFSESEKRCVFFYSGGKNNKNNFPTLESCEHCPRQVAKD 1847

QY 76 ICSMPQAGPCLASIPHWYKTKICSEFIYGGCGNNNNFQTEAICLVTCCK 129
1848 ICEIPAEGECANYTSTYDTQDACRFYGGCGNNENRFPTEESCLARCDR 1901

RESULT 16
ID IBP_CARCR STANDARD; PRT; 110 AA.
AC P00993;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chelonianin (basic protease inhibitor) (RPL1).
OS Carretta caretta (loggerhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Cheloniaidea; Cheloniidae; Carretta.
OX NCBI_TaxID=8467;
RN [1]
RC TISSUE=Egg white;
RA Kato I., Tomimaga N.;
RT "Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of
RT two tandem domains -- one Kunitz -- one of a new family.";
RL Fed. Proc. 38:832-832(1979)
CC -!- FUNCTION: The first domain inhibits trypsin; the second one
CC inhibits subtilisin.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC -!- CAUTION: As the paper only indicates the species as "red sea
CC turtle", the species indicated here is therefore an inference.
CC PIR; A01224; TITROR.
DR HSSP; P00974; 1K09.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP_BPTI; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Pyrrolidone carboxylic acid;
KW Serine protease inhibitor.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DOMAIN 8 58 BPTI/Kunitz inhibitor.
FT SITE 63 105 WAP.
FT SITE 18 19 Reactive bond for trypsin.
FT DISULFID 8 58 By similarity.
FT DISULFID 17 41 By similarity.
FT DISULFID 33 54 By similarity.
FT DISULFID 67 92 By similarity.
FT DISULFID 76 97 By similarity.
FT DISULFID 80 93 By similarity.
FT DISULFID 86 101 By similarity.
SQ SEQUENCE 110 AA; 269436243813418E CRC64;

Query Match      24.7%; Score 186; DB 1; Length 110;
Best Local Similarity 50.0%; Pred. No. 3.9e-10;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 73 RKDICSMPQAGPCLASIPHWYKTKICSEFIYGGCGNNNNFQTEAICLVTCCK 128
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DB 4 KRDCRLPPEQGPCCKGRIPRYFYPASRMCESEFIYGGCKGNKNNFKTKAECURACR 59

RESULT 17
QY 22685 PRELIMINARY; PRT; 988 AA.
ID Q22685
AC Q22685;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein T22F7.3.
GN Name=T22F7.3; ORFNames=T22F7.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Macri C.;
RT "The sequence of C. elegans cosmid T22F7.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR EMBL; U13071; AAL65793.1; -.
DR HSSP; P10646; 1ADZ.
DR InterAct; Q22685; -.
DR WormBase; WBGene00020702; T22F7.3.
DR WormPep; T22F7.3; CE30304.
DR CO; G01004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 1.
DR Pfam; PF00014; Kunitz_BPTI; 5.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 5.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WR1; 8.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 5.
KW Hypothetical protein.
SQ SEQUENCE 988 AA; 108702 MW; 6F62DAFB898C306B CRC64;

Query Match      24.5%; Score 184.5; DB 2; Length 988;
Best Local Similarity 34.3%; Pred. No. 4.7e-09;
Matches 35; Conservative 14; Mismatches 44; Indels 9; Gaps 2;

QY 37 KVECE-----VERIDQCTKPRDPENMKCCPFCGCKKCLDFRKDICSMPQAGPCLAS 89
402 KLVCEGNGNPLRIGEEWQRCETNADCPSSHSC--QGSCHKVCCPTAQSCLCTQPKRLGDSCTSA 459

QY 90 IPHWYKTKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 131
460 VRRYTNATRSCEMFQYTGCGQNNNNFTLMACQOKCRGIH 501
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Name=agCG49342; ORFNames=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008987; EAA01339.1; -.
DR HSSP; P10646; IIRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP_1; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS50092; TSPI; 5.
DR NON_TER
FT NON_TER
SQ SEQUENCE 2419 AA; 260249 MW; 58B078660983C946 CRC64;

Query Match 24.2%; Score 182; DB 2; Length 2419;
Best Local Similarity 33.8%; Pred. No. 1.9e-08;
Matches 35; Conservative 12; Mismatches 32; Indels 29; Gaps 3;

Qy 47 QCTKP-----KCCPF-----SCGKCLDFKIDIC 77
Dy 322 ECLPPDSEDCGEQTRWHFDAQNNCLTFTFGCHHNLNHFYEACMLACMSGPLATC 381
Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGCOCGNNNNFOTEICLVTC 127
Dy 382 SLPALQGFCKAYVPRWYNSQTGLCQSFVYGCCEGNGNFSREACBESC 431

RESULT 19
Q7PXZ1
ID Q7PXZ1 PRELIMINARY; PRT; 2419 AA.
AC Q7PXZ1.
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP12609 (Fragment).

Name=agCG49342; ORFNames=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008987; EAA01339.1; -.
DR HSSP; P10646; IIRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP_1; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS50092; TSPI; 5.
DR NON_TER
FT NON_TER
SQ SEQUENCE 2419 AA; 260249 MW; 58B078660983C946 CRC64;

Query Match 24.2%; Score 182.5; DB 2; Length 571;
Best Local Similarity 31.8%; Pred. No. 4.3e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCEPNM-----KCCPF-----SCGKCLDFKIDIC 77
Dy 322 ECLPPDSEDCGEQTRWHFDAQNNCLTFTFGCHHNLNHFYEACMLACMSGPLATC 381
Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGCOCGNNNNFOTEICLVTC 127
Dy 382 SLPALQGFCKAYVPRWYNSQTGLCQSFVYGCCEGNGNFSREACBESC 431

RESULT 19
Q7PXZ1
ID Q7PXZ1 PRELIMINARY; PRT; 2419 AA.
AC Q7PXZ1.
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP12609 (Fragment).

Name=agCG49342; ORFNames=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008987; EAA01339.1; -.
DR HSSP; P10646; IIRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP_1; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS50092; TSPI; 5.
DR NON_TER
FT NON_TER
SQ SEQUENCE 2419 AA; 260249 MW; 58B078660983C946 CRC64;

Query Match 24.2%; Score 182; DB 2; Length 2419;
Best Local Similarity 33.9%; Pred. No. 1.9e-08;
Matches 39; Conservative 12; Mismatches 32; Indels 32; Gaps 4;

Qy 46 DQCTKPR-----DCPENKCKCFSCG-----KKC-----LDPRK 74
Dy 1515 DVCHLPKISGFCPTHYNNMYDYAERNM-CAQFTYGGCLGNANRFESQEECKALCSVDDSK 1573
Qy 75 DICSMPOEAGPCLASIPHWYNNKTKICSEFIYGCOCGNNNNFOTEICLVTC 129
Dy 1574 PCQEPNEAGPCNGTFFERWYDKETDACHPFYGGCKGNKNYPTASCGYHCKK 1628

RESULT 20
Q9U8G8
ID Q9U8G8 PRELIMINARY; PRT; 3198 AA.
AC Q9U8G8.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lacunin precursor.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99457716; Pubmed=10528409; DOI=10.1016/S0965-1748(99)00064-8;
RA Nardi J.B., Martos R., Waiden K.K., Lampe D.J., Robertson H.M.;
RT "Expression of lacunin, a large multidomain extracellular matrix
RT protein, accompanies morphogenesis of epithelial monolayers in Manduca
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RESULT 21
Q6DRJ1
ID ID PRELIMINARY; PR7; 515 AA.
AC Q6DRJ1;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Serine protease inhibitor HGFAI.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15256591; DOI=10.1073/pnas.0403929101;
RA Amsterdam A.; Nissen R.M.; Sun Z.; Swindell E.C.; Farrington S.,
RA Hopkins N.;
RT "Identification of 315 genes essential for early zebrafish
RL development.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004).

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RESULT 22


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GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002350; Prot_inh_kazal.
DR InterPro; IPR011497; Prot_inh_kazal_2.
DR InterPro; IPR002223; Prot_inh_kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR Pfam; PF000409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
DR PROTEASE.
KW
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Query Match 23.0%; Score 173.5; DB 2; Length 576;
Best Local Similarity 31.8%; Pred. No. 3.1e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
Db 327 ECLPPDSEDCGEOTRWHFDAQANNCLTFTFGHCHRNLNHFYEAACMLACMSGPLAAC 386

Qy 78 SMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 127
Db 387 SLPALQGPCKAYAPRWAYNSQTGCQSFYGGCEGNGNFESREACEESC 436

RESULT 23
Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bikunin hlg.
GN ORFNames=UNQ9235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
PL Genome Res. 13:2265-2270(2003).
CC -i- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAQ88509.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
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DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002223; Prot_inh_kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
DR SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match 23.0%; Score 173.5; DB 2; Length 576;
Best Local Similarity 31.8%; Pred. No. 3.1e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
Db 327 ECLPPDSEDCGEOTRWHFDAQANNCLTFTFGHCHRNLNHFYEAACMLACMSGPLAAC 386

Qy 78 SMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 127
Db 387 SLPALQGPCKAYAPRWAYNSQTGCQSFYGGCEGNGNFESREACEESC 436

RESULT 24
Q6AX20 PRELIMINARY; PRT; 587 AA.
AC Q6AX20
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Alp2 A protein.
GN Name=alp2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC079801; AAH79801.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR ProDom; PD000222; Prot_Inh_Kunz-m.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 587 AA; 66870 MW; 7DF224C2138B94BF CRC64;

Query Match 23.0%; Score 173; DB 2; Length 587;
Best Local Similarity 46.0%; Pred. No. 3.5e-08;
Matches 29; Conservative 8; Mismatches 26; Indels 0; Gaps 0;

QY 66 GKCLDFRDKICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLV 125
DB 273 GKDITDVKSVCSEAITGPRAMPWRYFNLGQKCKFRFYGGCGGNRNFESEDYCMA 332

QY 126 TCK 128
DB 333 VCK 335

RESULT 25
Q708Z0 PRELIMINARY; PRT; 751 AA.
AC Q708Z0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amyloid-beta-like protein A precursor.
GN Name=ap1p2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Collin R.W.J., van Strien D., Leunissen J.A., Martens G.J.M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ608932; CAE75662.1; --
DR HSSP; Q16019; IAA;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW SIGNAL.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 751 amyloid-beta-like protein A.
SQ SEQUENCE 751 AA; 85200 MW; C5E8FE7302C36B58 CRC64;

Query Match 23.0%; Score 173; DB 2; Length 751;
Best Local Similarity 46.0%; Pred. No. 4.5e-08;
Matches 29; Conservative 8; Mismatches 26; Indels 0; Gaps 0;

QY 66 GKCLDFRDKICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLV 125
DB 281 GKDITDVKSVCSEAITGPRAMPWRYFNLGQKCKFRFYGGCGGNRNFESEDYCMA 340

QY 126 TCK 128
DB 341 VCK 343

RESULT 26
Q09983 PRELIMINARY; PRT; 1599 AA.
AC Q09983;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F30H5.3.
GN Name=F30H5.3; ORFNames=F30H5.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Stellyes L.;
RT "The sequence of C. elegans cosmid F30H5.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR EMBL; U29096; AAA68408.1; --
DR PIR; T16210; T16210.
DR HSSP; P10646; IADZ.
DR IntAct; Q09983; --


```
DR WormBase; WBGene00017937; F30H5.3.
DR WormPep; F30H5.3; CS01927.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 3.
DR Pfam; PF00014; Kunitz_BPTI; 5.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; EGF; 1.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WR1; 15.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 5.
KW Hypothetical protein.
SQ SEQUENCE 1599 AA; 171658 MW; AB5B6A1D86E9880D CRC64;

Query Match 22.9%; Score 172.5; DB 2; Length 1599;
Best Local Similarity 35.4%; Pred. No. 1e-07;
Matches 35; Conservative 13; Mismatches 42; Indels 9; Gaps 2;

Qy 37 KVECEV-----BEIDQTKPRDCPENNKCCPFCGKCKLDFRKDICSMPQEAQPCLAS 89
Db 518 LQCKYGTPLKIGSNQRCASADCPSTHEC--QSDHNVCPRPQAICSQLRLGDCQKS 575

Qy 90 IPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 128
Db 576 VRRYWNVAVTRACBIFDYTGCGGNNNFETLEQNTCE 614

RESULT 27
IBPC BOVIN STANDARD; PRT; 67 AA.
AC P00976;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Colostrum trypsin inhibitor (Colostrum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Cechova D., Jonakova V., Sorm F.
RT "Primary structure of trypsin inhibitor from cow colostrum (component B2).";
RL Collect. Czech. Chem. Commun. 36:3342-3357 (1971).
RN [2]
RP DISULFIDE BONDS.
RA Cechova D., Ber E.
RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
RL Collect. Czech. Chem. Commun. 39:680-688 (1974).
RN [3]
RP CHARACTERIZATION.
RA Cechova D., Muszynska G.
RX PubMed=11947537;
RA "Role of lysine 18 in active center of cow colostrum trypsin inhibitor.";
RL FEBS Lett. 8:84-86 (1970).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01207; TIBOC.
DR HSP; P02760; IBTK.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
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DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Glycoprotein; Serine protease inhibitor.
FT SITE 18 19 Reactive bond for trypsin.
FT DISULFID 8 58
FT DISULFID 17 41
FT DISULFID 33 54
FT CARBOHYD 27 27 N-linked (GlcNAc...).
SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;

Query Match 22.8%; Score 172; DB 1; Length 67;
Best Local Similarity 48.1%; Pred. No. 5.3e-09;
Matches 26; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

Qy 75 DICSMPOEAQPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 128
Db 6 DLQQLPQARGPCAKALLRYFYNSNACEPFTYGGCGGNNNFETTEMCLRICE 59

RESULT 28
Q7T363 PRELIMINARY; PRT; 516 AA.
AC Q7T363;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Zgc:64075.
GN ORFNames=zgc:64075;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; BC053239; AAH53239.1; -.
DR HSP; P10646; IADZ.
DR ZFIN; ZDB-GENE-040426-2169; zgc:64075.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR000601; PKD.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
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RP REVISIONS.
RA Jones S.J.M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/ebis/announcement/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; Z19157; CAA79569.1; -.
DR PIR; E88550; E88550.
DR PIR; S28291; S28291.
DR HSSP; P00981; 1DTK.
DR WormBase; WBGene00013846; ZC84.1.
DR WormPep; ZC84.1; CE15020.
DR InterPro; IPR006149; EB region.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 3.
DR Pfam; PF00014; Kunitz BPTI; 5.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 5.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WRI; 13.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 5.
KW Hypothetical protein; Repeat; Serine protease inhibitor.
FT DOMAIN 212 266 BPTI/Kunitz inhibitor 1.
FT DOMAIN 337 387 BPTI/Kunitz inhibitor 2.
FT DOMAIN 434 484 BPTI/Kunitz inhibitor 3.
FT DOMAIN 538 590 BPTI/Kunitz inhibitor 4.
FT DOMAIN 646 698 BPTI/Kunitz inhibitor 5.
SQ SEQUENCE 1416 AA; 152986 MW; 531CAC81CB22P70D CRC64;

Query Match 22.7%; Score 171; DB 1; Length 1416;
Best Local Similarity 30.4%; Pred. No. 1.3e-07;
Matches 35; Conservative 14; Mismatches 34; Indels 32; Gaps 3;

Qy 37 KVECEV-----EIDQCTKPRDCPENMK-----CPFSGCKKCLDFR 73
Db 380 KHECMYCARLCQRCRGLRGEARQCNNAQCPSSHECKADQGVCCP-----RK 430
Qy 74 KDICSMFQEGAGPCLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 128
Db 431 QTICAPLRIGDCTENVKRYWYNARTQCMFEVTGCGGNDNFDSDMDCQNFCK 485

RESULT 31
BTIA BOOMI
ID BTIA BOOMI STANDARD; PRT; 122 AA.
AC P83609;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Kunitz-type serine protease inhibitor BMTI-A (Fragments).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Larva;
RX PubMed=10615008; DOI=10.1016/S0162-3109(99)00074-0;
RA Tanaka A.S.; Andreotti R.; Gomes A.; Torquato R.J.S.; Sampaio M.U.;
RA Sampaio C.A.M.;
RT "A double headed serine proteinase inhibitor-human plasma kallikrein
and elastase inhibitor from Boophilus microplus larvae."
RL Immunopharmacology 45:171-177(1999).
CC -1- FUNCTION: Inhibits bovine trypsin, human chymotrypsin, human

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CC plasmin, human plasma kallikrein and human neutrophil elastase,
CC but not bovine thrombin, human factor Xa or porcine pancreatic
CC kallikrein. May play a role in blocking blood coagulation during
CC the larvae fixation on cattle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR InterPro; IPR002223; Kunitz BPTI.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
KW Direct protein sequencing; Repeat; Serine protease inhibitor.
FT DOMAIN 10 60 BPTI/Kunitz inhibitor 1.
FT DOMAIN 62 112 BPTI/Kunitz inhibitor 2.
FT DISULFID 10 60 By similarity.
FT DISULFID 35 56 By similarity.
FT NON CONS 69 70 By similarity.
FT DISULFID 71 121 By similarity.
FT DISULFID 80 104 By similarity.
FT DISULFID 96 117 By similarity.
FT SITE 19 20 Reactive bond (By similarity).
FT SITE 71 72 Reactive bond (By similarity).
FT NON TER 122 122
SQ SEQUENCE 122 AA; 13736 MW; 8F5B1F48E10C566F CRC64;

Query Match 22.6%; Score 170.5; DB 1; Length 122;
Best Local Similarity 46.7%; Pred. No. 1.3e-08;
Matches 35; Conservative 7; Mismatches 18; Indels 15; Gaps 3;

Qy 61 CPFSQ-----GKCKLDFRDKICSMFQEGAGPCLASIPHWYNNKTKICSEFIYGGCG 113
Db 56 CKASCPETEYEAKKCL-----ARP-ESGPCLAYMPWGYDSKLGQCQCFYIYGGCGDN 107
Qy 114 NNNFQTEAICLVTC 128
Db 108 DNKYTTEECCKSCK 122

RESULT 32
Q6ITB9
ID Q6ITB9 PRELIMINARY; PRT; 83 AA.
AC Q6ITB9;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Malgin-3.
OS Pseudechis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudechis.
OX NCBI_TaxID=8670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filipovich I.V.; Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; AY626926; AAT45402.1; -.
DR HSSP; Q16019; IAAp.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9103 MW; 315C361D8EC89221 CRC64;

Query Match 22.6%; Score 170; DB 2; Length 83;
Best Local Similarity 52.7%; Pred. No. 1e-08;
Matches 29; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

```


DE Hypothetical protein Y55F3BR.2.
GN Name=Y55F3BR.2; ORFNames=Y55F3BR.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bradshaw-Cordum H., Leonard S., Graves T.;
RT "The sequence of C. elegans cosmid Y55F3BR.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

RA Waterston R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 BPTI/Kunitz inhibitor domains.
DR EMBL; AC024830; AAF59608.3; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
KW Hypothetical protein.
SQ SEQUENCE 1297 AA; 142370 MW; 7C8FAA75CE07ED8C CRC64;
Query Match 22.2%; Score 167.5; DB 2; Length 1297;
Best Local Similarity 28.0%; Pred. No. 2.6e-07;
Matches 35; Conservative 13; Mismatches 34; Indels 43; Gaps 3;
QY 47 OCTPRDCP-----ENMKCCPFs-----CGKKCLDFR----- 73
DB 673 RCARDTDCPSTHTCAMEHQVCCPTPHREIQKYKGLDVSSSLKIVGSRHENYRNPGRGV 732
QY 74 -----KDI CSMPOEAGPCLASIPHWYKTKICSEFIYGGCGGNNNNPOTEAIC 123
DB 733 ARPNI FLIEEKTLCTEPLRVGDCQSVQRFWYNAETKTCSFLYTGCGGNNRNFSLNEC 792
QY 124 LVTCK 128
DB 793 QSYCK 797
RESULT 39
OS2504 PRELIMINARY; PRT; 1474 AA.
AC O62504;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein ZC84.6.
GN ORFNames=ZC84.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Thomas K.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR EMBL; Z19157; CAA79570.1; -.
DR PIR; D88550; D88550.
DR HSP; P31713; 1SHP.
DR WormBase; WBGene00013849; ZC84.6.
DR WormPep; ZC84.6; CE15024.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR


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Query Match      22.2%; Score 167; DB 2; Length 83;
Best Local Similarity 50.9%; Pred. No. 1.9e-08;
Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 73 RXDICSMPQEAAGPCLASIPHHWYKTKICSEFIYGGCGNNNFOTBAICLVTC 127
DB 27 RPDFCLPADTGCVRGPFSPFYNDPEKKCLEFIYGGCGNNNFITKECESTC 81

RESULT 43
Q6T6S5
ID Q6T6S5 PRELIMINARY; PRT; 90 AA.
AC Q6T6S5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kunitz protease inhibitor 2.
OS Bitis gabonica (Gaboon viper) (Gaboon viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OX NCBI_TaxID=8694;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15276202; DOI=10.1016/j.gene.2004.03.024;
RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
RA Ribeiro J.M.;
RT "Bitis gabonica (Gaboon viper) snake venom gland: toward a catalog for
RT the full-length transcripts (cDNA) and proteins.";
RL Gene 337:55-69(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RA Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY430413; AAR24535.1; -.
DR HSP; Q16019; IAP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI_1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 90 AA; 10006 MW; 2BEDC1D2020852AF CRC64;

Query Match      22.2%; Score 167; DB 2; Length 90;
Best Local Similarity 45.2%; Pred. No. 2.1e-08;
Matches 28; Conservative 10; Mismatches 20; Indels 4; Gaps 1;

QY 66 GKXCLDFRKDCSMQEAAGPCLASIPHHWYKTKICSEFIYGGCGNNNFOTBAICLV 125
DB 24 GKX----RPDFCYLPADTGCWAFNFRFYDSASKKCKFTYGGCGNNNFETRECRK 79

QY 126 TK 127
DB 80 KC 81

RESULT 44
Q6P2V8
ID Q6P2V8 PRELIMINARY; PRT; 342 AA.
AC Q6P2V8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC76314.
GN Name=MGC76314;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Schaefer C.W., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin I.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhardt D.S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the lipocalin family.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; BC064278; AAH64278.1; -.
DR HSP; P10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002968; Al-microglobin.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI_2.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR01215; ALMCGLOBULIN.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00179; LIPOCALIN.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Hypothetical protein; Lipocalin.
SQ SEQUENCE 342 AA; 38191 MW; D9B95BE25C8CB5A CRC64;

Query Match      22.1%; Score 166.5; DB 2; Length 342;
Best Local Similarity 32.9%; Pred. No. 8.7e-08;
Matches 47; Conservative 17; Mismatches 48; Indels 31; Gaps 7;

QY 3 LSGLLPILVFPFILLGDIQEPGHAEGILGKPCPKIKV-----ECEVEIDQCTKPRD-- 53
DB 148 LVGRSPDLRP-VLIDFQOQFALAQGV-----PDSIFLTITNSGECAPGDIE--VRPRRTQ 199

QY 54 ---CPE-----NMKCCPFSCGKKKLDPRKDCSMQEAAGPCLASIPHHWYKTKICSEF 105
DB 200 RAVLPEEEEGSGMENNPLSRNK-----GDSCLAPAFGPGCLGMHSRYFNSSTWACET 253

QY 106 IYGGCGGNNNFOTBAICLVTC 128
DB 254 KYGGCLGNNNFHSEKELQTCR 276
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RESULT 45
Q90WA1          PRELIMINARY;      PRT;      83 AA.
AC Q90WA1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textilin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=169397;
[1]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Flippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; AF402324; AAK95519.1; -.
DR HSPF; P25660; IUC6.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;

Query Match      22.0%; Score 166; DB 2; Length 83;
Best Local Similarity 50.9%; Pred. No. 2.4e-08;
Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Oy 73 RKDICSPQEPAGPCLASIPHWYKTKICSEFYGGCGQGNNNFQTEAICLVTC 127
Db 27 RPDCELADTGPCRVRFPFVYNPDKKCLEFYGGCGGNANNFITKECESIC 81

RESULT 46
Q6I750          PRELIMINARY;      PRT;      507 AA.
AC Q6I750;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatocyte growth factor activator inhibitor-1.
GN Name=HAI-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN
RP SEQUENCE FROM N.A.
RA Tezuki S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC EMBL; AB154834; BAD33971.1; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MANSC; 1.
DR PRINTS; PR00759; BASICTPASE.
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DR PRODOM; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00068; LDLRA_2; 1.
SQ SEQUENCE 507 AA; 56469 MW; 810043AE28C47AF3 CRC64;

Query Match      22.0%; Score 166; DB 2; Length 507;
Best Local Similarity 34.0%; Pred. No. 1.4e-07;
Matches 33; Conservative 17; Mismatches 39; Indels 8; Gaps 3;

Oy 40 CEVEEIDQCTKPRDCP---ENMKCCPFSCG---KKCLDFRKD--ICSMPOEAGPCLASIP 91
Db 324 CCTDGFLECDTDCPDGSDENTCEKYSSGFDELQSHFLSDKGYCAELPDTGCKENIP 383

Oy 92 HWYNNKTKICSEFYGGCGQGNNNFQTEAICLVTC 128
Db 384 RWTYNPFSECARFTYGGCYGNKNFKEQQCLESCE 420

RESULT 47
Q9GQR0          PRELIMINARY;      PRT;      2174 AA.
AC Q9GQR0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin precursor.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=dp cn bw;
RX MEDLINE=20530499; PubMed=11076767;
RA Kramerova I.A., Kawaguchi N., Nelson R.E., Fessler L.I., Chen Y.,
RA Kramerov A.A., Kusage-Gullberg M., Kramer J.M., Ackley B.D.,
RA Sieron A.L., Prockop D.J., Fessler J.H.;
RT "Papilin in development; a pericellular protein with a homology to the
RT ADAMTS metalloproteinases."
RL Development 127:5475-5485 (2000).
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AF205357; AAG37995.1; -.
DR HSSP; P12111; 1KTH.
DR FlyBase; FBgn0003137; Ppn.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR Pfam; PF00090; TSP_1-5.
DR Pfam; PF00095; WAP_1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00131; KU; 3.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 3.
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DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 5.
KW Matrix protein; Signal.
FT SIGNAL 1 26 Potential.
SQ SEQUENCE 2174 AA; 231935 MW; 038F707952623120 CRC64;

Query Match      22.0%; Score 165.5; DB 2; Length 2174;
Best Local Similarity 32.2%; Pred. No. 6.6e-07;
Matches 29; Conservative 16; Mismatches 42; Indels 3; Gaps 1;

QY 40 CEVEIDQCTKPRDCPENKCKCPFGSGKKCLDFRDKDICSMPQEAQCLASIPHWYNNKT 99
Db 1696 CEFQYGGCYGYNRFDLSLEQCGQTC--AAENLPTCEQPVESGFCAGNFERWYDNET 1752
QY 100 KICSEFIYGGCGNNNNQTEALCLVTCK 129
Db 1753 DICRPFYGGCGKGNKNYPTEHACYNCRQ 1782

RESULT 48
QYRQ8
ID Q7YRQ8 PRELIMINARY; PRT; 234 AA.
AC Q7YRQ8
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;
RA Du X., Deng F.M., Chand H.S., Kisiel W.;
RT "Molecular cloning, expression, and characterization of bovine tissue
factor pathway inhibitor-2";
RL Arch. Biochem. Biophys. 417:96-104 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Deng F.-M., Kisiel W., Sun T.-T.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DE EMBL; AY234861; AA084035.1; -.
DR HSSP; P00981; 1DTC.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26675 MW; 401BEC94D589B422 CRC64;

Query Match      21.9%; Score 165; DB 2; Length 234;
Best Local Similarity 49.1%; Pred. No. 8.3e-08;
Matches 27; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 75 DICMPQEAQCLASIPHWYNNKTICSEFIYGGCGNNNNFQTEALCLVTCK 129
Db 34 EICLLPDDGPCREARIPSYDYRYTQSCREFFYGGCGEGNANNFETLEACNEACWK 88

RESULT 49
Q6ZN14
ID Q6ZN14 PRELIMINARY; PRT; 283 AA.
AC Q6ZN14;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
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```
DE Hypothetical protein FLJ16032.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuoka K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DE EMBL; AK131196; BAD18391.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 8620657309866D30 CRC64;

Query Match      21.9%; Score 165; DB 2; Length 283;
Best Local Similarity 42.2%; Pred. No. 1e-07;
Matches 27; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 64 SCGKKCLDFRDKDICSMPQEAQCLASIPHWYNNKTICSEFIYGGCGNNNNFQTEALIC 123
Db 80 ACLACMSGLAACLSPALQGPCKAYAPWAYNSQTQCQSFVYGGCGNGNPFESREAC 139
QY 124 LVTC 127
Db 140 EESC 143

RESULT 50
SPTI_MOUSE
ID SPTI_MOUSE STANDARD; PRT; 507 AA.
AC Q9R097;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
activator inhibitor type 1) (HAI-1).
GN Name=Spint1; Synonyms=Hail;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RX MEDLINE=21299055; PubMed=11406276; DOI=10.1016/S0167-4781(01)00216-0;
RA Itoh H., Kataoka H., Meng J.Y., Hamasuna R., Kitamura N., Koono M.;
RT "Mouse hepatocyte growth factor activator inhibitor type 1 (HAI-1) and
type 2 (HAI-2)/placental bikunin genes and their promoters.";
RL Biochim. Biophys. Acta 1519:92-95 (2001).
CC -!- FUNCTION: Inhibitor of HGF activator (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- DOMAIN: This inhibitor contains two inhibitory domains.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
```



```

CC CC -!- SIMILARITY: Contains 1 MANSO domain.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.ebi-sib.ch/announce/
CC CC or send an email to license@sib-sib.ch).
CC CC -----
CC CC EMBL; AF099018; AAF02490.1; -.
CC CC HSSP; P31713; 1SHP.
CC CC MGD; MGI:1338033; Spint1.
CC CC InterPro; IPR002172; LDL_receptor_A.
CC CC InterPro; IPR011106; MANSO_N.
CC CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC CC Pfam; PF00014; Kunitz_BPTI; 2.
CC CC Pfam; PF00057; Ldl_recept_a; 1.
CC CC Pfam; PF07502; MANSO; 1.
CC CC PRINTS; PR00759; BASICPTASE.
CC CC ProDom; PD000222; Prot_Inh_Kunz-m; 2.
CC CC SMART; SM00131; KU; 2.
CC CC SMART; SM00192; LDLa; 1.
CC CC PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC CC PROSITE; PS0279; BPTI_KUNITZ_2; 2.
CC CC PROSITE; PS01209; LDLRA_1; FALSE_NEG.
CC CC PROSITE; PS00068; LDLRA_2; 1.
CC CC PROSITE; PS00986; MANSO; 1.
CC CC Glycoprotein; Repeat; Serine protease inhibitor; Signal.
CC CC SIGNAL 1 29
CC CC CHAIN 30 507 Kunitz-type protease inhibitor 1.
CC CC DOMAIN 51 134 MANSO.
CC CC DOMAIN 244 294 BPTI/Kunitz inhibitor 1.
CC CC DOMAIN 312 348 LDL-receptor class A.
CC CC DOMAIN 369 419 BPTI/Kunitz inhibitor 2.
CC CC SITE 254 255 Reactive bond (By similarity).
CC CC SITE 379 380 Reactive bond (By similarity).
CC CC SITE 244 294 By similarity.
CC CC DISULFID 253 277 By similarity.
CC CC DISULFID 269 290 By similarity.
CC CC DISULFID 369 419 By similarity.
CC CC DISULFID 378 402 By similarity.
CC CC DISULFID 394 415 By similarity.
CC CC CARBOHYD 229 229 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 501 501 N-linked (GlcNAc...) (Potential).
CC CC SEQUENCE 507 AA; 56676 MW; 20CB5DEDC46AA7 CRC64;

Query Match 21.9%; Score 165; DB 1; Length 507;
Best Local Similarity 32.3%; Pred. No. 1.8e-07;
Matches 32; Conservative 15; Mismatches 40; Indels 12; Gaps 2;

Qy 40 CEVEIIOCTKPRDCPENMKCPSPCGKKCLDF-----RKDTCMPQEAQPLAS 89
Db 324 CSIDGFLECDTDPDPCDSD--EATCEKYSTGDFDELQNIHFLSDKGYCAELPDTGFCKEN 381

Qy 90 IPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVCK 128
Db 382 IPRWYNPFBSRCARFTYGGCYGNKNFEEQQCLESCR 420

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Search completed: September 21, 2005, 16:40:08
Job time : 83.2625 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 14:52:13 ; Search time 66.2891 Seconds
(without alignments)
618.452 Million cell updates/sec

Title: US-10-807-204-2

Perfect score: 625

Sequence: 1 EGILGKPCPKIKVEVEEI.....GNNNFQTEAICLVTCCKYH 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A_Geneseq_16Dec04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	106	7	ADAI19801 Mature fo
2	625	100.0	131	7	ADAI19800 Engineere
3	625	100.0	131	7	ADAI19811 Engineere
4	603	96.5	131	7	ADAI19814 Human DJI
5	423	67.7	98	7	ADAI19808 Engineere
6	416	66.6	136	7	ADAI19808 Engineere
7	401.5	64.2	117	5	Aae27094 Human sec
8	401.5	64.2	117	5	Aae27165 Human gen
9	401.5	64.2	117	6	ABU65038 Human sec
10	401.5	64.2	117	8	ADG89847 Human sec
11	400	64.0	102	5	Aae27095 Human sec
12	400	64.0	102	5	Aae28009 Human gen
13	400	64.0	102	6	ABU65039 Human sec
14	400	64.0	102	8	ADG89848 Human sec
15	400	64.0	102	2	Aaw75219 Human sec
16	400	64.0	133	5	Aae26982 Human gen
17	400	64.0	133	5	Aae27120 Human gen
18	400	64.0	133	6	ABU64993 Human sec
19	400	64.0	133	7	ADAI19812 Human EPP
20	400	64.0	133	8	ADG89802 Human pro
21	400	64.0	154	3	Aay70010 Human pro
22	400	64.0	179	8	ABM85103 Human dia
23	352	56.3	134	7	ADAI19813 Mouse EPP
24	276	44.2	86	5	ABP69809 Human pol
25	276	44.2	86	6	ABJ26667 Human pro

26	276	44.2	101	4	ABBI2236 Human epp
27	246	39.4	43	7	ADAI19804 Engineere
28	242	38.7	64	4	AAEI13093 Human ser
29	236	37.8	58	4	AAEI13084 Human ser
30	236	37.8	58	4	AAAB60630 Kunitz do
31	236	37.8	58	7	ADAI1997 Human CAB
32	236	37.8	58	8	ADL16838 Human Kun
33	236	37.8	58	8	ADL16838 Human CAB
34	219	35.0	51	2	AAW75257 Fragment
35	219	35.0	51	5	AAAE27025 Human gen
36	219	35.0	51	5	AAAE27163 Human gen
37	219	35.0	51	8	ADG89845 Human sec
38	187	29.9	560	2	AAE62523 Hookworm
39	187	29.9	2858	4	ABB71150 Drosophil
40	187	29.9	3060	4	ABB58064 Drosophil
41	182.5	29.2	571	7	AAE39498 Cloned mo
42	182.5	29.2	571	7	AAE39459 Mouse GDF
43	182.5	29.2	571	7	ADG93670 Mouse GDF
44	181.5	29.0	101	8	ADQ66734 Novel hum
45	180	28.8	33	7	ADAI19806 Engineere
46	180	28.8	33	7	ADAI19809 Engineere
47	177	28.3	58	2	AAE99146 Aprotinin
48	175	28.0	43	4	AAE13096 Human ser
49	175	28.0	54	4	AAE13092 Trypsin i
50	173.5	27.8	503	5	ABJ01150 Ovary cel

ALIGNMENTS

RESULT 1

ADAI19801
ID ADAI19801 standard; protein; 106 AA.

XX AC ADAI19801;

XX DT 20-NOV-2003 (first entry)

XX DE Mature form of engineered human DJI1 protein SEQ ID NO:2.

XX KW DJI1; Kunitz-type protease inhibitor domain; antiinflammatory;
XX KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
XX KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX KW nephrotropic; antipneumonic; vulnary; protease inhibitor; Gene therapy;
XX KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX KW deep vein thrombosis; myocardial infarction; shock; septic shock;
XX KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX KW chronic inflammatory bowel disease; psoriasis.

XX OS Synthetic.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 8..36 /note = predicted disulfide bond

FT Disulfide-bond 15..40 /note = predicted disulfide bond

FT Disulfide-bond 23..35 /note = predicted disulfide bond

FT Disulfide-bond 29..44 /note = predicted disulfide bond

FT Domain 52..102 /note = predicted disulfide bond

FT Disulfide-bond 52..102 /note = Kunitz domain predicted by pfscan

FT Disulfide-bond 61..85 /note = predicted disulfide bond

FT Disulfide-bond 77..98 /note = predicted disulfide bond

XX WO2003070770-A2.

PD 28-AUG-2003.
 XX
 PF 18-FEB-2003; 2003WO-EP001629.
 XX
 XX 21-FEB-2002; 2002US-0358683P.
 PR (GENE-) GENEPROT INC.
 XX
 XX Bougueleret L, Bairoch A, Niknejad A;
 PI WPI; 2003-663849/62.
 XX
 DR New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX
 PS Claim 5; Page 71; 87pp; English.
 XX
 CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents the mature form of an engineered human
 CC DJ11 protein from the present invention.
 XX
 SQ Sequence 106 AA;
 Query Match 100.0%; Score 625; DB 7; Length 106;
 Best Local Similarity 100.0%; Pred. No. 8.7e-47;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKDICSMPQEAGP 60
 Db 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKDICSMPQEAGP 60
 Qy 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 106
 Db 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 106
 RESULT 2
 ID ADA19800
 AC ADA19800 standard; protein; 131 AA.
 XX
 AC ADA19800;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Engineered human DJ11 protein SEQ ID NO:1.
 DE
 XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;

KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..131
 FT /note= "eppin-like precursor"
 FT Peptide 1..25
 FT /label= signal
 FT Protein 26..131
 FT /note= "mature DJ11 protein"
 FT Disulfide-bond 33..61
 FT /note = predicted disulfide bond
 FT Disulfide-bond 40..65
 FT /note = predicted disulfide bond
 FT Disulfide-bond 48..60
 FT /note = predicted disulfide bond
 FT Disulfide-bond 54..69
 FT /note = predicted disulfide bond
 FT Domain 77..127
 FT /note = Kunitz domain predicted by pfscan
 FT Disulfide-bond 77..127
 FT /note = predicted disulfide bond
 FT Disulfide-bond 86..110
 FT /note = predicted disulfide bond
 FT Disulfide-bond 102..123
 FT /note = predicted disulfide bond
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 PI WPI; 2003-663849/62.
 DR N-PSDB; ADA19810.
 XX
 PT New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX
 PS Claim 5; Page 69-70; 87pp; English.
 XX
 CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as

CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 625; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.1e-46;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPEAGP 60
 Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPEAGP 85
 QY 61 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 106
 Db 86 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 131

RESULT 3

ID ADA19811 standard; protein; 131 AA.

AC ADA19811;

DT 20-NOV-2003 (first entry)

DE Engineered human DJ11 protein SEQ ID NO:12.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.

OS Homo sapiens.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-BF001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Disclosure; Page 84; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.

CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolysis,
 CC haemorrhage, and especially inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 625; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.1e-46;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPEAGP 60

Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 106

Db 86 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 131

RESULT 4

ADA19814

ID ADA19814 standard; protein; 131 AA.

XX ADA19814;

DT 20-NOV-2003 (first entry)

XX Human DJ11 protein SEQ ID NO:15.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Homo sapiens.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-BF001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX

CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoaritic and vulnery
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a human DJ11 protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.
 XX Sequence 131 AA;

Query Match 96.5%; Score 603; DB 7; Length 131;
 Best Local Similarity 98.1%; Pred. No. 8.6e-45;
 Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKCLDFRDKICSMPOEAGP 60
 Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKCLDFRDKICSMPOEAGP 85
 Qy 61 CLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTCCKYH 106
 Db 86 CLASIPHHWYNNKTKICSEFYGGSGQNNNNFQTEAICLVTCCKYH 131

RESULT 5
 ID ADA19808 standard; protein; 98 AA.
 XX ADA19808;
 XX 20-NOV-2003 (first entry)
 XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:9.
 XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoaritic; vulnery; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW Chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.
 DR New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX Disclosure; Page 82; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoaritic and vulnery
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a partial engineered human DJ11 protein
 CC amino acid sequence from the present invention.

XX Sequence 98 AA;

Query Match 67.7%; Score 423; DB 7; Length 98;
 Best Local Similarity 98.6%; Pred. No. 2.8e-29;
 Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKCLDFRDKICSMPOEAGP 60
 Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKCLDFRDKICSMPOEAGP 85
 Qy 61 CLASIPHHWYNNK 73
 Db 86 CLASIPHHWYNNK 98

RESULT 6
 ID ADA19815 standard; protein; 136 AA.
 XX ADA19815;
 XX 20-NOV-2003 (first entry)
 XX Mouse DJ11 protein SEQ ID NO:16.
 XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoaritic; vulnery; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 XX Chronic inflammatory bowel disease; psoriasis.
 OS Mus musculus.
 XX WO2003070770-A2.
 XX

PD 28-AUG-2003.
 XX
 PF 18-FEB-2003; 2003WO-EP001629.
 XX
 PR 21-FEB-2002; 2002US-0358683P.
 XX
 PA (GENE-) GENEPROT INC.
 XX
 PI Bougueleret L, Bairoch A, Niknejad A;
 XX
 XX WPI; 2003-663849/62.
 DR
 XX
 XX
 PT New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX
 XX
 PS Disclosure; Fig 1; 87pp; English.
 XX
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, anti-allergic, thrombolytic,
 CC anticoagulant, cardiac, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a mouse DJ11 protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.
 XX
 XX Sequence 136 AA;
 SQ
 Query Match 66.6%; Score 416; DB 7; Length 136;
 Best Local Similarity 60.6%; Pred. No. 1.5e-28;
 Matches 63; Conservative 20; Mismatches 21; Indels 0; Gaps 0;
 QY 1 EGLGKPCPKIKVECEVEIDICTKPRDCPENMKCCPFSCGKCLDFRDKICSMPEAGP 60
 DB 26 EGGFIRTCPRVRVKCEVERNECTRHQCPCNKKCCCLFSGKKCMDLRQVCSLQDDP 85
 QY 61 CLASIPHWYNNKTKICSEFFIYGGCGQNNNNFQTEAICLVTCCK 104
 DB 86 CLAYLPRWYNQETDLCTEFYGGCGQNNPNPSEIGCTVCKK 129
 RESULT 7
 AAE27094
 ID AAE27094 standard; protein; 117 AA.
 XX
 AC AAE27094;
 XX
 XX 13-DEC-2002 (first entry)
 XX
 DE Human secreted protein #1.
 XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 XX autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;

KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropic; vulnary; cytostatic; nootropic; cardiac;
 KW anti-HIV; tranquilliser; gout; antiparasitic.
 XX
 OS Homo sapiens.
 XX
 XX US2002077287-A1.
 PN
 XX 20-JUN-2002.
 PD
 XX 11-MAY-2001; 2001US-00852659.
 PF
 XX 11-SEP-1998; 98US-00152060.
 PR
 XX (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYU/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEI/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 XX WPI; 2002-598780/64.
 DR
 XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 XX
 XX Disclosure; Page 16; 209pp; English.
 PS
 XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE28593-AAE28599 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogeneic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders, e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine

PA (SOPP/) Soppet D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.
XX
XX
PI Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
XX WPI; 2004-042167/04.
XX
XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
XX Disclosure; SEQ ID NO 120; 320pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.
XX
SQ Sequence 117 AA;

Query Match 64.2%; Score 401.5; DB 8; Length 117;
Best Local Similarity 66.0%; Pred No. 2.4e-27;
Matches 66; Conservative 12; Mismatches 21; Indels 1; Gaps 1;
Qy 4 LKPCPKIKVCEVEIDQTKPRDCPENMKCCFPSCGKGLDKFRKDTCSMPQAGPCL 63
Db 14 LGR-CPKIRECEFEQDVTCKRQCQDNKCCVFCGKGLDLKQDCEMPKGTGCL 72

Qy 64 SIPHWYNNKTKICSEFIYGGCGGNNNNNFQTEAICLVTK 103
AAE27095
Db 73 YFLHWYDKDNTCSMFYGGCGGNNNNNFQSKANCLNTCK 112
RESULT 11
ID AAE27095 standard; protein; 102 AA.
XX
XX AAE27095;
AC AAE27095;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human secreted protein #2.
XX
KW Human; immunodeficiency; X-linked gammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotropic; vulnary; cytostatic; nootropic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.
XX
OS Homo sapiens.
XX
XX US2002077287-A1.
PN
PD 20-JUN-2002.
XX
XX
PF 11-MAY-2001; 2001US-00852659.
PR
PR 11-SEP-1998; 98US-00152060.
XX
XX (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) Soppet D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2002-598780/64.
XX
XX Novel human secreted polypeptides and polynucleotides for diagnosing,
PT preventing, treating immune, hyperproliferative, cardiovascular, of
PT neurological, reproductive disorders and identifying modulators of
PT therapeutic use.
XX
XX Disclosure; Page 16; 209pp; English.
XX
XX AD44636-AD44676 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
CC AAE27000-AAE27025 represent human secreted protein fragments or their
CC variants. The secreted proteins and genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Specific uses are described for each of the 28 genes, based on
CC the tissues in which they are most highly expressed and include

CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogeneic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders. e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention
 XX
 SQ Sequence 102 AA;

Query Match 64.0%; Score 400; DB 5; Length 102;
 Best Local Similarity 66.7%; Pred. No. 2.9e-27;
 Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
 QY 8 CPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKCKLDFRKIDICSMPOEAGPCLASIPH 67
 DB 2 CPKIRECECFQERDVCTKDRQCQDNKKCCVFCGKCKLQKQDVCMPKGTGCLAYFLH 61
 QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
 DB 62 WYDKNDTCSMFYGGCGNNNNFQSKANCLNTCK 97

RESULT 12

AAE28009
 ID AAE28009 standard; protein; 102 AA.

AC AAE28009;

XX 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein fragment #2.

DE Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 KW vulnery.

XX Homo sapiens.

OS US2002076756-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00853161.

XX 02-FEB-2001; 2001US-0265583P.

XX (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;

WPI; 2002-574454/61.

XX New nucleic acid molecules encoding 28 human secreted proteins, useful
 PT for diagnosing, preventing, treating or ameliorating medical conditions
 PT and as food additives or preservatives.

XX Disclosure; Page 17; 209pp; English.

XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
 CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Secreted protein sequences of the invention are useful for the
 CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
 CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
 CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
 CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
 CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
 CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
 CC polypeptides can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues and in chemotaxis. They can also be used as food
 CC additives or preservative to increase or decrease storage capabilities,
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
 CC and other nutritional components. The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention
 XX

SQ Sequence 102 AA;

Query Match 64.0%; Score 400; DB 5; Length 102;
 Best Local Similarity 66.7%; Pred. No. 2.9e-27;
 Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 8 CPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKCKLDFRKIDICSMPOEAGPCLASIPH 67
 DB 2 CPKIRECECFQERDVCTKDRQCQDNKKCCVFCGKCKLQKQDVCMPKGTGCLAYFLH 61
 QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
 DB 62 WYDKNDTCSMFYGGCGNNNNFQSKANCLNTCK 97

RESULT 13

ABU65039

ID ABU65039 standard; peptide; 102 AA.

XX ABU65039;

XX 15-MAY-2003 (first entry)

XX Human secreted protein gene 24, protein #3.

XX Secreted protein; immunodeficiency; multiple sclerosis;

XX severe combined immunodeficiency; autoimmune disorder; cancer;

XX rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;

XX inflammatory condition; septic shock; inflammatory bowel disease;

PT cancers, CNS disorders or immune system disorders.
XX Claim 1; Page 167-168; 201pp; English.
XX This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAV34277) for increasing the stability of the fused protein
CC as compared to the human protein only. The invention relates to 28 novel
CC genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino
CC acid sequences AAW75196-W75235) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 28 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAV34286 for described uses)
XX
SQ

Sequence 133 AA;

Query Match 64.0%; Score 400; DB 2; Length 133;
Best Local Similarity 66.7%; Pred. No. 3.7e-27;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
Qy 8 CPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKCKLDFRKDICSMPQEGPCLASIPH 67
Dy 33 CPKIRECEFEQERDVCTKDRQCQDNKKCCVFCGKCKLCLDLKQDVCEMPKETGCPCLAYFLH 92
Qy 68 WYNNKTKICSEFYGGCGQNNNFQTEAICLVTK 103
Dy 93 WYDCKDNTCSMFYGGCGQNNNFQSKANCLNTCK 128

RESULT 16

AAE26982

ID AAE26982 standard; protein; 133 AA.

XX AAE26982;

DT 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:34.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotrophic; vulnery; cytostatic; nootropic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21

FT Protein 22..133 /label= Signal_peptide

FT /note= "Human mature secreted protein"

XX US2002077287-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00852659.

XX 11-SEP-1998; 98US-00152060.

XX (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX WPI; 2002-598780/64.
DR N-PSDB; AAD44659.

XX Novel human secreted polypeptides and polynucleotides for diagnosing,
PT preventing, treating immune, hyperproliferative, cardiovascular,
PT neurological, reproductive disorders and identifying modulators of
PT therapeutic use.

PS Claim 11; Page 185-186; 209pp; English.

XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
CC AAE27000-AAE27025 represent human secreted protein fragments or their
CC variants. The secreted proteins and genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Specific uses are described for each of the 28 genes, based on
CC the tissues in which they are most highly expressed and include
CC developing products for the diagnosis or treatment of immunodeficiencies,
CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
CC bowel disease), cancers e.g. gastric, ovarian, lung, liver, bladder and
CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
CC sarcoidosis and allogenic transplant rejection, blood-related disorder
CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
CC lung cancer, allergic disorders, pneumonitis, renal disorders e.g. acute
CC glomerulonephritis, neurological diseases, liver disorders, endocrine
CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
CC infectious diseases and reproductive system disorders e.g. endometriosis.
CC The present sequence represents a human secreted protein of the invention

XX Sequence 133 AA;

Query Match 64.0%; Score 400; DB 5; Length 133;

Best Local Similarity 66.7%; Pred. No. 3.7e-27;

Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 8 CPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKCKLDFRKDICSMPQEGPCLASIPH 67

Dy 33 CPKIRECEFEQERDVCTKDRQCQDNKKCCVFCGKCKLCLDLKQDVCEMPKETGCPCLAYFLH 92

Qy 68 WYNNKTKICSEFYGGCGQNNNFQTEAICLVTK 103

Dy 93 WYDCKDNTCSMFYGGCGQNNNFQSKANCLNTCK 128


```
RESULT 17
AAE27120
ID AAE27120 standard; protein; 133 AA.
XX
AC AAE27120;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:75.
XX
KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiac; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnery.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Signal_peptide
FT Protein 22..133
FT /note= "Mature human secreted protein"
XX
US2002076756-A1.
XX
20-JUN-2002.
XX
11-MAY-2001; 2001US-00853161.
XX
02-FEB-2001; 2001US-0265583P.
XX
(RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEI/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GRE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
WPI: 2002-574454/61.
XX
N-PSDB; AAD44877.
XX
New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
Claim 11; Page 185-186; 209pp; English.
XX
AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
angio genesis), cardiovascular disorders (e.g. cardiac arrest), nervous
system disorders (e.g. Alzheimer's disease), infections caused by fungi,
bacteria and viruses and ocular disorders (e.g. corneal infection). The
polypeptides can also be used to aid wound healing and epithelial cell
proliferation, to prevent skin aging due to sunburn, to maintain organs
before transplantation, for supporting cell culture of primary tissues,
to regenerate tissues and in chemotaxis. They can also be used as food
additives or preservative to increase or decrease storage capabilities,
fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
and other nutritional components. The present sequence represents a human
secreted protein of the invention
Sequence 133 AA;
Query Match 64.0%; Score 400; DB 5; Length 133;
Best Local Similarity 66.7%; Pred. No. 3.7e-27;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIKVEGEVEIEIOCTKPRDCPENMKCCPFCGKCKLDLFRKIDICSMFQEGPCLASIPH 67
DB 33 CPKIRECEFEQERDVCTKROQDNKKCCVFCGKCKLDLQKQVCEMPKETGPGCLAYFLH 92
QY 68 WYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCK 103
DB 93 WYDKKONTCSMFVYGGCGGNNNNFQSKANCLNTCK 128
RESULT 18
ABU64993
ID ABU64993 standard; protein; 133 AA.
XX
AC ABU64993;
XX
DT 15-MAY-2003 (first entry)
XX
DE Human secreted protein gene 24, protein #1.
XX
KW Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
KW body height; hair colour; human.
XX
OS Homo sapiens.
XX
US2002172994-A1.
XX
21-NOV-2002.
XX
11-MAY-2001; 2001US-00852797.
XX
14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
```


CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a human EPPIN protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.
 XX
 SQ Sequence 133 AA;

Query Match 64.0%; Score 400; DB 7; Length 133;
 Best Local Similarity 66.7%; Pred. No. 3.7e-27;
 Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
 QY 8 CPKIKVEVEBIDQCTPRDCPENMKCCPFSCGKKCLDFRDKICSMFQEAQPCIASIPH 67
 DB 33 CPKIRECECFQERDVCTKDRQCQDNKKCCVFCGKKCLDLKQDVCMPKSTGFCPLAYFLH 92
 QY 68 WMYNKKTKICSEFIYGGCGGNNNFQTEAICLVTK 103
 DB 93 WMYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 128

RESULT 20
 ADG89802
 ID ADG89802 standard; protein; 133 AA.

AC ADG89802;

XX 11-MAR-2004 (first entry)

XX Human protein from secreted protein gene 24 #1.

XX Secreted protein; gene therapy; neural disorder; immune system disorders;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; cancer; systemic lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
 KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
 KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
 KW myocardial infarction; AIDS; infection; human.

XX Homo sapiens.

XX US2003225009-A1.

XX 04-DEC-2003.

XX 30-JAN-2002; 2002US-00058993.

XX 14-MAR-1997; 97US-0040710P.

XX 14-MAR-1997; 97US-0040762P.

XX 30-MAY-1997; 97US-0048100P.

XX 30-MAY-1997; 97US-0048189P.

XX 30-MAY-1997; 97US-0048357P.

XX 30-MAY-1997; 97US-0050934P.

XX 06-JUN-1997; 97US-0048970P.

XX 05-SEP-1997; 97US-0057765P.

XX 19-DEC-1997; 97US-0068368P.

XX 12-MAR-1998; 98WO-US004858.

XX 11-SEP-1998; 98US-00152060.

XX 02-FEB-2001; 2001US-0265583P.

XX 11-MAY-2001; 2001US-00852659.

XX 11-MAY-2001; 2001US-00852797.

XX 11-MAY-2001; 2001US-00853161.

XX (ROSE/) ROSEN C A.

XX (RUBE/) RUBEN S M.

XX (LIY/) LI Y.

XX (ZENG/) ZENG Z.

XX (KIYAW/) KYAW H.

XX (FISC/) FISCHER C L.

XX (LIHH/) LI H.

PA (GENTZ/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (HAST/) HASTINGS G A.
 XX

PI Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM, Hastings GA;

XX WPI; 2004-042167/04.
 DR N-PSDB; ADG89761.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
 PT treating diseases associated with aberrant expression or activity of the
 PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

PS Claim 11; SEQ ID NO 75; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridisable to the nucleotide sequences, a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment, a
 CC epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the specification, a polynucleotide which
 CC encodes a species homologue of the above amino acid sequences, a
 CC polynucleotide capable of hybridising under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridise
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant vector
 CC comprising the above nucleic acid molecule, making a recombinant host
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC comprising a sequence that is at least 95% identical to the polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosis or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular
 CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis, asthma,
 CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, atherosclerosis,
 CC nephritis, Parkinson's disease, Alzheimer's disease,
 CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a protein from
 CC one of the 28 disclosed secreted protein genes.

XX Sequence 133 AA;

Query Match 64.0%; Score 400; DB 8; Length 133;

Best Local Similarity 66.7%; Pred. No. 3.7e-27;

Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 8 CPKIKVEVEBIDQCTPRDCPENMKCCPFSCGKKCLDFRDKICSMFQEAQPCIASIPH 67

DB 33 CPKIRECECFQERDVCTKDRQCQDNKKCCVFCGKKCLDLKQDVCMPKSTGFCPLAYFLH 92

QY 68 WMYNKKTKICSEFIYGGCGGNNNFQTEAICLVTK 103

Db	93	WYDKKONTCSMFVYGGCGNNNNFQSKANCLINTCK	128
RESULT 21			
ID	AAV70010		
XX	AAV70010 standard; protein; 164 AA.		
AC	AAV70010;		
XX			
XX	05-JUN-2000 (first entry)		
DT	Human Protease and associated protein-4 (PPRG-4).		
XX			
XX	Protease and associated protein-4; PPRG-4; anti-PPRG antibody; diagnosis;		
KW	treatment; cell proliferative disorder; cancer; cirrhosis;		
KW	arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder;		
KW	AIDS; Addison's disease; adult respiratory distress syndrome; allergy;		
KW	ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic;		
KW	hepatototropic; antiinflammatory; virucide; antipapillary; anti-HIV;		
KW	antiallergic; immunosuppressive; antidiabetic; antianaemic;		
XX	neuroprotective; human.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Modified-site	157	
FT		/note= "Potential Phosphorylation site"	
XX			
FN	WO200009709-A2.		
XX			
PD	24-FEB-2000.		
XX			
PP	06-AUG-1999; 99WO-US017818.		
XX			
PR	10-AUG-1998; 98US-0096114P.		
PR	11-FEB-1999; 99US-0119768P.		
XX			
PA	(INCY-) INCYTE PHARM INC.		
XX			
PI	Bandman O, Hillman JL, Baughn MR, Azimzai Y, Guegler KJ;		
PI	Corley NC, Yue H, Tang YI, Reddy R, Patterson C, Au-Young J;		
PI	Shih LL, Lu DAM;		
XX			
DR	WPI; 2000-224346/19.		
DR	N-PSDB; AAZ50921.		
XX			
FT	New human proteases, useful for diagnosis, treatment and prevention of		
FT	cell proliferative disorders such as atherosclerosis.		
XX			
PS	Claim 1; Page 77; 114pp; English.		
XX			
CC	The present sequence is that of human protease and associated protein-4		
CC	(PPRG-4), which is expressed in reproductive tissues. It is encoded by		
CC	cDNA identified in incyte clone 2012492 derived from TESTNOT03 cDNA		
CC	library. It has been identified as a protease as it includes a Kunitz		
CC	family signature sequence. Anti-PPRG antibodies can be used as		
CC	therapeutic antagonists, reagents for diagnosis and monitoring diseases		
CC	and for isolating PPRG. PPRG nucleotide sequence can be used as probe or		
CC	primer for diagnosis and monitoring of PPRG-related diseases and gene		
CC	mapping. PPRG can be used in the treatment of cell proliferative		
CC	disorders like cancer, arteriosclerosis, atherosclerosis, bursitis,		
CC	cirrhosis and hepatitis, and immune disorders like AIDS, Addison's		
CC	disease, adult respiratory distress syndrome, allergies, ankylosing		
CC	spondylitis and amyloidosis		
XX			
SQ	Sequence 164 AA;		
Query Match	64.0%; Score 400; DB 3; Length 164;		
Best Local Similarity	66.7%; Pred. No. 4.5e-27;		
Matches	64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;		
Qy	8	CPKIVECEVEBEIDQCTKPRCPENMKCCPFSCGKKCLDFRDKSCMPQEAQPLAS1PH	67
	: :		
Db	64	CPKIRECEFEQERDVCTKDRQCQDNKKCCVFCGKKCLDKQDVCMPKETGTCPLAYFLH	123
Qy	68	WYNKTKKICSEFYGGCGNNNNNFQTEAICLVTK	103
	: :		
Db	124	WYDKKONTCSMFVYGGCGNNNNNFQSKANCLNTCK	159
RESULT 22			
ABM85103			
ID	ABM85103 standard; protein; 179 AA.		
XX	ABM85103;		
AC	ABM85103;		
XX			
DT	18-NOV-2004 (first entry)		
XX			
DE	Human diagnostic and therapeutic pprotein SEQ ID NO:5352.		
XX			
KW	gene therapy; human diagnostic and therapeutic polynucleotide; dithp.		
XX			
OS	Homo sapiens.		
XX			
FN	WO2004023973-A2.		
XX			
PD	25-MAR-2004.		
XX			
PF	12-SEP-2003; 2003WO-US028227.		
XX			
PR	12-SEP-2002; 2002US-0410259P.		
PR	12-SEP-2002; 2002US-0410260P.		
XX			
PA	(INCY-) INCYTE CORP.		
XX			
PI	Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;		
PI	Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;		
PI	Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;		
PI	Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin BH;		
PI	Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;		
PI	Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;		
PI	Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;		
PI	Patury S, Shi X, Suarez CJ;		
XX			
DR	WPI; 2004-329368/30.		
DR	N-ESDB; ACN43755.		
XX			
FT	New diagnostic and therapeutic polynucleotides and polypeptides, useful		
FT	in diagnosing a condition, disease or disorder associated with human		
FT	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or		
FT	in gene mapping.		
XX			
PS	Claim 27; Page; 190pp; English.		
XX			
CC	The invention relates to novel diagnostic and therapeutic polynucleotides		
CC	selected from one of the 2722 sequences defined in the specification. A		
CC	polynucleotide of the invention may have a use in gene therapy. The human		
CC	diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be		
CC	used to diagnose a particular condition, disease or disorder associated		
CC	with human molecules, e.g. cell proliferative disorders,		
CC	autoimmune/inflammatory disorder, developmental disorder, endocrine		
CC	disorder, neurological disorders, gastrointestinal disorders, or		
CC	infections caused by virus, bacteria, fungi or parasite. The dithp		
CC	molecules may also be used in genetic mapping, in identifying individuals		
CC	from minute biological samples, in detecting single nucleotide		
CC	polymorphisms, as molecular weight markers, and for somatic or germline		
CC	gene therapy. The present sequence represents a dithp protein of the		
CC	invention. Note: The sequence data for this patent is not represented in		
CC	the printed specification, but was obtained in electronic format directly		
CC	from WIPO at www.wipo.int/pct/en/sequences/listing.htm		
XX			
SQ	Sequence 179 AA;		
Query Match	64.0%; Score 400; DB 8; Length 179;		
Best Local Similarity	66.7%; Pred. No. 4.9e-27;		
Matches	64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;		

CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 86 AA;

Query Match 44.2%; Score 276; DB 5; Length 86;
 Best Local Similarity 98.0%; Pred. No. 1.4e-16;
 Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 49

Db 26 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 74

RESULT 25

ABJ26667

ID ABJ26667 standard; protein; 86 AA.

XX AC ABJ26667;

XX DT 01-MAY-2003 (first entry)

XX DE Human protein modification + maintenance molecule protein SEQ ID No 21.

XX KW Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
 KW cerebroprotective; antiparkinsonian; nootropic; antiinflammatory;
 KW antiulcer; hepatotropic; gynaecological; antibacterial; virucide;
 KW protozoacide; antiparasitic; cell proliferative disease; PMOD;
 KW protein modification and maintenance molecule; immunogenic fragment;
 KW cancer; autoimmune; inflammatory disease; neurological disorder;
 KW gastrointestinal; developmental; vesicle trafficking disorder; infection;
 KW protein-protein interaction; drug-target interaction;
 KW gene expression profile; human.

XX OS Homo sapiens.

XX FN WO2003000844-A2.

XX PD 03-JAN-2003.

XX PF 18-JUN-2002; 2002WO-US019360.

XX PR 22-JUN-2001; 2001US-0300508P.

PR 06-JUL-2001; 2001US-0303445P.

PR 13-JUL-2001; 2001US-0305405P.

PR 09-AUG-2001; 2001US-0311442P.

PR 24-AUG-2001; 2001US-0314821P.

PR 29-AUG-2001; 2001US-0315992P.

PR 03-MAY-2002; 2002US-0378205P.

XX (INCY-) INCYTE GENOMICS INC.

XX PI Gandhi AR, Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggan BM;
 PI Warren BA, Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Yue H;
 PI Forsythe IJ, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang J;
 PI Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG;
 PI Walia NK, Mason PM, Gururajan R, Lee S, Becha SD, Lee SY, Tran UK;
 PI Elliott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zebbarjadian Y;

XX WPI; 2003-184039/18.

DR N-PSDB; ABT23220.

XX PT New isolated human PMOD polypeptide and polynucleotide, useful for
 PT diagnosing, treating and preventing diseases or conditions associated
 PT with the aberrant PMOD expression, e.g. cancer, AIDS, arteriosclerosis and
 PT infections.

XX PS Claim 76; Page 196; 225pp; English.

XX The invention relates to an isolated polypeptide comprising: any of 28
 CC sequences of 48-1286 amino acids; a natural amino acid sequence at least
 CC 90% identical to the 28 amino acid sequences, 94% identical to a sequence
 CC of 703 or 277 amino acids, 96% identical to a sequence of 414 amino
 CC acids, or 97% identical to a sequence of 242 amino acids, all given in
 CC the specification; or a biologically active or immunogenic fragment of
 CC the isolated polypeptide. The polypeptides and polynucleotides are useful
 CC in diagnosing, treating and preventing diseases or conditions associated
 CC with the decreased expression of protein modification and maintenance
 CC molecules (PMOD), such as cell proliferative diseases (e.g. cancer,
 CC atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS,
 CC allergies), neurological disorders (e.g. stroke, Parkinson's disease,
 CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g.
 CC endometriosis), developmental, vesicle trafficking disorders, and
 CC infections (e.g. bacterial, viral, parasitic, protozoal). These are also
 CC useful in assessing the effects of exogenous compounds on the expression
 CC of nucleic acid and amino acid sequences of PMOD. The PMOD or its
 CC fragments are useful in screening compounds for effectiveness as agonist
 CC or antagonist of the polypeptides, or in altering the expression of the
 CC target polynucleotide and compounds that specifically bind to or modulate
 CC the activity of the polypeptide. The microarray is useful in monitoring
 CC or measuring protein-protein interactions, drug-target interactions, and
 CC gene expression profiles. This sequence represents a human PMOD protein
 CC of the invention
 XX

SQ Sequence 86 AA;

Query Match 44.2%; Score 276; DB 6; Length 86;
 Best Local Similarity 98.0%; Pred. No. 1.4e-16;

Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 49

Db 26 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 74

RESULT 26

ABB12236

ID ABB12236 standard; peptide; 101 AA.

XX AC ABB12236;

XX DT 11-JAN-2002 (first entry)

XX DE Human eppin-1 homologue, SEQ ID NO:2606.

XX KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokines; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.

OS Homo sapiens.

XX WO200157188-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US003800.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;
 XX WPI: 2001-457740/49.
 DR N-PSDB; ABA09480.
 XX Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 XX Claim 20; Page 318; 1963pp; English.
 XX
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 XX Sequence 101 AA;
 SQ
 Query Match 44.2%; Score 276; DB 4; Length 101;
 Best Local Similarity 98.0%; Pred. No. 1.7e-16;
 Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EGILGPCPKIKVECEVEIDQCTKPRDCPENMKCCPFSGKCKLDFRK 49
 DB 41 EGILGPCPKIKVECEVEIDQCTKPRDCPENMKCCPFSGKCKLDFRK 89
 RESULT 27
 ADA19804
 ID ADA19804 standard; protein; 43 AA.
 XX
 XX ADA19804;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Engineered human DV11 partial amino acid sequence SEQ ID NO:5.
 DE
 XX DV11: Kunitz-type protease inhibitor domain; antiinflammatory;
 XX antiallergic; thrombolytic; anticoagulant; cardiant; vasotrophic;
 KW

KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO2003070770-A2.
 XX
 XX 28-AUG-2003.
 XX
 XX 18-FEB-2003; 2003WO-EP001629.
 XX
 XX 21-FEB-2002; 2002US-0358683P.
 XX
 XX (GENE-) GENEPROT INC.
 XX
 XX Bougueleret L, Bairoch A, Niknejad A;
 PI
 XX WPI: 2003-663849/62.
 XX
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX
 XX Disclosure; Page 79; 87pp; English.
 PS
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antibacterial, immunosuppressive,
 CC anticoagulant, cardiant, vasotrophic, antiallergic, thrombolytic,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a partial engineered human DJ11 protein
 CC amino acid sequence from the present invention.
 XX
 XX Sequence 43 AA;
 SQ
 Query Match 39.4%; Score 246; DB 7; Length 43;
 Best Local Similarity 97.7%; Pred. No. 3e-14;
 Matches 42; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 PCPKIKVECEVEIDQCTKPRDCPENMKCCPFSGKCKLDFRK 49
 DB 1 PCPKIKVECEVEIDQCTKPRDCPENMKCCPFSGKCKLDFRK 43
 RESULT 28
 AAE13093
 ID AAE13093 standard; peptide; 64 AA.
 XX
 XX AAE13093;
 XX

DT 28-JAN-2002 (first entry)
DE Human serine proteinase inhibitor BTL.009 C-terminal peptide.
XX
KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
OS Homo sapiens.
XX
PN US6294648-B1.
XX
PD 25-SEP-2001.
XX
PF 20-JUL-1999; 99US-00358569.
XX
PR 20-JUL-1999; 99US-00358569.
XX
PA (FARB) BAYER CORP.
XX
PI Delaria K, Rocznia K, Davies C;
XX
DR WPI; 2001-662224/76.
XX
PT New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
PS Disclosure; Col 6; 16pp; English.
XX
CC The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL.009 C-terminal peptide containing Kunitz domain which is used in the
CC exemplification of the invention
XX
SQ Sequence 64 AA;
Query Match 38.7%; Score 242; DB 4; Length 64;
Best Local Similarity 65.5%; Pred. No. 9.9e-14;
Matches 38; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY 46 DFRKDCSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFOTEALCLVTCK 103
Db 1 DLKQDVCEMPKETGTPCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 58
RESULT 29
AAE13084
ID AAE13084 standard; peptide; 58 AA.
XX
AC AAE13084;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human serine proteinase inhibitor BTL.009 peptide.
XX
KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW

KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
OS Homo sapiens.
XX
PN US6294648-B1.
XX
PD 25-SEP-2001.
XX
PF 20-JUL-1999; 99US-00358569.
XX
PR 20-JUL-1999; 99US-00358569.
XX
PA (FARB) BAYER CORP.
XX
PI Delaria K, Rocznia K, Davies C;
XX
DR WPI; 2001-662224/76.
XX
PT New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
PS Claim 1; Col 15-16; 16pp; English.
XX
CC The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL.009 peptide corresponding to Kunitz domain used in the
CC exemplification of the invention. Note: The present sequence shown in
CC column 14 and sequence listing of the specification lacks 3 amino acid
CC residues at the C-terminal end
XX
SQ Sequence 58 AA;
Query Match 37.8%; Score 236; DB 4; Length 58;
Best Local Similarity 66.1%; Pred. No. 3e-13;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 48 RKDTCSPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFOTEALCLVTCK 103
Db 1 KQDVCEMPKETGTPCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 56
RESULT 30
AAE60630
ID AAE60630 standard; protein; 58 AA.
XX
AC AAE60630;
XX
DT 27-APR-2001 (first entry)
XX
DE Kunitz domain, SEQ ID NO:8, used to identify BTL.010 protein.
XX
KW Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;
KW proteinase-3 inhibitor; Kunitz domain; emphysema;
KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
KW platelet activation; blood coagulation; neutrophil activation;
KW monocyte activation; angioplasty; inflammatory disease; lung injury;
KW vascular injury; nephrotropic; antirheumatic; antiarthritic.
XX

OS Unidentified.
 XX US6180607-B1.
 XX 30-JAN-2001.
 XX 05-AUG-1999; 99US-00369494.
 XX 05-AUG-1999; 99US-00369494.
 XX (DAVI/) DAVIES C.
 XX (CHEN/) CHEN D.
 XX (ROCZ/) ROCZNIK S.
 XX Davies C, Chen D, Rocznik S;
 XX WPI; 2001-190860/19.
 XX Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful
 XX for treating emphysema, cystic fibrosis, adult respiratory distress
 XX syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
 XX Disclosure; Col 6; 17pp; English.
 XX The invention relates to a novel human serine protease inhibitor of the
 XX Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and
 XX AAB60634). The BTL.010 protein is thought to preferentially inhibit
 XX neutral serine proteases such as elastase and proteinase-3, relative to
 XX trypsin-like and chymotrypsin-like proteases. A substantial proportion of
 XX the BTL.010 protein Kunitz domain (AAB60631) was identified via homology
 XX searching in the GenBank high throughput genomic (HTG) DNA sequence
 XX database using the Kunitz domain sequences AAB60630, and was confirmed as
 XX being novel using the Kunitz domain sequences AAB60632, and AAB60633.
 XX This sequence information was extended to provide a larger region of
 XX BTL.010 protein sequence data (AAB60634) by identifying an open reading
 XX frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain
 XX fragment in a 399 bp fragment of human genomic DNA (AAF59750),
 XX corresponding to bases 16016-16414 of GenBank accession number AC004846.
 XX The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from
 XX the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical
 XX compositions comprising it, may be used for inhibiting protease activity,
 XX particularly that of leukocyte elastase, in the prevention, treatment or
 XX amelioration of medical conditions such as emphysema, idiopathic
 XX pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,
 XX rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010
 XX compositions of the invention modulate at least one physiological
 XX condition such as platelet activation, blood coagulation, neutrophil
 XX activation, or monocyte activation. BTL.010 is also useful for the
 XX prophylactic or therapeutic treatment of patients undergoing angioplasty,
 XX and for the treatment of inflammatory diseases and diseases involving
 XX lung and vascular injury. The present sequence represents a Kunitz domain
 XX sequence used to identify the BTL.010 protein

Query Match 37.8%; Score 236; DB 4; Length 58;
 Best Local Similarity 66.1%; Pred. No. 3e-13;
 Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 48 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTK 103
 Db 1 KQDVCEMPKETGPCLAYFLHWYDKDNTCSMFVYGGCGQNNNFQSKANCLNTCK 56
 RESULT 31
 ADF41997
 ID ADF41997 standard; protein; 58 AA.
 XX ADF41997;
 XX 12-FEB-2004 (first entry)
 XX Human CAB37 Kunitz domain peptide.

XX albumin fusion; Kunitz domain; cytostatic; haemostatic;
 KW hereditary angioedema; cancer; bleeding; gene therapy; human; CAB37.
 XX Homo sapiens.
 XX WO2003066824-A2.
 XX 14-AUG-2003.
 XX 07-FEB-2003; 2003WO-US003616.
 XX 07-FEB-2002; 2002US-0355547P.
 XX (AVET) AVENTIS BEHRING GMBH.
 XX (AVET) AVENTIS BEHRING LLC.
 XX (DELZ) DELTA BIOTECHNOLOGY LTD.
 XX (DYAX-) DYAX CORP.
 XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
 PI Ley AC;
 XX WPI; 2003-731497/69.
 XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
 PT useful for preparing a composition for treating a patient with hereditary
 PT angioedema or angioedema-related disease, cancer or bleeding disorder.
 XX Disclosure; Page 20; 110pp; English.
 XX The invention relates to a novel albumin fusion protein comprising a
 CC Kunitz domain peptide or its fragment or variant and an albumin or its
 CC fragment or variant. The fusion protein of the invention demonstrates
 CC cytostatic and haemostatic activities and may be useful for preparing a
 CC composition for treating a patient with hereditary angioedema, an
 CC angioedema-related disease, cancer, a cancer-related disease or a
 CC bleeding disorder, as well as during gene therapy procedures. The current
 CC sequence is that of the human Kunitz domain peptide of the invention.
 XX Sequence 58 AA;
 Query Match 37.8%; Score 236; DB 7; Length 58;
 Best Local Similarity 66.1%; Pred. No. 3e-13;
 Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 48 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTK 103
 Db 1 KQDVCEMPKETGPCLAYFLHWYDKDNTCSMFVYGGCGQNNNFQSKANCLNTCK 56
 RESULT 32
 ADL16838
 ID ADL16838 standard; peptide; 58 AA.
 XX ADL16838;
 XX 06-MAY-2004 (first entry)
 XX Human Kunitz domain (KD) peptide.
 XX BTL.010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;
 KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 KW inflammatory disease; oxidative burst; platelet activation;
 KW blood coagulation; gene therapy; human; KD.
 XX Homo sapiens.
 XX US6689582-B1.
 XX 10-FEB-2004.
 XX 12-MAY-2000; 2000US-00569670.


```

XX 05-AUG-1999; 99US-00369494.
XX (FARB ) BAYER PHARM CORP.
XX
XX Davies C, Chen D, Roczniak S;
XX WPI; 2004-141424/14.
XX
XX New isolated polynucleotide encoding BTL010 serine proteinase, useful
XX for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
XX respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
XX glomerulonephritis.
XX
XX Disclosure; SEQ ID NO 8; 17pp; English.
XX
XX The invention relates to BTL010, a human serine proteinase inhibitor of
XX the Kunitz family and its corresponding nucleic acid sequence. The
XX sequences of the invention are useful for treating diseases, e.g.
XX emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
XX syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
XX glomerulonephritis or inflammatory diseases. The BTL010 protein is also
XX useful for preventing neutrophil and monocyte activation and formation of
XX active oxygen species during the oxidative burst of stimulated
XX granulocytes. It is also useful for reducing platelet activation and
XX blood coagulation. BTL010 DNA is useful in gene therapy. The present
XX sequence is human Kunitz domain (KD) peptide.
XX
XX Sequence 58 AA;
XX
XX Query Match 37.8%; Score 236; DB 8; Length 58;
XX Best Local Similarity 66.1%; Pred. No. 3e-13;
XX Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
XX
XX 48 RKDTCSPQEPAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTCCK 103
XX :.:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 1 KQDVCEMPKETGPCLAYFLHWYDKDNTCSMFYGGCGQNNNFQSKANCLNTCK 56
XX
XX RESULT 33
XX ADR89980
XX ID ADR89980 standard; peptide; 58 AA.
XX
XX ADR89980;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human CAB37 protein kunitz domain peptide.
XX
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;
XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
XX cytosstatic; haemostatic; CAB37 protein; human.
XX
XX Homo sapiens.
XX
XX US2004171794-A1.
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX (LADN/) LADNER R C.
XX PA (LEVA/) LEV A C.
XX
XX Ladner RC, Ley AC;
XX WPI; 2004-625120/60.
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
XX for the treatment of e.g. cystic fibrosis and related disease.
XX
XX Disclosure; SEQ ID NO 5; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
XX designated DPI-14 for inhibiting human neutrophil elastase, fused to
XX albumin. The invention is useful for treating cystic fibrosis and related
XX diseases, hereditary angioedema, cancer and related diseases including
XX chronic obstructive pulmonary disease, asthma, bronchitis, acute
XX respiratory syndrome, pneumonia and bleeding. The invention acts as a
XX cytosstatic and haemostatic agent. The present sequence is the human CAB37
XX protein (A4) kunitz domain peptide. This sequence is used in the
XX invention.
XX
XX Sequence 58 AA;
XX
XX Query Match 37.8%; Score 236; DB 8; Length 58;
XX Best Local Similarity 66.1%; Pred. No. 3e-13;
XX Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
XX
XX 48 RKDTCSPQEPAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTCCK 103
XX :.:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 1 KQDVCEMPKETGPCLAYFLHWYDKDNTCSMFYGGCGQNNNFQSKANCLNTCK 56
XX
XX RESULT 34
XX AAW75257
XX ID AAW75257 standard; protein; 51 AA.
XX
XX AAW75257;
XX
XX 29-JAN-1999 (first entry)
XX
XX Fragment of human secreted protein encoded by gene 24.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX Homo sapiens.
XX
XX WO98040483-A2.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-US004858.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057765P.
XX 19-DEC-1997; 97US-0068368P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
XX Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JW;
XX Ferrie AM;
XX
XX WPI; 1998-520811/44.
XX N-PSDB; AAV34309.
XX
XX Isolated human polynucleotide(s) encoding secretory peptide(s) - used to
XX develop products for the diagnosis and treatment of e.g. inflammation,
XX cancers, CNS disorders or immune system disorders.

```


XX PS Disclosure; Page 24; 201pp; English.

XX CC This sequence represents a fragment of a secreted human protein encoded

CC by the nucleic acid molecule designated Gene 24 (AAV34309). The gene can

CC be used to generate fusion proteins by linking to the gene to a human

CC immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of

CC the fused protein as compared to the human protein only. The invention

CC relates to 28 novel genes and their fragments (nucleic acid sequences:

CC AAV34286-V34325; amino acid sequences AAV75196-W75235) which are useful

CC for preventing, treating or ameliorating medical conditions e.g. by

CC protein or gene therapy. Also, pathological conditions can be diagnosed

CC by determining the amount of the new polypeptides in a sample or by

CC determining the presence of mutations in the new polynucleotides.

CC Specific uses are described for each of the 28 polynucleotides, based on

CC which tissues they are most highly expressed in (see AAV34286 for

CC described uses)

XX Sequence 51 AA;

SQ Query Match 35.0%; Score 219; DB 2; Length 51;

Best Local Similarity 68.6%; Pred. No. 7.9e-12;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 52 CSMPOAGCLASIPHHWYNNKTKICSEPIYGGCGQNNNNFOTEAICLVTC 102

DB 1 CEMPKEGTCLAYFLHWYDKDNTCSMFVYGGCGQNNNNFQSKANCLNTC 51

RESULT 35

AAE27025

ID AAE27025 standard; protein; 51 AA.

AC AAE27025;

XX 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein variant, SEQ ID NO:118.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;

KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;

KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;

KW respiratory disorder; asthma; allergy; gastrointestinal disorder;

KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;

KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;

KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;

KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;

KW respiratory disorder; rhinitis; sinusitis; neurological disease;

KW endocrine disorder; Addison's disease; reproductive system disorder;

KW endometriosis; vasotropic; vulnery; cytostatic; nootropic; cardiant;

KW anti-HIV; tranquilliser; gout; antiparasitic.

XX Homo sapiens.

XX US2002077287-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00852659.

XX 11-SEP-1998; 98US-00152060.

XX (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEIV/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

XX Ferrie AM;

DR WPI; 2002-598780/64.

XX Novel human secreted polypeptides and polynucleotides for diagnosing,

PT preventing, treating immune, hyperproliferative, cardiovascular,

PT neurological, reproductive disorders and identifying modulators of

PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted

CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.

CC AAE27000-AAE27025 represent human secreted protein fragments or their

CC variants. The secreted proteins and genes are useful for preventing,

CC treating or ameliorating medical conditions, e.g., by protein or gene

CC therapy. Specific uses are described for each of the 28 genes, based on

CC the tissues in which they are most highly expressed and include

CC developing products for the diagnosis or treatment of immunodeficiencies,

CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe

CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus

CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune

CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,

CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions

CC including septic shock, sepsis, reperfusion injury, inflammatory bowel

CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders

CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory

CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and

CC breast), central nervous system (CNS) disorders e.g., ischaemic brain

CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's

CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,

CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,

CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,

CC sarcoidosis and allogenic transplant rejection, blood-related disorder

CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative

CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,

CC lung cancer, allergic disorders, pneumonitis, renal disorders, endocrine

CC glomerulonephritis, neurological diseases, liver disorders, endocrine

CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,

CC infectious diseases and reproductive system disorders e.g. endometriosis.

CC The present sequence represents a human secreted protein variant of the

CC invention

XX Sequence 51 AA;

SQ Query Match 35.0%; Score 219; DB 5; Length 51;

Best Local Similarity 68.6%; Pred. No. 7.9e-12;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 52 CSMPOAGCLASIPHHWYNNKTKICSEPIYGGCGQNNNNFOTEAICLVTC 102

DB 1 CEMPKEGTCLAYFLHWYDKDNTCSMFVYGGCGQNNNNFQSKANCLNTC 51

RESULT 36

AAE27163

ID AAE27163 standard; protein; 51 AA.

XX AAE27163;

XX 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein fragment kunitz-type domain.

XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;

KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;

KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;

KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnary.
XX
XX
OS Homo sapiens.
XX
XX US2002076756-A1.
XX
XX 20-JUN-2002.
XX
XX 11-MAY-2001; 2001US-00853161.
XX
XX 02-FEB-2001; 2001US-0265583P.
XX
XX (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEI/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2002-574454/61.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
XX Disclosure; Page 16; 209pp; English.
XX
XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment Kunitz-type domain referred to in the
XX disclosure of the invention
XX
XX Sequence 51 AA;

Query Match 35.0%; Score 219; DB 5; Length 51;
Best Local Similarity 68.6%; Pred. No. 7.9e-12;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 52 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 102

Db 1 CEMPKEGTGPCLAYFLHWYDKDNTCSMFYVGCGQNNNNFQSKANCLNTC 51
RESULT 37
ADG89845
ID ADG89845 standard; protein; 51 AA.
XX
XX ADG89845;
AC
XX
XX 11-MAR-2004 (first entry)
XX
XX Human secreted protein gene 24 protein #3.
XX
XX Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.
XX
XX Homo sapiens.
OS
XX
XX US2003225009-A1.
XX
XX 04-DEC-2003.
XX
XX 30-JAN-2002; 2002US-00058993.
XX
XX 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
PR 11-MAY-2001; 2001US-00852659.
PR 11-MAY-2001; 2001US-00852797.
PR 11-MAY-2001; 2001US-00853161.
XX
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEI/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.
XX
XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
XX WPI; 2004-042167/04.
XX
XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX


```

XX   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
XX   Disclosure; SEQ ID NO 40242; 21pp + Sequence Listing; English.
XX
XX   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABU16176-ABLJ0511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX   SQ      Sequence 2858 AA;
          Query Match           29.9%; Score 187; DB 4; Length 2858;
          Best Local Similarity 33.3%; Pred. No. 2.le-07;
          Matches 38; Conservative 13; Mismatches 33; Indels 30; Gaps 5;
QY       21 DQCTKPR---DCPENM-----KCCPF---SCG-----KKCLD----FRKD 50
DB       1748 DRCALPQTGDCESEKLAKWHFSESEKRCVPFYSGCGGNKNFPFLSCECHCPRQVAKD 1807
QY       51 ICSNPQAGCLASIPHWYNKTKICSEFIYGGCGGNNNNFOTEALCVTCKK 104
DB       1808 ICEIPAEGVCANYVTSMYYDTQDACRQRFYGGCGGNENRFPTEESCLARCDR 1861

RESULT 40
ABB58064
ID     ABB58064 standard; protein; 3060 AA.
XX
XX     ABB58064;
XX
XX     26-MAR-2002 (first entry)
XX
XX     Drosophila melanogaster polypeptide SEQ ID NO 984.
XX
XX     Drosophila; developmental biology; cell signalling; insecticide;
KW     pharmaceutical.
XX
XX     Drosophila melanogaster.
XX
XX     WO200171042-A2.
XX
XX     27-SEP-2001.
XX
XX     23-MAR-2001; 2001WO-US009231.
XX
XX     23-MAR-2000; 2000US-0191637P.
PR     11-JUL-2000; 2000US-00614150.
XX
XX     (PEKE ) PE CORP NY.
PA
XX
XX     Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX     WPI; 2001-656860/75.
DR     N-PSDB; ABL02167.
XX
XX     New isolated nucleic acid detection reagent for detecting 1000 or more
PT     genes from Drosophila and for elucidating cell signaling and cell-cell
PT     interactions.
XX
XX     Disclosure; SEQ ID NO 984; 21pp + Sequence Listing; English.
XX
XX     The invention relates to an isolated nucleic acid detection reagent
CC     capable of detecting 1000 or more genes from Drosophila. The invention is
CC     useful in developmental biology and in elucidating cell signalling and
CC     useful in developmental biology and in elucidating cell signalling and
```


used to modulate GDF-8 for treatment of muscular disorders such as
 muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
 myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
 progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
 congestive obstructive pulmonary disease, congenital myopathy (myotonia),
 familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
 Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
 carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
 and other muscle wasting syndromes such as traumatic or chronic injury to
 muscle, metabolic disorders such as diabetes types 1 or 2, impaired
 glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
 induced by trauma and obesity, adipose tissue disorder such as obesity,
 and bone degenerative conditions such as osteoporosis, osteopaenia,
 osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
 premature gonadal failure, vitamin D deficiency, androgen suppression,
 secondary hyperparathyroidism, nutritional deficiencies and anorexia
 nervosa. The present sequence is cloned mouse GDF (growth and
 differentiation factor)-associated serum protein (GASP)
 Sequence 571 AA;

Query Match 29.2%; Score 182.5; DB 7; Length 571;
 Best Local Similarity 31.8%; Pred. No. 1.1e-07;
 Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
 QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKC 52
 DB 322 ECLKPPDSEDCGEQTRWHFDAQANCLTFTGCHCHNLNHFETAEACLMACWSGPLATC 381
 QY 53 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 102
 DB 382 SLPALQGPCKAYVPRWAYNSQTGLQCSFYVGGCEGNGNFFESRACEESC 431

RESULT 42

AAE39459
 ID AAE39459 standard; protein; 571 AA.

AC AAE39459;

DT 18-DEC-2003 (first entry)

XX Mouse GDF-associated serum protein (GASP)1 protein.

XX Mouse: GDF-associated serum protein; GASP; amyotrophic lateral sclerosis;
 growth and differentiation factor; GDF; chronic glucocorticoid therapy;
 familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
 progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
 bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
 muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
 carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
 nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;
 androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;
 metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
 myotonia; neuroprotective; obesity; immunomodulator; diabetes.

OS Mus sp.

XX Key Location/Qualifiers
 FT Domain 105..170
 FT /note= "Follistatin domain"

XX US2003162714-A1.

XX 28-AUG-2003.

XX 21-FEB-2003; 2003US-00369736.

XX 21-FEB-2002; 2002US-0357845P.

XX 20-DEC-2002; 2002US-043644P.

XX (AMHP) WYETH.

XX

PI Hill JJ, Wolfman NM;

XX WPI; 2003-756055/71.

DR N-PSDB; AAD59923.

XX Composition containing growth and differentiation factor-associated serum
 protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
 for diagnosis.

PS Disclosure; Fig 6C; Opp; English.

XX The present invention relates to the use of a protein GDF (growth and
 differentiation factor)-associated serum protein (GASP) 1 comprising
 at least one follistatin domain to modulate the level or activity of
 growth and differentiation factor (GDF) -8. Administration of GASP1 is
 used to modulate GDF-8 for treatment of muscular disorders such as
 muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
 myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
 progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
 congestive obstructive pulmonary disease, congenital myopathy (myotonia),
 familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
 Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
 carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
 and other muscle wasting syndromes such as traumatic or chronic injury to
 muscle, metabolic disorders such as diabetes types 1 or 2, impaired
 glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
 induced by trauma and obesity, adipose tissue disorder such as obesity,
 and bone degenerative conditions such as osteoporosis, osteopaenia,
 osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
 premature gonadal failure, vitamin D deficiency, androgen suppression,
 secondary hyperparathyroidism, nutritional deficiencies and anorexia
 nervosa. The present sequence is mouse GDF (growth and differentiation
 factor)-associated serum protein (GASP)
 Sequence 571 AA;

Query Match 29.2%; Score 182.5; DB 7; Length 571;

Best Local Similarity 31.8%; Pred. No. 1.1e-07;

Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKC 52

DB 322 ECLKPPDSEDCGEQTRWHFDAQANCLTFTGCHCHNLNHFETAEACLMACWSGPLATC 381

QY 53 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 102

DB 382 SLPALQGPCKAYVPRWAYNSQTGLQCSFYVGGCEGNGNFFESRACEESC 431

RESULT 43

ADD93670

ID ADD93670 standard; protein; 571 AA.

XX ADD93670;

XX 29-JAN-2004 (first entry)

XX Mouse GDF-associated serum protein 1 (GASP1).

XX Mouse: GDF-associated serum protein 1; GASP1; antidiabetic; anorectic;
 osteopathic; gene therapy.

OS Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..29 /note= "Signal peptide"

FT Protein 30..571 /note= "Mature protein"

FT Domain 105..170 /note= "Follistatin domain"

FT Modified-site 313 /note= "potential N-glycosylation site"

FT

FT

OS Synthetic.
OS Homo sapiens.
PN WO2003070770-A2.
XX
PD 28-AUG-2003.
XX
XX
PF 18-FEB-2003; 2003WO-EP001629.
XX
PR 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
PA Bougueleret L, Bairoch A, Niknejad A;
PI WPI; 2003-663849/62.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Disclosure; Page 80; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.
XX
XX Sequence 33 AA;
XX
Query Match 28.8%; Score 180; DB 7; Length 33;
Best Local Similarity 97.0%; Pred. No. 1.3e-08;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 74 TKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 106
DB 1 TKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 33
RESULT 46
ADA19809
ID ADA19809 standard; peptide; 33 AA.
XX
AC ADA19809;
XX
XX 20-NOV-2003 (first entry)
XX
XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:10.
XX
XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiatic; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
XX

KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2003070770-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
PA Bougueleret L, Bairoch A, Niknejad A;
PI WPI; 2003-663849/62.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Disclosure; Page 82-83; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.
XX
XX Sequence 33 AA;
XX
Query Match 28.8%; Score 180; DB 7; Length 33;
Best Local Similarity 97.0%; Pred. No. 1.3e-08;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 74 TKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 106
DB 1 TKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 33
RESULT 47
AAR99146
ID AAR99146 standard; protein; 58 AA.
XX
XX AAR99146;
XX
XX 12-FEB-1997 (first entry)
XX

DE Aprotinin-like Kunitz domain.
XX
XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX
XX Synthetic.
OS
XX WO9620278-A2.
FN
XX
XX PD 04-JUL-1996.
XX
XX PF 15-DEC-1995; 95WO-US016349.
XX
XX PR 16-DEC-1994; 94US-00358160.
XX
XX PA (PROT-) PROTEIN ENG CORP.
XX
XX PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX
XX DR WPI; 1996-321851/32.
XX
XX PT New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX
XX PS Example 23; Page 47; 105pp; English.
XX
XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211
XX
XX SQ Sequence 58 AA;

Query Match 28.3%; Score 177; DB 2; Length 58;
Best Local Similarity 56.4%; Pred. No. 4e-08; Mismatches 19; Indels 0; Gaps 0;
Matches 31; Conservative 5;

QY 48 RKDSCMPQAGPCILASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 102
DB 1 RPDFCLLPAGTGPCRAMIPRFYNAKSGKCEPFYGGCGGNNNFQTEECRRTC 55

RESULT 48
AAE13096
ID AAE13096 standard; peptide; 43 AA.
AC AAE13096;
XX
XX DT 28-JAN-2002 (first entry)
XX
XX Human serine proteinase inhibitor BTL.009 peptide fragment #2.
DE
XX Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angiodysplasia;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
XX OS Homo sapiens.
XX
XX PN US6294648-B1.

XX 25-SEP-2001.
XX
XX PD 20-JUL-1999; 99US-00358569.
XX
XX PR 20-JUL-1999; 99US-00358569.
XX
XX PA (FARB) BAYER CORP.
XX
XX PI Delaria K, Rocznik S, Davies C;
XX
XX DR WPI; 2001-662224/76.
XX
XX PT New isolated protein for inhibiting human serine proteinase activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
XX PS Disclosure; Col 5-6; 16pp; English.
XX
XX The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL.009 peptide fragment related to the invention
XX
XX SQ Sequence 43 AA;

Query Match 28.0%; Score 175; DB 4; Length 43;
Best Local Similarity 69.0%; Pred. No. 4.5e-08;
Matches 29; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 62 LASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 103
DB 1 LAYFLHWYDKKONTCSMFYGGCGGNNNFQSKANCLNTCK 42

RESULT 49
AAE13092
ID AAE13092 standard; peptide; 54 AA.
AC AAE13092;
XX
XX DT 28-JAN-2002 (first entry)
XX
XX DE Trypsin inhibitor peptide.
XX
XX BTL.009 protein; serine proteinase inhibitor; cytostatic; therapeutic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angiodysplasia;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW trypsin inhibitor.
XX
XX OS Unidentified.
XX
XX PN US6294648-B1.
XX
XX PD 25-SEP-2001.
XX
XX PF 20-JUL-1999; 99US-00358569.
XX
XX PR 20-JUL-1999; 99US-00358569.
XX
XX PA (FARB) BAYER CORP.

XX Delaria K, Rocznik S, Davies C;
XX WPI; 2001-662224/76.
XX New isolated protein for inhibiting human serine protease activity in the
XX treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
XX Disclosure; Col 5-6; 16pp; English.
XX
XX The invention relates to human BTL 009 protein, a serine proteinase
XX inhibitor of the Kunitz family that exhibits greater potency towards
XX neutral serine proteinases. BTL 009 protein is found to inhibit leukocyte
XX elastase, chymotrypsin-like protease and trypsin-like protease. BTL 009
XX protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
XX adult respiratory distress syndrome, cystic fibrosis, rheumatoid
XX arthritis, organ failure, glomerulonephritis, other inflammatory diseases
XX and diseases involving lung and vascular injury. BTL 009 is also useful
XX for preventing neutrophil and monocyte activation and formation of active
XX oxygen species during the oxidative burst of stimulated granulocytes.
XX BTL 009 is useful for reducing platelet activation and blood coagulation
XX and for the prophylactic or therapeutic treatment of patients undergoing
XX angioplasty. The present sequence is trypsin inhibitor peptide related to
XX the invention
XX
XX Sequence 54 AA;

Query Match 28.0%; Score 175; DB 4; Length 54;
Best Local Similarity 50.0%; Pred. No. 5.5e-08;
Matches 27; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
QY 50 DICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103
Db 1 DICQLPQARGPCAKALLRYFNSTNACEPFTYGGCGGNNNNFETEMCLRICE 54

RESULT 50
ABJ01150
ID ABJ01150 standard; protein; 503 AA.
XX
XX AC ABJ01150;
XX
XX DT 28-NOV-2002 (first entry)
XX
XX DE Ovary cell-specific amino acid sequence 96.
XX
XX KW Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
XX KW ovary specific protein; ovarian cancer; breast cancer; vaccine;
XX KW gene therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO200238606-A2.
XX
XX PD 16-MAY-2002.
XX
XX PF 07-NOV-2001; 2001WO-US046459.
XX
XX PR 08-NOV-2000; 2000US-0246640P.
XX
XX PA (DIAD-) DIADEXUS INC.
XX
XX PI Sun Y, Recipon H, Salceda S, Liu C;
XX
XX DR WPI; 2002-519297/55.
XX
XX PT Polypeptide and polynucleotides present in normal and neoplastic ovary
XX PT cells, useful for identifying, monitoring, staging, diagnosing,
XX PT preventing and treating ovarian cancer, and non-cancerous disease states
XX PT in the ovary.
XX
XX PS Claim 11; Page 244-245; 247pp; English.
XX

CC The invention comprises amino acid and DNA sequences which are present in
CC normal and neoplastic ovary cells. The DNA and protein sequences of the
CC invention are useful for determining the presence of an ovary specific
CC nucleic acid or an ovary specific protein in a sample. The DNA and
CC protein sequences of the invention are useful for diagnosing and
CC monitoring the presence and metastasis of ovarian cancer and breast
CC cancer. Amino acids ABJ01055 - ABJ01155 represent the ovary cell specific
CC protein sequences of the invention
XX
XX Sequence 503 AA;

Query Match 27.8%; Score 173.5; DB 5; Length 503;
Best Local Similarity 31.8%; Pred. No. 6.1e-07;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;
QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKCIC 52
Db 258 ECLKPPDSEDGEGQTRWHFPAQANNCLTFTFGHCHRNLNHFETVEACMLACMSGPLAAC 317
QY 53 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
Db 318 SLPALQGPCKAYAPRWAYNSQTQCQSFYGGCGGNNNNFESREACEESC 367

Search completed: September 21, 2005, 16:36:50
Job time : 67.2891 secs

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Qy 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
Db 93 WMYDKONTCSMFYGGCGNNNNFQSKANCLNTCK 128

RESULT 2

US-09-358-569D-10

; Sequence 10, Application US/09358569D

; Patent No. 6294648

; GENERAL INFORMATION:

; APPLICANT: Delaria, Kathy

; APPLICANT: Rocznia, Steve

; APPLICANT: Davies, Christopher

; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

; FILE REFERENCE: MSB-7259

; CURRENT APPLICATION NUMBER: US/09/358,569D

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 64

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Extension of

; OTHER INFORMATION: Seq Id 1

US-09-358-569D-10

Query Match 38.7%; Score 242; DB 3; Length 64;

Best Local Similarity 65.5%; Pred. No. 1e-17;

Matches 38; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 46 DPKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103

Db 1 DLKQDVCMPKETGTGCLAYFLHWYDKKONTCSMFYGGCGNNNNFQSKANCLNTCK 58

RESULT 3

US-09-369-494-8

; Sequence 8, Application US/09369494

; Patent No. 6180607

; GENERAL INFORMATION:

; APPLICANT: Davies, Christopher

; APPLICANT: Chen, Dadong

; APPLICANT: Rocznia, Steve

; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

; FILE REFERENCE: MSB-7260

; CURRENT APPLICATION NUMBER: US/09/369,494

; CURRENT FILING DATE: 1999-08-05

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 58

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:fragment from

; OTHER INFORMATION: computer database

US-09-369-494-8

Query Match 37.8%; Score 236; DB 3; Length 58;

Best Local Similarity 66.1%; Pred. No. 3.7e-17;

Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 48 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103

Db 1 KQDVCMPKETGTGCLAYFLHWYDKKONTCSMFYGGCGNNNNFQSKANCLNTCK 56

RESULT 4

US-09-569-670-8

; Sequence 8, Application US/09569670

; Patent No. 6689582

; GENERAL INFORMATION:

; APPLICANT: Davies, Christopher

; APPLICANT: Chen, Dadong

; APPLICANT: Rocznia, Steve

; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

; FILE REFERENCE: MSB-7260

; CURRENT APPLICATION NUMBER: US/09/569,670

; CURRENT FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 58

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:fragment from

; OTHER INFORMATION: computer database

US-09-569-670-8

Query Match 37.8%; Score 236; DB 4; Length 58;

Best Local Similarity 66.1%; Pred. No. 3.7e-17;

Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 48 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103

Db 1 KQDVCMPKETGTGCLAYFLHWYDKKONTCSMFYGGCGNNNNFQSKANCLNTCK 56

RESULT 5

US-09-358-569D-8

; Sequence 8, Application US/09358569D

; Patent No. 6294648

; GENERAL INFORMATION:

; APPLICANT: Delaria, Kathy

; APPLICANT: Rocznia, Steve

; APPLICANT: Davies, Christopher

; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

; FILE REFERENCE: MSB-7259

; CURRENT APPLICATION NUMBER: US/09/358,569D

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 54

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:derived from

; OTHER INFORMATION: EST sequence database

US-09-358-569D-8

Query Match

Best Local Similarity 37.3%; Score 233; DB 3; Length 54;

Matches 37; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 50 DICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103

Db 1 DVCEMPKETGTGCLAYFLHWYDKKONTCSMFYGGCGNNNNFQSKANCLNTCK 54

RESULT 6

US-09-358-569D-1

; Sequence 1, Application US/09358569D

; Patent No. 6294648

; GENERAL INFORMATION:

; APPLICANT: Delaria, Kathy

; APPLICANT: Rocznia, Steve

; APPLICANT: Davies, Christopher

; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

; FILE REFERENCE: MSB-7259

; CURRENT APPLICATION NUMBER: US/09/358,569D

; CURRENT FILING DATE: 1999-07-20


```
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match      37.0%; Score 231; DB 3; Length 55;
Best Local Similarity 65.5%; Pred. No. 1.1e-16;
Matches 36; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 48 RNDICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFOTEICLVTC 102
Db 1 KQDVCEMPKETGPCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 7
US-08-358-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 16-DEC-1994
; APPLICATION NUMBER: US/08/358,160
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
```

```
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-113

Query Match      29.8%; Score 186; DB 1; Length 66;
Best Local Similarity 50.0%; Pred. No. 5.3e-12;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 48 RNDICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFOTEICLVTC 103
Db 4 KRDCRLPPEQGPKGRIPRYFYFNPASRMCSFIYGGCKGNKNFKTKAECVRACR 59

RESULT 8
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain,;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; FILING DATE: 15-JUL-1993
; APPLICATION NUMBER: US/08/93,285
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:7;
; LENGTH: 79
5466783-7

Query Match      29.8%; Score 186; DB 6; Length 79;
Best Local Similarity 50.0%; Pred. No. 6.3e-12;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 48 RNDICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFOTEICLVTC 103
Db 4 KRDCRLPPEQGPKGRIPRYFYFNPASRMCSFIYGGCKGNKNFKTKAECVRACR 59

RESULT 9
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain,;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:7;
; LENGTH: 79
5466783-7

Query Match      29.8%; Score 186; DB 6; Length 79;
Best Local Similarity 50.0%; Pred. No. 6.3e-12;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
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Qy 48 RDCSMQEPAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
Db 4 KRDICRLPPEQGFCGKGRIPRYFYNPASRCSEFIYGGCKGNKNFNKTAECVACR 59

RESULT 10
US-08-358-160-71
; Sequence 71, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-71

Query Match 28.3%; Score 177; DB 1; Length 58;
Best Local Similarity 56.4%; Pred. No. 3.8e-11; Indels 0; Gaps 0;
Matches 31; Conservative 5; Mismatches 19;

Qy 48 RDCSMQEPAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
Db 4 KRDICRLPPEQGFCGKGRIPRYFYNPASRCSEFIYGGCKGNKNFNKTAECVACR 59

Db 1 RPDFCLLPATGPCRAMIPRFYNNAKSGKCEPFIYGGCGGNNNNFKTEECRTC 55

RESULT 11
US-09-358-569D-13
; Sequence 13, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: sequence derived from EST database
US-09-358-569D-13

Query Match 28.0%; Score 175; DB 3; Length 43;
Best Local Similarity 69.0%; Pred. No. 4.5e-11; Indels 0; Gaps 0;
Matches 29; Conservative 4; Mismatches 9;

Qy 62 LASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
Db 1 LAYFLHWYDKKNTCSMFYVGGCGGNNNNFQSKANCLNTCK 42

RESULT 12
US-09-358-569D-9
; Sequence 9, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-9

Query Match 28.0%; Score 175; DB 3; Length 54;
Best Local Similarity 50.0%; Pred. No. 5.7e-11; Indels 0; Gaps 0;
Matches 27; Conservative 10; Mismatches 17;

Qy 50 DICSMQEPAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
Db 1 DLCLPQARGPCAKLLRYFYNNSTSNACEPFIYGGCGGNNNNFETEMCLRC 54

RESULT 13
US-08-358-160-123
; Sequence 123, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.


```
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-18

Query Match 27.7%; Score 173; DB 1; Length 58;
Best Local Similarity 50.0%; Pred. No. 9.8e-11;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 103
Db 1 RPDFQQLGYSAGPCVAMFPFYNGASMACQTFVYGGCGNGNFFVTEKDLQTCR 56

RESULT 16
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain.;Kretzmer, Kuniko K.;Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 26
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION NUMBER: US/08/93,285
; FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
; US-09-910-430-8
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```
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4
; LENGTH: 77
5466783-4

Query Match 27.0%; Score 169; DB 6; Length 77;
Best Local Similarity 46.3%; Pred. No. 3.3e-10;
Matches 25; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 103
Db 6 DLCLPQARGPCKAALLRYFYBSTSNACEPTYGGCGGNNNFETTCLEICE 59

RESULT 17
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain.;Kretzmer, Kuniko K.;Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4
; LENGTH: 77
5466783-4

Query Match 27.0%; Score 169; DB 6; Length 77;
Best Local Similarity 46.3%; Pred. No. 3.3e-10;
Matches 25; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 103
Db 6 DLCLPQARGPCKAALLRYFYBSTSNACEPTYGGCGGNNNFETTCLEICE 59

RESULT 18
US-09-910-430-8
; Sequence 8, Application US/09910430
; Patent No. 6794166
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Leboullie, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CF1
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
; US-09-910-430-8
```


QY 48 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103
DB 1 RPDFCOLGYSAGPCVAMPFRIFYNGTSMACETFYGGCGMGNGNFFVTEKDCLQTCR 56

RESULT 21
US-07-664-989B-48
; Sequence 48, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-48

Query Match 26.6%; Score 166; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 5e-10;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
QY 48 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 1 RPDFCLEPPYTGPCVAMPFRIFYNAKAGLCQTFYGGCGMGNGNFKSAEDCMRTC 55

RESULT 22
US-07-664-989B-51
; Sequence 51, Application US/07664989B

; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-51

Query Match 26.6%; Score 166; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 5e-10;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
QY 48 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 1 RPDFCLEPPYTGPCIAFFRYFNAKAGLCQTFYGGCGMGNGNFKSAEDCMRTC 55

RESULT 23
US-08-358-160-1
; Sequence 1, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ


```
/
/ TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
/ NUMBER OF SEQUENCES: 234
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W. Suite 300
/ CITY: Washington
/ STATE: District of Columbia
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/358,160
/ FILING DATE: 16-DEC-1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/133,031
/ FILING DATE: 13-OCT-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/009,319
/ FILING DATE: 26-JAN-1993
/ APPLICATION NUMBER: US 07/664,989
/ FILING DATE: 01-MAR-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/487,063
/ FILING DATE: 02-MAR-1990
/ APPLICATION NUMBER: US 07/240,160
/ FILING DATE: 02-SEP-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cooper, Iver P.
/ REGISTRATION NUMBER: 28,005
/ REFERENCE/DOCKET NUMBER: LEY=1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 58 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-358-160-1
/
/ Query Match 26.6%; Score 166; DB 1; Length 58;
/ Best Local Similarity 47.3%; Pred. No. 5e-10;
/ Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
/
/ QY 48 RKDICSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFOTEICLVTC 102
/ Db 1 RPDFCLEPPYTGFCVAMPFRFYNAKAGLCQTFYGGCGMGNNGNFKSAEDCMRTC 55
/
/ RESULT 24
/ US-08-358-160-15
/ Sequence 15, Application US/08358160
/ Patent No. 5663143
/ GENERAL INFORMATION:
/ APPLICANT: LEY, Arthur C.
/ APPLICANT: LADNER, Robert C.
/ APPLICANT: GUTERMAN, Sonia K.
/ APPLICANT: ROBERTS, Bruce L.
/ APPLICANT: MARKLAND, William
/ APPLICANT: KENT, Rachel B.
/ TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
/ TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
/ NUMBER OF SEQUENCES: 234
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/
```

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W. Suite 300
/ CITY: Washington
/ STATE: District of Columbia
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/358,160
/ FILING DATE: 16-DEC-1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/133,031
/ FILING DATE: 13-OCT-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/009,319
/ FILING DATE: 26-JAN-1993
/ APPLICATION NUMBER: US 07/664,989
/ FILING DATE: 01-MAR-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/487,063
/ FILING DATE: 02-MAR-1990
/ APPLICATION NUMBER: US 07/240,160
/ FILING DATE: 02-SEP-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cooper, Iver P.
/ REGISTRATION NUMBER: 28,005
/ REFERENCE/DOCKET NUMBER: LEY=1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 58 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-358-160-15
/
/ Query Match 26.6%; Score 166; DB 1; Length 58;
/ Best Local Similarity 48.2%; Pred. No. 5e-10;
/ Matches 27; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
/
/ QY 48 RKDICSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFOTEICLVTC 103
/ Db 1 KEDFCOLGYSAGPCVAMPFRFYNGTSMACETFOYGGCGMGNNGNFFTEKDCLOTCT 56
/
/ RESULT 25
/ US-08-358-160-26
/ Sequence 26, Application US/08358160
/ Patent No. 5663143
/ GENERAL INFORMATION:
/ APPLICANT: LEY, Arthur C.
/ APPLICANT: LADNER, Robert C.
/ APPLICANT: GUTERMAN, Sonia K.
/ APPLICANT: ROBERTS, Bruce L.
/ APPLICANT: MARKLAND, William
/ APPLICANT: KENT, Rachel B.
/ TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
/ TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
/ NUMBER OF SEQUENCES: 234
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/
```


STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEV=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-26

Query Match 26.6%; Score 166; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 5e-10;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPQEAGPCLASIPHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 102
Db 1 RPDFCLEPPYTGPCIAFFPRFYNAKAGLCQTFVYGGCMGNGNFKSAEDCMRTC 55

RESULT 26
US-08-358-160-27
Sequence 27, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEV, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington

STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEV=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-27

Query Match 26.6%; Score 166; DB 1; Length 62;
Best Local Similarity 47.3%; Pred. No. 5.4e-10;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPQEAGPCLASIPHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 102
Db 5 RPDFCLEPPYTGPCIAFFPRFYNAKAGLCQTFVYGGCMGNGNFKSAEDCMRTC 59

RESULT 27
US-09-270-767-46540
Sequence 46540, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46540
LENGTH: 107
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-46540

Query Match 26.6%; Score 166; DB 4; Length 107;
Best Local Similarity 39.1%; Pred. No. 9.4e-10;

Matches 27; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

[illegible]

RECORD 28
US-07-664-989B-49
; Sequence 49, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409sel
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; STREET: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004

Query Match	26.4%	Score 165;	DB 1;	Length 58;
Best Local Similarity	47.3%	Pred. No. 6.4e-10;		
Matches	26: Conservative	8: Mismatches	21: Indels	0: Gaps

Qy	48	RKDICMPQEAGPCLASIPHHWYKTKICSEFIYGCGQNNNFQTEAICLVTC	102
Db	1	RPDFCIPEPPYTGCVAIFRYFYNAKAGLCOTEFYGGCMGNGNFKSABDCMRTC	55

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RESULT 29
US-08-358-160-24
; Sequence 24, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEV, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BROWDY AND NEIMARK
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-24

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Query Match 26.4%; Score 165; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 6.4e-10;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 48 RKDTCMPQEGAPCLASIPHHWNKTKICSEFYGGCGQNNNNFQTEAICLVTC 102

nb 1 RPDGCEPPYTPGCVATPPRYFNAKAGLCOTFVYGGCMGNNGNFKSAEDCMRTC 55


```
RESULT 30
US-08-358-160-9
; Sequence 9, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-9

Query Match 26.2%; Score 164; DB 1; Length 58;
Best Local Similarity 48.2%; Pred. No. 8.1e-10;
Matches 27; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 48 RKDSCMPQAGCPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 103
Db 1 KEDSCQLGYSAGFCVAMPFRIFYNGTSMACETFIQGGCGNGNNGNFFVTEKDLQTCR 56

RESULT 31
US-08-829-876-211
```

```
; Sequence 211, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-211

Query Match 26.2%; Score 164; DB 2; Length 61;
Best Local Similarity 46.3%; Pred. No. 8.5e-10;
Matches 25; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

Qy 49 KDICMPQAGCPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 102
Db 4 REVCSEAETGTCRAAIQHMYFDVTEGKCAPFFYGGCGNNRNNFDTEECNAVC 57

RESULT 22
US-08-829-876-214
; Sequence 214, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
```


ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 4.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/664,989B
FILING DATE: 19910301
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-664-989B-84

Query Match 26.1%; Score 163; DB 1; Length 58;

Best Local Similarity 47.3%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGPCLASIPHWYKTKICSEFIYGGCGQNNNFOTEICLVTC 102
DB 1 RPDFCLPPYTGPCVAMFPRFYFNAGLQTFMYGGCGQKGNFNKSAEDCMRTC 55

RESULT 38

US-08-358-160-12
Sequence 12, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-12

Query Match 26.1%; Score 163; DB 1; Length 58;

Best Local Similarity 48.2%; Pred. No. 1e-09;
Matches 27; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGPCLASIPHWYKTKICSEFIYGGCGQNNNFOTEICLVTC 103
DB 1 RPDFCQLGYSTGPCVAMFPRFYNGTSMACETFOYGGCMGNGNFFVTEKDCLOTCR 56

RESULT 39

US-08-358-160-61
Sequence 61, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031


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; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-61

Query Match 26.1%; Score 163; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RNDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 1 RPDFCLEPPYTCVAMPFRPYNAKAGLCQTFMYGGCGKGNFKSAEDCWRTC 55

RESULT 40
US-08-463-155A-56
; Sequence 56, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-155A-56

Query Match 26.1%; Score 163; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 2 REVCSQAEDGFCRAAIPRWYFDVTEGKCAPFIYGGCGGNNNNFDTSEYCAAVC 55

RESULT 41
US-08-463-432B-56
; Sequence 56, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,432B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-432B-56

Query Match 26.1%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 2 REVCSQAEDGFCRAAIPRWYFDVTEGKCAPFIYGGCGGNNNNFDTSEYCAAVC 55

RESULT 42
US-08-676-124-69
; Sequence 69, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; FROM FROM THE KUNITZ DOMAINS
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-155A-56

Query Match 26.1%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 2 REVCSQAEDGFCRAAIPRWYFDVTEGKCAPFIYGGCGGNNNNFDTSEYCAAVC 55

RESULT 41
US-08-463-432B-56
; Sequence 56, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,432B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-432B-56

Query Match 26.1%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 2 REVCSQAEDGFCRAAIPRWYFDVTEGKCAPFIYGGCGGNNNNFDTSEYCAAVC 55

RESULT 42
US-08-676-124-69
; Sequence 69, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; FROM FROM THE KUNITZ DOMAINS
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-180

Query Match 26.1%; Score 163; DB 2; Length 61;
Best Local Similarity 46.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 4 REVCSQAETGCRAGIPRWYFDVTGKCAPFFYGGCGGNNNNFDTTEYCMAVC 57

RESULT 47
US-08-829-876-218
; Sequence 218, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelt, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-218

Query Match 26.1%; Score 163; DB 2; Length 61;
Best Local Similarity 46.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 4 REVCSQAETGCRAGIPRWYFDVTGKCAPFFYGGCGGNNNNFDTTEYCMAVC 57

RESULT 48
US-09-234-874A-180
; Sequence 180, Application US/09234874A
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; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-874A-180

Query Match 26.1%; Score 163; DB 3; Length 61;
Best Local Similarity 46.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 4 REVCSQAETGCRAGIPRWYFDVTGKCAPFFYGGCGGNNNNFDTTEYCMAVC 57

RESULT 49
US-09-234-874A-218
; Sequence 218, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-874A-218

Query Match 26.1%; Score 163; DB 3; Length 61;
Best Local Similarity 46.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Qy 49 KDICMPQEGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db :::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 REVSCQAEGPCRAAIYHVFDTVEGKCAPFFYGGCGGNRNNFDTBEYCMAVC 57

RESULT 50
US-09-234-873A-180
; Sequence 180, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
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;
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-873A-180

Query Match 26.1%; Score 163; DB 4; Length 61;
Best Local Similarity 46.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 49 KDICMPQEGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db :::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 REVSCQAETGCRAGIPRWTFDVTGKCAPFFYGGCGGNRNNFDTBEYCMAVC 57

Search completed: September 21, 2005, 16:42:18
Job time : 20.3864 secs
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:33:14 ; Search time 66.2891 Seconds
(without alignments)
650.835 Million cell updates/sec

Title: US-10-807-204-2

Perfect score: 625

Sequence: 1 EGILGKPCPKIKVEVEEI.....GNNNNFQTEAICLVCTCKYH 106

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Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

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Published Applications AA:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	106	16	US-10-807-204-2
2	625	100.0	131	16	US-10-807-204-1
3	625	100.0	131	16	US-10-807-204-12
4	603	96.5	131	16	US-10-807-204-15
5	423	67.7	98	16	US-10-807-204-9
6	415	66.6	136	16	US-10-807-204-16
7	401.5	64.2	117	9	US-09-852-659A-119
8	401.5	64.2	117	15	US-10-058-993-120
9	400	64.0	102	9	US-09-852-659A-120
10	400	64.0	102	15	US-10-058-993-121
11	400	64.0	133	9	US-09-853-161-75

12	400	64.0	133	9	US-09-852-659A-75
13	400	64.0	133	9	US-09-852-797-75
14	400	64.0	133	15	US-10-058-993-75
15	400	64.0	133	16	US-10-807-204-13
16	352	56.3	134	16	US-10-807-204-14
17	276	44.2	86	17	US-10-480-988-21
18	276	44.2	101	15	US-10-276-774-2606
19	258	41.3	43	16	US-10-807-204-5
20	236	37.8	58	16	US-10-361-997-5
21	236	37.8	58	17	US-10-931-153-21
22	219	35.0	51	15	US-10-058-993-118
23	197	31.5	759	17	US-10-825-692-48
24	184	29.4	64	10	US-09-896-095-160
25	184	29.4	64	14	US-10-038-722-103
26	184	29.4	64	15	US-10-115-134-17
27	182.5	29.2	571	14	US-10-369-736-3
28	182.5	29.2	571	14	US-10-369-736-49
29	182.5	29.2	571	14	US-10-369-738-3
30	182.5	29.2	571	14	US-10-369-738-49
31	182.5	29.2	571	19	US-11-028-058-3
32	182.5	29.2	571	19	US-11-028-058-49
33	180	28.8	33	16	US-10-807-204-7
34	180	28.8	33	16	US-10-807-204-10
35	177	28.3	58	14	US-10-038-722-5
36	175	28.0	67	10	US-09-896-095-147
37	175	28.0	67	14	US-10-038-722-90
38	175	28.0	67	15	US-10-115-134-4
39	173.5	27.8	503	14	US-10-007-280A-233
40	173.5	27.8	576	9	US-09-794-589-2
41	173.5	27.8	576	14	US-10-315-380-2
42	173.5	27.8	576	14	US-10-369-736-7
43	173.5	27.8	576	14	US-10-369-738-7
44	173.5	27.8	576	19	US-11-028-058-7
45	173.5	27.8	640	14	US-10-369-736-5
46	173.5	27.8	640	14	US-10-369-738-5
47	173.5	27.8	640	19	US-11-028-058-5
48	173	27.7	58	14	US-10-038-722-17
49	173	27.7	58	14	US-10-038-722-18
50	173	27.7	58	14	US-10-038-722-19

ALIGNMENTS

RESULT 1
US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN


```

; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-2

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Query Match          100.0%; Score 625; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.4e-52;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGLDFRDKDICSMPQEAGP 60
DB 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGLDFRDKDICSMPQEAGP 60

QY 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 106
DB 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 106

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RESULT 2
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015 US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:

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; NAME/KEY: SIGNAL
; LOCATION: (1)...(25)
; OTHER INFORMATION: predicted by SignalP 2.0
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (48)...(60)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (54)...(69)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(127)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (86)...(110)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (102)...(123)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-1

Query Match          100.0%; Score 625; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.8e-52;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGLDFRDKDICSMPQEAGP 60
DB 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 106
DB 86 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 131

RESULT 3
US-10-807-204-12
; Sequence 12, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015 US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 12
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-12

Query Match      100.0%; Score 625; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.8e-52;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCKYH 106
Db 86 CLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCKYH 131

RESULT 4
US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-15

Query Match      96.5%; Score 603; DB 16; Length 131;
Best Local Similarity 98.1%; Pred. No. 2.3e-50;
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCKYH 106
Db 86 CLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCKYH 131

RESULT 5
US-10-807-204-9
; Sequence 9, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-9

Query Match      96.5%; Score 603; DB 16; Length 131;
Best Local Similarity 98.1%; Pred. No. 2.3e-50;
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCKYH 106
Db 86 CLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCKYH 131

RESULT 6
US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-16

Query Match      66.6%; Score 416; DB 16; Length 136;
Best Local Similarity 60.6%; Pred. No. 2.5e-32;
Matches 63; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

QY 1 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGFFRTCTPRVVKCEVEERNECTRHQCPCNKKRCLFSCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCK 104
Db 86 CLAYLPRWYNNQETDLCTEFYGGCGGNNNNFSEGICTVWCKK 129

RESULT 7
US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
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; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-9

Query Match      67.7%; Score 423; DB 16; Length 98;
Best Local Similarity 98.6%; Pred. No. 3.9e-33;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNK 73
Db 86 CLASIPHHWYNNK 98

RESULT 6
US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-16

Query Match      66.6%; Score 416; DB 16; Length 136;
Best Local Similarity 60.6%; Pred. No. 2.5e-32;
Matches 63; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

QY 1 EGILGPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGFFRTCTPRVVKCEVEERNECTRHQCPCNKKRCLFSCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCK 104
Db 86 CLAYLPRWYNNQETDLCTEFYGGCGGNNNNFSEGICTVWCKK 129

RESULT 7
US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
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Best Local Similarity 66.7%; Pred. No. 6.6e-31; Mismatches 21; Indels 0; Gaps 0;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIVKEVEEIDQCTKPRDCPENMKCCPFCGKCKCLDFRDKDICSMPQOAGPCLASIPH 67
DB 2 CPKIREEEFQERDVCTKRDQCQDNKKCCVFCGKCKCLDLKQDVCMPKGTGCLAYFLH 61
QY 68 WYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
DB 62 WYDKKDNCTSMFVYGGCGGNNNNFQSKANCLNTCK 97
RESULT 10
US-10-058-993-121
; Sequence 121, Application US/10058993
; Patent No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/048,710
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/048,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-121
Query Match 64.0%; Score 400; DB 15; Length 102;
Best Local Similarity 66.7%; Pred. No. 6.6e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIVKEVEEIDQCTKPRDCPENMKCCPFCGKCKCLDFRDKDICSMPQOAGPCLASIPH 67
DB 2 CPKIREEEFQERDVCTKRDQCQDNKKCCVFCGKCKCLDLKQDVCMPKGTGCLAYFLH 61
QY 68 WYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
DB 62 WYDKKDNCTSMFVYGGCGGNNNNFQSKANCLNTCK 97

RESULT 11
US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-75
Query Match 64.0%; Score 400; DB 9; Length 133;
Best Local Similarity 66.7%; Pred. No. 8.5e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIVKEVEEIDQCTKPRDCPENMKCCPFCGKCKCLDFRDKDICSMPQOAGPCLASIPH 67
DB 33 CPKIREEEFQERDVCTKRDQCQDNKKCCVFCGKCKCLDLKQDVCMPKGTGCLAYFLH 92
QY 68 WYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
DB 93 WYDKKDNCTSMFVYGGCGGNNNNFQSKANCLNTCK 128
RESULT 12
US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14

Thu Sep 22 07:16:47 2005

Db 33 CPKIRECEFBQERDVCTKDRQCQDNKKCCVFCGKCKLDLKDQVCMPEKGTGCLAYFLH 92
QY 68 WYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
Db 93 WYDCKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 128

RESULT 15
US-10-807-204-13
; Sequence 13, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015-US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-13

Query Match 64.0%; Score 400; DB 16; Length 133;
Best Local Similarity 66.7%; Pred. No. 8.5e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKCKLDLFRKIDICSMPOEAGPCLASIPH 67
Db 33 CPKIRECEFBQERDVCTKDRQCQDNKKCCVFCGKCKLDLKDQVCMPEKGTGCLAYFLH 92
QY 68 WYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
Db 93 WYDCKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 128

RESULT 16
US-10-807-204-14
; Sequence 14, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015-US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-14

Query Match 56.3%; Score 352; DB 16; Length 134;
Best Local Similarity 55.7%; Pred. No. 3.6e-26;
Matches 54; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

QY 8 CPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKCKLDLFRKIDICSMPOEAGPCLASIPH 67
Db 33 CPKIRECEFBQERDVCTKDRQCQDNKKCCVFCGKCKLDLKDQVCMPEKGTGCLAYFLH 92
QY 68 WYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 104
Db 93 WYDCKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 128

RESULT 17
US-10-480-988-21
; Sequence 21, Application US/10480988
; Publication No. US20050069877A1
; GENERAL INFORMATION:
; APPLICANT: Gandhi, Ameena R.; Kable, Amy E.;
; APPLICANT: Swarnakar, Anita; Hafalia, April J.A.;
; APPLICANT: Tran, Bao; Duggan, Brendan M.;
; APPLICANT: Warren, Bridget A.; Ison, Craig H.;
; APPLICANT: Honchellu, Cynthia D.; Nguyen, Dannel B.;
; APPLICANT: Lu, Dyung Aina M.; Lee, Ernestine A.;
; APPLICANT: Yue, Henry; Forsythe, Ian J.;
; APPLICANT: Barroso, Ines; Ramkumar, Javalaxmi;
; APPLICANT: Griffin, Jennifer A.; Li, Joana X.;
; APPLICANT: Yang, Junming; Thangavelu, Kavitha;
; APPLICANT: Gietsen, Kimberly J.; Ding, Li;
; APPLICANT: Baughn, Mariah R.; Borowsky, Mark L.;
; APPLICANT: Yao, Monique G.; Chawla, Narinder K.;
; APPLICANT: Mason, Patricia M.; Gururajan, Rajagopal;
; APPLICANT: Lee, Sally; Bessa, Shanya D.;
; APPLICANT: Lee, Soo Yeun; Tran, Uyen K.;
; APPLICANT: Elliott, Vicki S.; Luo, Wen;
; APPLICANT: Sprague, William W.; Tang, Y. Tom;
; APPLICANT: Lu, Yan; Zebajadian, Yeganeh
; TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
; FILE REFERENCE: PP-1040 USN
; CURRENT APPLICATION NUMBER: US/10/480,988
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: PCT/US02/19360
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/300,508
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/303,445
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/305,405
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/311,442
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: US 60/314,821
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/315,992
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/378,205
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7675588CD1
US-10-480-988-21

Query Match 44.2%; Score 276; DB 17; Length 86;
Best Local Similarity 98.0%; Pred. No. 5e-19;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EGI LGKPCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKCKLDLFRK 49
Db 26 EGI LGKPCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKCKLDLFRK 74

RESULT 18
US-10-276-774-2606
; Sequence 2606, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2606
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2606

Query Match 44.2%; Score 276; DB 15; Length 101;
Best Local Similarity 98.0%; Pred. No. 5.8e-19;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EGILGKPCPKIRKEVEBEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 49
Db 41 EGILGKPCPKIRKEVEBEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 89

RESULT 19
US-10-807-204-5
; Sequence 5, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Anos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-5

Query Match 41.3%; Score 258; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.4e-17;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PCPKIRKEVEBEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 49
Db 1 PCPKIRKEVEBEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 43

RESULT 20
US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles

; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5

Query Match 37.8%; Score 236; DB 16; Length 58;
Best Local Similarity 66.1%; Pred. No. 2.4e-15;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
Qy 48 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTK 103
Db 1 KQDVCEMPKETGPCLAYFLHWYDKKONTCSMFYGGCGQNNNNFQSKANCLNTCK 56

RESULT 21
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-PEGYLATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match 37.8%; Score 236; DB 17; Length 58;
Best Local Similarity 66.1%; Pred. No. 2.4e-15;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
Qy 48 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTK 103
Db 1 KQDVCEMPKETGPCLAYFLHWYDKKONTCSMFYGGCGQNNNNFQSKANCLNTCK 56

RESULT 22
US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Roben et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161


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; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-058-993-118

Query Match      35.0%; Score 219; DB 15; Length 51;
Best Local Similarity 68.6%; Pred. No. 9.3e-14;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 52 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 102
Db 1 CEMPKEIGFLAYFLHWDYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 51

RESULT 23
US-10-825-692-48
; Sequence 48, Application US/10825692
; Publication No. US20050042232A1
; GENERAL INFORMATION:
; APPLICANT: Hotez, Peter
; APPLICANT: Ashcom, James
; APPLICANT: Bdamchian, Mahnaz
; APPLICANT: Zhan, Bin
; APPLICANT: Wang, Yan
; APPLICANT: Hawdon, John
; APPLICANT: Loukas, Alexander
; APPLICANT: Williamson, Angela
; APPLICANT: Jones, Brian
; APPLICANT: Bethony, Jeffrey
; APPLICANT: Goud, Gaddam
; APPLICANT: Botazzi, Maria E.
; APPLICANT: Mendez, Susana
; TITLE OF INVENTION: Hookworm Vaccine
; FILE REFERENCE: 03740007aa
; CURRENT APPLICATION NUMBER: US/10/825,692
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/329,533
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 60/332,007
; PRIOR FILING DATE: 2001-11-23
; PRIOR APPLICATION NUMBER: US 60/375,404
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: PCT US02/33106
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Ancylostoma caninum
; US-10-825-692-48

Query Match      31.5%; Score 197; DB 17; Length 759;
Best Local Similarity 46.1%; Pred. No. 1.6e-10;
Matches 35; Conservative 13; Mismatches 26; Indels 2; Gaps 1;

QY 31 ENMKCCPESCCKKCL--DFRKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGN 88
Db 560 ETMEDCTFTCEORLAKPELEKDVCSQPITAGCRASIPRYGVDKSKKCKVKFTYGGCKGN 619

QY 89 NNNFQTEAICLVTKK 104
Db 620 GNRFFTKNECEKTKR 635

RESULT 24
US-09-896-095-160
; Sequence 160, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Caretta sp.
; US-09-896-095-160

Query Match      29.4%; Score 184; DB 10; Length 64;
Best Local Similarity 48.2%; Pred. No. 2.7e-10;
Matches 27; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 103
Db 4 KRDIKRLPPEQFCCKGRLPYFYNPASRMCESFIYGGCKGNKKNFKTKAECVRACR 59

RESULT 25
US-10-038-722-103
; Sequence 103, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS RHE INHIBITORS
; FILE REFERENCE: LEY-1B
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; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 64
; TYPE: PRP
; ORGANISM: Caretta sp.
US-10-038-722-103

Query Match      29.4%; Score 184; DB 14; Length 64;
Best Local Similarity 48.2%; Pred. No. 2.7e-10;
Matches 27; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY    48 RKDICSMPGAGPCLASIPHHWYNKTKICSFHYGGCGGNNNFQTBAICLVTC 103
Db     :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
          4 KRDIQLPEQGFCGRLPFYFNPSRMCESFIYGCKGNKNPKTKAECVRACR 59

RESULT 26
US-10-115-134-17
Sequence 17, Application US/10115134
Publication No. US2003023977A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur Charles
APPLICANT: GUTERMAN, Sonia Kosow
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel Baribault
APPLICANT: ROBERTS, Bruce Lindsey
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
FILE REFERENCE: LEY=1C
CURRENT APPLICATION NUMBER: US/10/115,134
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 08/849,406
PRIOR FILING DATE: 2001-07-21
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 64
TYPE: PRP
ORGANISM: Caretta sp.
US-10-115-134-17

Query Match      29.4%; Score 184; DB 15; Length 64;
Best Local Similarity 48.2%; Pred. No. 2.7e-10;
Matches 27; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY    48 RKDICSMPGAGPCLASIPHHWYNKTKICSFHYGGCGGNNNFQTBAICLVTC 103
Db     :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
          4 KRDIQLPEQGFCGRLPFYFNPSRMCESFIYGCKGNKNPNFKTKAECVCR 59

RESULT 27
US-10-369-736-3
Sequence 3, Application US/10369736
Publication No. US20030162714A1
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: WOLFMAN, NEIL M.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/10/369,736
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
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<p> ; NUMBER OF SEQ ID NOS: 53 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 3 ; LENGTH: 571 ; TYPE: PRT ; ORGANISM: Mus sp. US-10-369-738-3 </p> <p> Query Match 29.2%; Score 182.5; DB 14; Length 571; Best Local Similarity 31.8%; Pred. No. 3.1e-09; Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3; </p> <p> QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 52 DB 322 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHHNLNHFETYEACMLACMSGPLATC 381 </p> <p> QY 53 SMPQEAGPCLASIPHHWYKTKICSEFYGGCGQNNNNFQTEAICLVTC 102 DB 382 SLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCEGNGNPFESREACEESC 431 </p> <p> RESULT 30 US-10-369-738-49 ; Sequence 49, Application US/10369738 ; Publication No. US20030180306A1 ; GENERAL INFORMATION: ; APPLICANT: HILL, JENNIFER J. ; APPLICANT: WOLFMAN, NEIL M. ; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS ; FILE REFERENCE: 08702.0014-00 ; CURRENT APPLICATION NUMBER: US/10/369,738 ; CURRENT FILING DATE: 2003-02-21 ; PRIOR APPLICATION NUMBER: 60/357,846 ; PRIOR FILING DATE: 2002-02-21 ; PRIOR APPLICATION NUMBER: 60/434,645 ; PRIOR FILING DATE: 2002-12-20 ; NUMBER OF SEQ ID NOS: 53 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 49 ; LENGTH: 571 ; TYPE: PRT ; ORGANISM: Mus sp. US-10-369-738-49 </p> <p> Query Match 29.2%; Score 182.5; DB 14; Length 571; Best Local Similarity 31.8%; Pred. No. 3.1e-09; Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3; </p> <p> QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 52 DB 322 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHHNLNHFETYEACMLACMSGPLATC 381 </p> <p> QY 53 SMPQEAGPCLASIPHHWYKTKICSEFYGGCGQNNNNFQTEAICLVTC 102 DB 382 SLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCEGNGNPFESREACEESC 431 </p>	<p> ; PRIOR FILING DATE: 2002-12-20 ; NUMBER OF SEQ ID NOS: 53 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 3 ; LENGTH: 571 ; TYPE: PRT ; ORGANISM: Mus sp. US-11-028-058-3 </p> <p> Query Match 29.2%; Score 182.5; DB 19; Length 571; Best Local Similarity 31.8%; Pred. No. 3.1e-09; Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3; </p> <p> QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 52 DB 322 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHHNLNHFETYEACMLACMSGPLATC 381 </p> <p> QY 53 SMPQEAGPCLASIPHHWYKTKICSEFYGGCGQNNNNFQTEAICLVTC 102 DB 382 SLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCEGNGNPFESREACEESC 431 </p> <p> RESULT 32 US-11-028-058-49 ; Sequence 49, Application US/11028058 ; Publication No. US20050106154A1 ; GENERAL INFORMATION: ; APPLICANT: HILL, JENNIFER J. ; APPLICANT: WOLFMAN, NEIL M. ; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS ; FILE REFERENCE: 08702.0015-00 ; CURRENT APPLICATION NUMBER: US/11/028,058 ; CURRENT FILING DATE: 2005-01-04 ; PRIOR APPLICATION NUMBER: US/10/369,736 ; PRIOR FILING DATE: 2003-02-21 ; PRIOR APPLICATION NUMBER: 60/357,846 ; PRIOR FILING DATE: 2002-02-21 ; PRIOR APPLICATION NUMBER: 60/434,645 ; PRIOR FILING DATE: 2002-12-20 ; NUMBER OF SEQ ID NOS: 53 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 49 ; LENGTH: 571 ; TYPE: PRT ; ORGANISM: Mus sp. US-11-028-058-49 </p> <p> Query Match 29.2%; Score 182.5; DB 19; Length 571; Best Local Similarity 31.8%; Pred. No. 3.1e-09; Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3; </p> <p> QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 52 DB 322 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHHNLNHFETYEACMLACMSGPLATC 381 </p> <p> QY 53 SMPQEAGPCLASIPHHWYKTKICSEFYGGCGQNNNNFQTEAICLVTC 102 DB 382 SLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCEGNGNPFESREACEESC 431 </p>
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, PRIOR APPLICATION NUMBER: PCT/EP03/01629
, PRIOR FILING DATE: 2003-02-18
, PRIOR APPLICATION NUMBER: US 60/358,683
, PRIOR FILING DATE: 2002-02-21
, NUMBER OF SEQ ID NOS: 16
, SOFTWARE: FastSEQ for Windows Version 4.0
, SEQ ID NO 7
, LENGTH: 33
, TYPE: PRT
, ORGANISM: Homo sapiens
US-10-807-204-7

```

```

Query Match      28.8%; Score 180; DB 16; Length 33;
Best Local Similarity 97.0%; Pred. No. 3.5e-10;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      74      TKICSEFIYGGCGGNNNNNFOTEICLVTCCKYH 106
          |||||
Db      1      TKICSEFIYGGSGGNNNNNFOTEICLVTCCKYH 33
          |||||

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RESULT 34
US-10-807-204-10
; Sequence 10, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015 US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-10

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[illegible]

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RESULT 35
US-10-038-722-5
; Sequence 5, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349

```

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; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5

```

```

Query Match      28.3%; Score 177; DB 14; Length 58;
Best Local Similarity 56.4%; Pred. No. 1.2e-09;
Matches 31; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 48 RKDICSMPQBPAGCLASIPHWYNNKTKTISEFTYGGCGGNNNNFQEAICLVTC 102
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dh 1 RNPFCILPAGTGPCRAMT PRFYNAKSGKCEPFTYGGCGGNNNNFKTEECRRTC 55
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 36
US-09-896-095-147
; Sequence 147, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896.095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 147
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-896-095-147

```

	Query Match	28.0%	Score 175;	DB 10;	Length 67;
Best Local Similarity	50.0%;	Pred. No. 2.1e-09;			
Matches	27;	Conservative 10;	Mismatches 17;	Indels 0;	Gaps 0
Qv	50	DICSMPEAGPCLASIPHHWYNNKTKICSFYGGCGGNNNNFOTEAILCVTK	103		
ph	6	DICOLPOARGPCKAALLRFYNTSFAPEPTFYGGCGGNNNNFETTEICLR	59		

RESULT 37
US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.


```

; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Query Match      28.0%; Score 175; DB 14; Length 67;
Best Local Similarity 50.0%; Pred.No.2.le-09;
Matches 27; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy    50 DICSMPQEAGPCLASIPHWYNKTKICSEFIYGGCGNNNFFOTEALCLVTCK 103
       |::|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::
Db    6 DLQLPQARGPKAALLRYFNSTSNACEPFYGGCGNNNFETTEMCLRICE 59
       ||::|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::

RESULT 38
US-10-115-134-4
; Sequence 4, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-115-134-4

Query Match      28.0%; Score 175; DB 15; Length 67;
Best Local Similarity 50.0%; Pred.No.2.le-09;
Matches 27; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy    50 DICSMPQEAGPCLASIPHWYNKTKICSFYIGGCGNNNFFOTEALCLVTCK 103
       |:|::|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::
Db    6 DLQLPQARGPKAALLRYFNSTSNACEPFYIGGCGNNNFETTEMCLRICE 59
       |:|::|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::

RESULT 39
US-10-007-280A-233
; Sequence 233, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Hervé
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Proteins
; FILE REFERENCE: DBX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A
```



```
; SEQ ID NO 5
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-736-5

Query Match      27.8%; Score 173.5; DB 14; Length 640;
Best Local Similarity 31.8%; Pred. No. 2.6e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDTC 52
DB 391 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHPETYEACMLACMSGPLAAC 450

QY 53 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 451 SLPALQGPCKAYAPRWAYNSQTGCOSFVYGGCGEGNNGNFESREACEESC 500

RESULT 46
US-10-369-738-5
; Sequence 5, Application US/10359738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-738-5

Query Match      27.8%; Score 173.5; DB 14; Length 640;
Best Local Similarity 31.8%; Pred. No. 2.6e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDTC 52
DB 391 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHPETYEACMLACMSGPLAAC 450

QY 53 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 451 SLPALQGPCKAYAPRWAYNSQTGCOSFVYGGCGEGNNGNFESREACEESC 500

RESULT 47
US-10-369-738-5
; Sequence 5, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
```

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-058-5

Query Match      27.8%; Score 173.5; DB 19; Length 640;
Best Local Similarity 31.8%; Pred. No. 2.6e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDTC 52
DB 391 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHPETYEACMLACMSGPLAAC 450

QY 53 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 451 SLPALQGPCKAYAPRWAYNSQTGCOSFVYGGCGEGNNGNFESREACEESC 500

RESULT 48
US-10-038-722-17
; Sequence 17, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, ARTHUR C.
; APPLICANT: GUTERMAN, SONIA K.
; APPLICANT: MARKLAND, WILLIAM
; APPLICANT: KENT, RACHEL B.
; APPLICANT: ROBERTS, BRUCE L.
; APPLICANT: LADNER, ROBERT C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-038-722-17

Query Match      27.7%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 2.9e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103
DB 1 RPDFCQLGYSAGPCVAMPFRFYNGTSMACQTFVYGGCMGNGNFVTEKDLQTCR 56

RESULT 49
US-10-038-722-18
; Sequence 18, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, ARTHUR C.
; APPLICANT: GUTERMAN, SONIA K.
; APPLICANT: MARKLAND, WILLIAM
; APPLICANT: KENT, RACHEL B.
; APPLICANT: ROBERTS, BRUCE L.
; APPLICANT: LADNER, ROBERT C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY-1B
```



```
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      27.7%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 2.9e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPQEGAPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTK 103
DB 1 RPDFCQLGYSAGPCVAMPFRYPYNGASMACQTFVYGGCGNGNGNFVTEKDCLQTCR 56

RESULT 50
US-10-038-722-19
; Sequence 19, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-038-722-19

Query Match      27.7%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 2.9e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPQEGAPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTK 103
DB 1 RPDFCQLGYSAGPCVAMPFRYPYNGTSMACETFYVYGGCGNGNGNFVTEKDCLQTCR 56
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Search completed: September 21, 2005, 16:45:53
Job time : 67.2891 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:21:48 ; Search time 15.3215 Seconds
(without alignments)
665.663 Million cell updates/sec

Title: US-10-807-204-2

Perfect score: 625

Sequence: 1 EGILGKPCPKIKVCEVEBEI.....GNNNNQTEAICLVTKCKYH 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	29.8	110	1 TITTOR	basic proteinase i
2	184.5	29.5	1522	2 H88380	protein T22F7.3 [i
3	172.5	27.6	1599	2 T16210	hypothetical prote
4	172	27.5	67	1 TIBOC	trypsin inhibitor,
5	171	27.4	1416	2 E88550	protein ZC84.1 [im
6	171	27.4	2844	2 S28291	hypothetical prote
7	168	26.9	922	2 T23573	hypothetical prote
8	165	26.4	1474	2 D88550	protein ZC84.6 [im
9	161	25.8	62	2 A44180	taicatoxin serine
10	161	25.8	747	2 JH0773	Alzheimer's disease
11	160	25.6	57	2 A59204	basic proteinase i
12	160	25.6	252	2 JG0185	hepatocyte growth
13	160	25.6	1743	2 T26859	hypothetical prote
14	157	25.1	58	1 T1HABK	isoinhibitor K (BP
15	157	25.1	111	2 S41082	amyloid precursor
16	157	25.1	337	1 T1PGBI	alpha-1-microglobu
17	157	25.1	751	2 A49974	beta-amyloid precu
18	157	25.1	763	2 A49321	amyloid beta (A4)
19	157	25.1	765	2 S42880	amyloid precursor-
20	155.5	24.9	2150	2 T32497	hypothetical prote
21	154	24.6	484	4 A32761	hypothetical Alzhe
22	154	24.6	770	1 QRHUA4	Alzheimer's disease
23	153	24.5	62	2 S19327	venom basic protei
24	152	24.3	62	2 S07451	proteinase inhibit
25	152	24.3	76	2 S06678	Alzheimer's disease
26	152	24.3	76	2 S03607	Alzheimer's disease
27	152	24.3	352	1 HCHU	alpha-1-microglobu
28	152	24.3	352	1 T1BOBI	alpha-1-microglobu
29	151	24.2	65	1 T1VIVC	venom basic protei

30	151	24.2	100	2 A32282	Alzheimer's disease
31	149.5	23.9	62	2 S01802	chymotrypsin inhib
32	149.5	23.9	249	2 T32060	hypothetical prote
33	149	23.8	57	1 T1FHPB	proteinase inhibit
34	149	23.8	76	2 S04855	Alzheimer's disease
35	149	23.8	123	2 A29652	inter-alpha-trypsi
36	148.5	23.8	62	2 S01803	chymotrypsin inhib
37	147.5	23.6	372	2 JC2556	alpha-1-microglobu
38	147	23.5	125	1 T1HOBI	basic proteinase i
39	146	23.4	100	1 T1BO	lipoprotein-associ
40	146	23.4	300	2 S12143	hypothetical prote
41	146	23.4	805	2 T34212	protein C37C3_6a [
42	146	23.4	1558	2 C89114	hypothetical prote
43	146	23.4	2167	2 T34395	uterine plasmin/tr
44	145	23.2	122	1 A55115	tissue factor path
45	145	23.2	299	2 I46937	short epsilon-dend
46	144	23.0	57	2 B59399	venom basic protei
47	144	23.0	59	1 T1EPED	isoaprotinin G1 -
48	144	23.0	59	2 S00371	Long epsilon-dendr
49	144	23.0	59	2 A59399	serum basic protei
50	144	23.0	60	1 T1BOR	

ALIGNMENTS

RESULT 1

TITTOR

basic proteinase inhibitor - loggerhead

C:Species: Caretta caretta (loggerhead)

C>Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A01224

R:Kato, I.; Tominaga, N.

Fed. Proc. 38, 832, 1979

A:Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tan

A:Reference number: A01224

A:Accession: A01224

A:Molecule type: protein

A:Residues: 1-110 <KAT>

A:Cross-references: UNIPROT:P00993

C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inh

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:8-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:63-105/Domain: antileukoproteinase repeat homology <ALP>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8-58,17-41,33-54,67-93,76-97,80-92,86-101/Diulfide bonds: #status predicted

F:18/Inhibitory site: Lys (trypsin) #status predicted

Query Match 29.8%; Score 186; DB 1; Length 110;

Best Local Similarity 50.0%; Pred. No. 8.7e-10;

Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 48 RKDICSMPQEAQPCLASPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103

Db 4 KRDICRLPPEQCKGRIPRYFPNPSRMCSEFIYGGCKGNKFNFKTAEQVACR 59

RESULT 2

H88380

protein T22F7.3 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: H88380

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/c_el

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an

A:Accession: H88380

A>Status: preliminary

A:Molecule type: DNA

493/1; 2555/1; 2720/1; 2739/3; 2819/1
F;220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BP11>
F;343-375/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>
F;442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BP13>
F;546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BP14>
F;654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BP15>
F;1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BP16>
F;1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BP17>
F;1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BP18>
F;1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BP19>
F;2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BP10>

Query Match 27.4%; Score 171; DB 2; Length 2844;
Best Local Similarity 30.4%; Pred. No. 2.4e-07;
Matches 35; Conservative 14; Mismatches 34; Indels 32; Gaps 3;

QY 12 KVECEV-----EEDQCTKPRDCPENMK-----CCPFCGKGLDPR 48
DB 388 KHECEMYCARLQCRGSPRLRIGEGAQRCQNNACQPSHCEKADQGVCCP-----RK 438

QY 49 KDICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 103
DB 439 QTICAPLRIGDCTENVKRYWYNARTQCFEYTCQGNNDNNFDSIMDCQNFCK 493

RESULT 7
T23573
hypothetical protein K10D3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23573
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19762
A;Accession: T23573
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-922 <W1>
A;Cross-references: UNIPROT:Q21418; EMBL:Z75545; PIDN:CAA99886.1; GSPDB:GN00019; CESP:K10D3
A;Experimental source: clone K10D3
C;Genetics:
A;Gene: CESP:K10D3.4
A;Map position: 1
A;Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 26.9%; Score 168; DB 2; Length 922;
Best Local Similarity 38.0%; Pred. No. 1.8e-07;
Matches 35; Conservative 8; Mismatches 29; Indels 20; Gaps 3;

QY 32 NMKC-----CP--FSC-----GKKCLDFRKDICSMPOEAGPCLASIPHHWYN 71
DB 371 NMESPTGSGANCPSTHSCESTSGSTTFGVCVCPROYVCKLPREGNGCTYSNRWFN 430

QY 72 KTKICSEFYGGCGQNNNNFQTEAICLVTC 103
DB 431 ARTGNCEEFYSGCGQNNANFETVKEQDYCR 462

RESULT 8
D88550
protein ZC84.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D88550
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele
A;Accession: D88550
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-1474 <STO>
A;Cross-references: UNIPROT:O62504; GB:chr_III; PIDN:CAA79570.1; PID:G3881447; GSPDB:GN00019
C;Genetics:
A;Gene: ZC84.6
A;Map position: 3

Query Match 26.4%; Score 165; DB 2; Length 1474;
Best Local Similarity 27.8%; Pred. No. 4.9e-07;
Matches 32; Conservative 16; Mismatches 35; Indels 32; Gaps 3;

QY 12 KVECEV-----EEDQCTKPRDCPENMK-----CCPFCGKGLDPR 48
DB 385 RIDCELYCARLQCRGNPLRIGDVTQSCASNNDSPSSHECKWDQVCCP-----RM 435

QY 49 KDICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 103
DB 436 QTICQPLRVGNCDRSVRRYWSAATRECQSPYTGCGQNDNNFETLVDCQTFCR 490

RESULT 9
A44180
taicatoxin serine proteinase inhibitor component - Australian taipan
C;Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44180
R;Possani, L.D.; Martin, B.M.; Yatani, A.; Mochca-Morales, J.; Zamudio, F.Z.; Gurrola, C.;
Toxicon 30, 1343-1364, 1992
A;Title: Isolation and physiological characterization of taicatoxin, a complex toxin w.
A;Reference number: A44180; MUID:93134601; PMID:1485334
A;Accession: A44180
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-62 <POS>
A;Cross-references: UNIPROT:O7LZB4
A;Experimental source: subsp. scutellatus, venom
A;Note: sequence extracted from NCBI backbone (NCBI:122482)
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 25.8%; Score 161; DB 2; Length 62;
Best Local Similarity 49.1%; Pred. No. 9e-08;
Matches 27; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 48 RKDICSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 102
DB 3 RPKFCHLPKPFPCRAAIPRFYNNPHSKQCEFIYGGCHGNANKFTPDCECYTC 57

RESULT 10
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:G263150; PIDN:AAB24853.1; PID:G963151
A;Experimental source: larva
A;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 25.8%; Score 161; DB 2; Length 747;
Best Local Similarity 44.4%; Pred. No. 6.5e-07;
Matches 24; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 102

A;Molecule type: DNA
A;Residues: 1-1743 <NIL>
A;/Cross-references: UNIPROT:Q9XWX5; EMBL:AL032623; PIDN:CAA21511.1; CESP:Y43F8B.3
C;Experimental source: clone Y43F8B
C;Genetics:
A;Gene: CESP:Y43F8B.3
A;/Introns: 65/1; 92/2; 128/1; 229/1; 367/1; 422/1; 486/2; 523/1; 571/1; 628/1; 857/2; 942/

Query Match 25.6%; Score 160; DB 2; Length 1743;
Best Local Similarity 30.8%; Pred. No. 1.5e-06;
Matches 36; Conservative 9; Mismatches 50; Indels 22; Gaps 2;

Qy 8 CPKTKVEBEIIOCTPRDCPENKKCCPPSGGKG--CLDPKDICSMPQEAGPCLASI 65
Db 1621 CPHGKPVDTHSLTTTGITDTCGRDHVCHSVSRGSTVCPCPDSPASFCVLRAADFGPCNREI 1680

Qy 66 PHWYNKKTICSEFIYGCGCNNNNFOTE-----AACLVTC 102
Db 1681 PRWAYDKASGGCKKFIFGCQCGLNLNFDINOCVAEFTGCGGNLFNVSIADCQATC 1737

RESULT 14
TIHABK
isoinhibitor K (BPI type) - Roman snail
C;Species: Helix pomatia (Roman snail)
C;/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;/Accession: A91232; A01225
R;Tschesche, H.; Dietl, T.
Eur. J. Biochem. 58, 439-451, 1975
A;/Title: The amino-acid sequence of iso-inhibitor K from snails (*Helix pomatia*). A sequen
A;/Reference number: A91232; PMID:76043680; PMID:1183446
A;/Accession: A91232
A;/Molecule type: protein
A;/Residues: 1-58 <TSC>
A;/Cross-references: UNIPROT:P00994
R;Dietl, T.; Tschesche, H.
Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976
A;/Title: Die Disulfidbruecken des Trypsin-Kallikrein-Inhibitors K aus Weinbergsschnecken
A;/Reference number: A91666; PMID:76141310; PMID:3462
A;/Contents: annotation; disulfide bonds
C;/Comment: This is one of several iso-inhibitors of broad specificity that are secreted in
C;/Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homolo
C;/Keywords: pyroglutamic acid; serine proteinase inhibitor
F;/7-57/Domain: animal kunitz-type proteinase inhibitor homology <BPT>
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;/7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 25.1%; Score 157; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 1.9e-07;
Matches 26; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

Qy 48 RKDICSMPEAGPCIASIPHWWYNKTKCSFYIGGCCGNNNNFOTEAICLVTC 102
Db 3 RPSFCNLPAETGPCKASFQYYINSKGGCCQQFIYGCRCNQNRFTDTQQCCGV 57

RESULT 15
S41082
anyloid precursor protein homolog - human (fragment)
C;/Species: Homo sapiens (man)
C;/Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;/Accession: S41082
R;Peterson, L.C.; Bjorn, S.E.; Norris, F.; Norris, K.; Sprecher, C.; Foster, D.C.
FEBS Lett. 338, 53-57, 1994
A;/Title: Expression, purification and characterization of a kunitz-type protease inhibit
A;/Reference number: S41082; MOID:94139895; PMID:8307156
A;/Accession: S41082
A;/Status: preliminary
A;/Molecule type: DNA
A;/Residues: 1-111 <PET>
A;/Cross-references: UNIPROT:O7MWL3
F:/59-109/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 25.1%; Score 157; DB 2; Length 111;
 Best Local Similarity 45.5%; Pred. No. 3.2e-07;
 Matches 25; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTK 103
 DB 56 KAVCSQEMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNNRNFSEDYCMVCK 110

RESULT 16
 TIPGBI
 alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
 N;Alternate names: bikunin; IRI; PI-14 (inhibitory fragment of ITI)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 30-Jun-1987 #sequence revision 04-Feb-2000 #text_change 09-Jul-2004
 C;Accession: S11066; S13493; A01208
 R;Gebhard, W.; Schreitmuller, T.; Vetr, H.; Wachter, B.; Hochtraesser, K.
 FEBS Lett. 269, 32-36, 1990
 A;Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microglobulin
 A;Reference number: S11066; MUID:90353595; PMID:1696914
 A;Accession: S11066
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-337 <GEB>
 A;Cross-references: UNIPROT:P04366; EMBL:X53685; NID:g1877; PIDN:CAA37725.1; PID:g1878
 R;Tavakkol, A.
 Biochim. Biophys. Acta 1088, 47-56, 1991
 A;Title: Molecular cloning of porcine alpha (1)-microglobulin/HI-30 reveals developmental
 A;Reference number: S13493; MUID:91113729; PMID:1703444
 A;Accession: S13493
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 'M', 3-48, 'M', 50-337 <TAV>
 A;Cross-references: GB:X52087; NID:g1881; PIDN:CAA36306.1; PID:g1882
 A;Note: the authors translated the codon GNG for residue 2 as a Met initiation codon
 R;Hochtraesser, K.; Wachter, B.; Albrecht, G.J.; Reislinger, P.
 Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
 A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
 A;Reference number: A90685; MUID:85225967; PMID:2408637
 A;Accession: A01208
 A;Molecule type: protein
 A;Residues: 212-258, 'Q', 260-269, 'S', 271-277, 'Q', 279-282, 'A', 284, 'IR', 287-292, 'A', 294-310
 C;Comment: This inhibitory fragment, released from native IRI after limited proteolysis
 first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
 C;Comment: The amino acid at position P2' (228-Met) appears to determine the specificity
 nd elastase; those with leucine interact strongly.
 C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
 C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
 F;20-173/Domain: lipocalin homology <LIP>
 F;216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F;272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F;216-266, 225-249, 241-262, 272-322, 281-305, 297-318/Disulfide bonds: #status predicted
 F;226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
 F;235/Binding site: carboxylate (Asn) (covalent) #status experimental
 F;282/Inhibitory site: Arg (trypsin) #status predicted

Query Match 25.1%; Score 157; DB 1; Length 337;
 Best Local Similarity 44.6%; Pred. No. 7.8e-07;
 Matches 29; Conservative 7; Mismatches 27; Indels 2; Gaps 1;

QY 41 GKIKLDFRK-DICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAIC 98
 DB 203 GQPVADFSKKEDSCQLGYSQGLGMIKRYFYNGSSMACETFYGGCGGNGNNFVSEKEC 262

QY 99 LVTK 103
 DB 263 LQTCR 267

RESULT 17
 A49374
 beta-amyloid precursor protein 2 homolog APLP2 - mouse
 C;Species: Mus musculus (house mouse)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A49374
 R;Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
 J. Biol. Chem. 269, 2637-2644, 1994
 A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid
 A;Reference number: A49974; MUID:94132029; PMID:8300594
 A;Accession: A49974
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-751 <SLU>
 A;Cross-references: UNIPROT:Q60709; GB:U15571; NID:g558467; PIDN:AAA50603.1; PID:g558467
 A;Note: sequence extracted from NCBI backbone (NCBIP:144636)
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 25.1%; Score 157; DB 2; Length 751;
 Best Local Similarity 45.5%; Pred. No. 1.5e-06;
 Matches 25; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTK 103
 DB 307 KAVCSQEMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNNRNFSEDYCMVCK 361

RESULT 18
 A49321
 amyloid beta (A4) homolog 2 precursor - human
 N;Alternate names: CDEI-binding protein
 C;Species: Homo sapiens (man)
 C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A49321; S34644; S40519
 R;Spröcher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster,
 Biochemistry 32, 4481-4486, 1993
 A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: e.
 A;Reference number: A49321; MUID:93250009; PMID:8485127
 A;Accession: A49321
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-763 <SPR>
 A;Cross-references: UNIPROT:Q06481; GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g30016
 A;Experimental source: placenta
 A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)
 A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
 R;von der Kammer, H.; Klaidiny, J.; Hanes, J.; Scheit, K.H.
 submitted to the EMBL Data Library, April 1993
 A;Description: The human homologue of the murine CDEI binding protein is an amyloid pre
 A;Reference number: S34644
 A;Accession: S34644
 A;Molecule type: mRNA
 A;Residues: 1-763 <VON>
 A;Cross-references: EMBL:222572; NID:g394763; PIDN:CAA80295.1; PID:g394764
 R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.
 Nature Genet. 5, 95-99, 1993
 A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer'
 A;Reference number: S40519; MUID:94035131; PMID:8220435
 A;Accession: S40519
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-763 <WAS>
 A;Cross-references: GB:I27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
 C;Genetics:
 A;Gene: GDB:APLP2; APPL2
 A;Cross-references: GDB:139159; OMIM:104776
 A;Map position: 11q23-11q25
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; transmembrane protein
 F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 25.1%; Score 157; DB 2; Length 763;
 Best Local Similarity 45.5%; Pred. No. 1.5e-06;
 Matches 25; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTK 103

Db 307 KAVCSQEAAMTGPCRAVPMRWYFDLSKGKVRFYGGCGGNRRNFESDYCMVACK 361

RESULT 19

S42880

amyloid precursor-like protein - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: S42880; S47528

R/Sandbrink, R.; Masters, C.L.; Beyreuther, K.

submitted to the EMBL Data Library, March 1994

A/Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid precursor

A/Reference number: S42880

A/Accession: S42880

A/Molecule type: mRNA

A/Residues: 1-765 <SAN>

A/Cross-references: UNIPROT:P15943; EMBL:X77934

R/Sandbrink, R.; Masters, C.L.; Beyreuther, K.

Biochim. Biophys. Acta 1219, 167-170, 1994

A/Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor

A/Reference number: S47528; MUID:94368849; PMID:8086458

A/Accession: S47528

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-765 <SA2>

A/Cross-references: EMBL:X77934

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

C/Keywords: alternative splicing

F/312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 25.1%; Score 157; DB 2; Length 765;

Best Local Similarity 45.5%; Pred. No. 1.5e-06;

Matches 25; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Qy 49 KDICSMPOEAGPCLASIPHWYKTKICSEFYGGCGGNRRNFQTEAICLVCK 103

Db 309 KAVCSQEAAMTGPCRAVPMRWYFDLSKGKVRFYGGCGGNRRNFESDYCMVACK 363

RESULT 20

T32497

hypothetical protein C08G9.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: T32497

R/Geisel, C.; Stellyes, L.

submitted to the EMBL Data Library, December 1997

A/Description: The sequence of C. elegans cosmid C08G9.

A/Reference number: Z21179

A/Accession: T32497

A/Status: preliminary; translated from GB/EMBL/DBDJB

A/Molecule type: DNA

A/Residues: 1-2150 <GEI>

A/Cross-references: UNIPROT:O44131; EMBL:AF036687; PIDN:AAB88311.1; GSPDB:GN00022; CESP:

A/Experimental source: strain Bristol N2; clone C08G9

C/Genetics:

A/Gene: CESP:C08G9.2

A/Map position: 4

A/Introns: 242/1; 306/1; 340/3; 485/1; 545/1; 736/2; 791/1; 829/1; 886/3; 942/1; 1079/2;

Query Match 24.9%; Score 155.5; DB 2; Length 2150;

Best Local Similarity 25.2%; Pred. No. 4.6e-06;

Matches 38; Conservative 18; Mismatches 34; Indels 61; Gaps 5;

Qy 13 VECEVEIDQCTKPRCP-----ENMK--CC----- 36

Db 1773 IETRTQOYSCQTSTVCPVGYYCTAFDDNMHVCCPGANSIKSIGEHNGLTCPHGDPFSS 1832

Qy 37 -----PFSC-----GKK-----CLDFRKDICSMPOEAGPCLASIPHWY 71

Db 1833 LADGTPFSCVLTNGCPATHYCSMTMPGQKIGICCVSKRYVNCNLQORDAGPCTATVTRFFYS 1892

A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:G178863; PIDN:AAA51768.1; PID:G178865
R;Pirelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:G178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-530, 'QWLMPVTPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:G178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.O.; Power, M.D.; Lieberburg, I.; van Duinen
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M7896; NID:G178618; PIDN:AAA51727.1; PID:G178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716, 'F', 718-737 <MUR>
A;Cross-references: GB:S57865; NID:G236720; PIDN:AAB19991.1; PID:G236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijeman, E.M.; Alonso, M.E.; Pulat, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692, 'G', 694-718 <KAM1>
A;Cross-references: GB:S45135; NID:G257377; PIDN:AAB23645.1; PID:G257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Status: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:G257379; PIDN:AAB23646.1; PID:G257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfad
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288, 'V', 365-770 <KAN>

A;Cross-references: GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:G28526
A;Note: alternative splice form APP(695)
R;Rabakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A;Cross-references: GB:M16765; NID:G178539; PIDN:AAA51722.1; PID:G178540
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756, 'S', 758-770 <GO1>
A;Cross-references: GB:M15533; NID:G178706; PIDN:AAA35540.1; PID:G178707
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van K
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:G177957; PIDN:AAA51564.1; PID:G177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DVR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PID:G929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeHitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; D
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CAA30050.1; PID:G28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:G929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three i
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <VIT1>
A;Accession: B30320

[illegible]

RESULT 27

HCHU
 A:Title: 1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human
 N:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) protein rich protein
 N:Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor
 C:Species: Homo sapiens (man)
 C:Date: 15-Oct-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
 C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; P90450; B39079; A61580; B253217
 R:Vetr, H.; Gebhard, W.
 Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
 A:Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
 A:Reference number: S13433; MUID:91214554; PMID:1708673
 A:Accession: S13433
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-352 <VET1>
 A:Cross-references: UNIPROT:P02760; EMBL:X54816; NID:G24475; PIDN:CAA38595.1; PID:982561
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Seabouee, R.; Salier, J.P.; Leveillard, T.; Mart Eur. J. Biochem. 191, 131-139, 1990
 A:Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene
 A:Reference number: S10778; MUID:90336621; PMID:1696200
 A:Accession: S10778
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-202 <DIA>
 R:Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
 Nucleic Acids Res. 14, 7839-7850, 1986
 A:Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-1
 A:Reference number: A93642; MUID:87040757; PMID:2430261
 A:Accession: A93642
 A:Molecule type: mRNA
 A:Residues: 1-352 <KAW>
 A:Cross-references: GB:X04494; NID:G24478; PIDN:CAA28182.1; PID:G24479
 R:Lopez Otin, C.; Grubb, A.O.; Mendes, E.
 Arch. Biochem. Biophys. 228, 544-554, 1984
 A:Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge
 A:Reference number: A90074; MUID:84126849; PMID:6198962
 A:Accession: A90074
 A:Molecule type: protein
 A:Residues: 20-56,58-202 <LOP>
 A:Experimental source: individual with tubular proteinuria
 A>Note: no evidence of sequence heterogeneity could be found, in spite of persistent het
 R:Takagi, T.; Takagi, K.; Kawai, T.
 Biochem. Biophys. Res. Commun. 98, 997-1001, 1981
 A:Title: Complete amino acid sequence of human alpha-1-microglobulin.
 A:Reference number: A90225; MUID:81184038; PMID:6164372
 A:Accession: A90225
 A:Molecule type: protein
 A:Residues: 20-47;58-136,138-141,'T',143-144,146-198 <TAK>
 A:Experimental source: pooled urine of patients with tubular proteinuria
 R:Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempart, K.; Salier, J.P.
 Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
 A:Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in
 A:Reference number: A90686; MUID:85225968; PMID:2408638
 A:Accession: A90686
 A:Molecule type: protein
 A:Residues: 206-290,'VI',293-342,'E',344-350 <REI>
 R:Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Druেকে, T.; Daudon, M.
 Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
 A:Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ca
 A:Reference number: P90450; MUID:93221481; PMID:8466493
 A:Accession: P90450
 A:Molecule type: protein
 A:Residues: 206-214,'X' <ATM1>
 R:Englild, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.
 J. Biol. Chem. 266, 747-751, 1991
 A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood pro
 A:Reference number: A39079; MUID:91093267; PMID:1898736
 A:Accession: B39079
 A:Molecule type: protein
 A:Residues: 206-225 <ENG1>

R:Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
 Int. J. Biochem. 23, 1201-1203, 1991
 A:Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inh
 A:Reference number: A61580; MUID:92175157; PMID:1794445
 A:Accession: A61580
 A:Molecule type: protein
 A:Residues: 214,'X',216-222,'X' <CHI>
 R:McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.
 J. Biol. Chem. 261, 5378-5383, 1986
 A:Title: Two apparent human endothelial cell growth factors from human hepatoma cells ar
 A:Reference number: A92583; MUID:86168278; PMID:3007499
 A:Accession: B25604
 A:Molecule type: protein
 A:Residues: 206-214,'X',216-230,'X',232-239,'X',241-248,'XX',251-252,'X',254 <MCK>
 R:Englild, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
 J. Biol. Chem. 264, 15975-15981, 1989
 A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
 A:Reference number: A92736; MUID:89380192; PMID:2476436
 A:Accession: C34245
 A:Molecule type: protein
 A:Residues: 206-225 <ENG2>
 R:Traboni, C.; Cortese, R.
 Nucleic Acids Res. 14, 6340, 1986
 A:Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobul
 A:Reference number: A25303; MUID:86312901; PMID:2428011
 A:Accession: A25303
 A:Molecule type: mRNA
 A:Residues: 1-218,'HW' <TRA>
 A>Note: this mRNA sequence appears to contain errors after residue 218
 R:Calero, M.; Escribano, J.; Grubb, A.; Mendez, E.
 J. Biol. Chem. 269, 384-389, 1994
 A:Title: Location of a novel type of interpolypeptide chain linkage in the human protei
 A:Reference number: A53110; MUID:94103241; PMID:7506257
 A:Accession: A53110
 A:Molecule type: protein
 A:Residues: 45-57 <CAL1>
 R:Vetr, H.; Koegler, M.; Gebhard, W.
 FEBS Lett. 245, 137-140, 1989
 A:Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inh
 A:Reference number: S03552; MUID:89171290; PMID:2466696
 A:Accession: S03552
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 206-352 <VET2>
 R:Malik, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Four
 Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
 A:Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolatio
 A:Reference number: S28928; MUID:93039735; PMID:1384548
 A:Accession: S28930
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-215 <MAL>
 R:Morelle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalski, C.; Fourne
 Eur. J. Biochem. 221, 881-888, 1994
 A:Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of in
 A:Reference number: S43466; MUID:94229087; PMID:7513643
 A:Accession: S43466
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-221 <MOR>
 R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilecek, J.
 Biochemistry 33, 7423-7429, 1994
 A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comp
 A:Reference number: A53642; MUID:94271799; PMID:7516184
 A:Accession: A53642
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-217 <WIS>
 R:Calero, M.; Mendez, E.; Garcia, E.
 Biochim. Biophys. Acta 1249, 91-99, 1995
 A:Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin
 A:Reference number: S55688; MUID:95284116; PMID:7539295
 A:Accession: S55688

A;Reference number: A01223
A;Accession: A01223
A;Molecule type: protein
A;Residues: 1-65 <RIT>
A;Cross-references: UNIPROT:P00992
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;7-57,16-40,32-53/Disulfide bonds: #status predicted
F;17/inhibitory site: Leu (chymotrypsin) #status predicted

Query Match 24.2%; Score 151; DB 1; Length 65;
Best Local Similarity 47.3%; Pred. No. 7.2e-07;
Matches 26; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 102
DB 3 RPKFCYLPADPGRCCLAYMPFRFYNPASNCKEKFYGGCGGNANNFKTWDECRHTC 57

RESULT 30
A32282
Alzheimer's disease amyloid beta protein precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 09-Jul-2004
C;Accession: A32282
R;Yamada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 158, 906-912, 1989
A;Title: Structure and expression of the alternatively-spliced forms of mRNA for the mouse Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology <BPI>
A;Reference number: A32282; MUID:89149813; PMID:2493250
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <YAM>
A;Cross-references: UNIPROT:P12023; GB:M24397; NID:G200350; PIDN:AAA39929.1; PID:G200350
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology <BPI>
F;11-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 24.2%; Score 151; DB 2; Length 100;
Best Local Similarity 44.4%; Pred. No. 1e-06;
Matches 24; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

QY 49 KOICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 102
DB 8 REVCSQAEPTGPRAMISRWYFDVTGKCVFFYGGCGGNRNNFDEEYCMAVC 61

RESULT 31
S01802
Chymotrypsin inhibitor I - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01802
R;Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A;Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A;Reference number: S01802; MUID:89228538; PMID:3072972
A;Accession: S01802
A;Molecule type: protein
A;Residues: 1-62 <SAS>
A;Cross-references: UNIPROT:P10831
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor
F;9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 23.9%; Score 149.5; DB 2; Length 62;
Best Local Similarity 54.4%; Pred. No. 9.4e-07;
Matches 31; Conservative 4; Mismatches 21; Indels 1; Gaps 1;

QY 49 KDICSMP-OBAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 104
DB 6 KPICEQAFGNSGPCFAYIKLYSYNQTKCKEEFYGGCGGNDRNFRFTLAECEQCKIK 62

RESULT 32
T32060
hypothetical protein R12A1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32060
R;Pauley, A.; Andrews, S.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid R12A1.
A;Reference number: Z21118
A;Accession: T32060
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-249 <PAU>
A;Cross-references: UNIPROT:O16701; EMBL:AF016680; PIDN:AAB66164.1; GSPDB:GN00023; CESP
A;Experimental source: strain Bristol N2; clone R12A1
C;Genetics:
A;Gene: CESP:R12A1.3
A;Map position: 5
A;Introns: 75/1; 139/1

Query Match 23.9%; Score 149.5; DB 2; Length 249;
Best Local Similarity 31.1%; Pred. No. 2.8e-06;
Matches 33; Conservative 16; Mismatches 46; Indels 11; Gaps 3;

QY 8 CPK-IKVECEVEIIDQCTKPRDCPENMKCC-----PFSCGKKCLD----PRKDICSMPQ 56
DB 88 CRRPLGISVFQDNTTIGCWMDSNCPGQKCCVEPNVTNSATRICRDPVGIASISICSLPL 147

QY 57 EAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 102
DB 148 AVGSCTAPAVRFYYDASSGRCNQFMYSGGGNANNFQSLSSCGTC 193

RESULT 33
TIFHBP
proteinase inhibitor - flesh fly (Sarcophaga bullata)
C;Species: Sarcophaga bullata
C;Date: 07-Feb-1992 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C;Accession: A37294
R;Papayannopoulos, I.A.; Biemann, K.
Protein Sci. 1, 278-288, 1992
A;Title: Amino acid sequence of a protease inhibitor isolated from Sarcophaga bullata d
A;Reference number: A37294; MUID:93284121; PMID:1304909
A;Accession: A37294
A;Molecule type: protein
A;Residues: 1-57 <PAP>
A;Cross-references: UNIPROT:P26228
A;Experimental source: hemolymph
C;Superfamily: basic proteinase inhibitor
C;Keywords: serine proteinase inhibitor
F;8-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;6-56,15-39,31-52/Disulfide bonds: #status predicted
F;16/inhibitory site: Arg (chymotrypsin) #status predicted

Query Match 23.8%; Score 149; DB 1; Length 57;
Best Local Similarity 48.1%; Pred. No. 9.8e-07;
Matches 26; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 49 KDICSMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 102
DB 3 KSACLPQKVGPCRKSDFFVFFYNADTKACEEFYGGCGGNDRNFRNTKECEKIC 56

RESULT 34
S04855
Alzheimer's disease amyloid A4 protein - mouse (fragment)
C;Species: Mus musculus domesticus (western European house mouse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04855
R;Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.

C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precursor
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
F:17/inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:73/inhibitory site: Arg (trypsin) #status predicted

Query Match 23.5%; Score 147; DB 1; Length 125;
Best Local Similarity 42.9%; Pred. No. 2.7e-06;
Matches 24; Conservative 9; Mismatches 23; Indels 0; Gaps 0;

QY 48 RKDSCMPQEAAGPCLASIPHWYNNKTKCSFYGGCGGNNNNFQTEAICLVTC 103
DB 3 KEDSQDLHAQPGCLGMSIRYFNGTSMACETFYGGCLGNGNFASQKCEICLTCK 58

RESULT 39

TIBO
N:Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPTI; cationic kallikrein
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence revision 22-Jul-1994 #text change 09-Jul-2004
C:Accession: S00277; A30333; S10546; S02486; S28197; A90162; A90736; A90927; A34
R:Creighton, T.E.; Charles, I.G.
J. Mol. Biol. 194, 11-22, 1987
A:Title: Sequences of the genes and polypeptide precursors for two bovine protease inhib
A:Reference number: S00274; MUID:87283904; PMID:2441071
A:Accession: S00277
A:Molecule type: DNA; mRNA
A:Residues: 1-100 <CR2>
A:Cross-references: UNIPROT:P00974; GB:M20934; GB:X05274; NID:g162767; PIDN:AAD13685.1;
R:Creighton, T.E.; Charles, I.G.
Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987
A:Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.
A:Reference number: A90926; MUID:88295740; PMID:2456884
A:Accession: A30333
A:Molecule type: DNA
A:Residues: 1-100 <CRE>
A:Cross-references: GB:M20934; GB:X05274; NID:g162767; PIDN:AAD13685.1; PID:g162769
R:Kingston, I.B.; Anderson, S.
Biochem. J. 233, 443-450, 1986
A:Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic e
A:Reference number: S10546; MUID:86158754; PMID:2420326
A:Accession: S10546
A:Molecule type: DNA
A:Residues: 34-97 <KIN>
R:Fioretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
Biol. Chem. Hoppe-Seyler 369(Suppl.), 37-42, 1988
A:Title: Aprotinin-like isoforms in bovine organs.
A:Reference number: S02485; MUID:89076531; PMID:2462435
A:Accession: S02486
A:Molecule type: protein
A:Residues: 36-93 <PIO>
R:Ikemita, M.; Jones, C.S.; Kamo, M.; Tsugita, A.; Kizuki, K.; Moriya, H.
Protein Seq. Data Anal. 5, 7-11, 1992
A:Title: Purification and characterization of the major cationic kallikrein inhibitor in
A:Reference number: S28197; MUID:93150003; PMID:1283464
A:Accession: S28197
A:Molecule type: protein
A:Residues: 36-93 <IKE>
R:Kasell, B.; Laskowski, M.
Biochem. Biophys. Res. Commun. 20, 463-468, 1965
A:Title: The basic trypsin inhibitor of bovine pancreas. V. The disulfide linkages.
A:Reference number: A90162; MUID:66083012; PMID:5860161
A:Contents: annotation; disulfide bonds
A:Accession: A90162
A:Molecule type: protein
A:Residues: 36-93 <RAS>
R:Andrer, F.A.; Hornle, S.
J. Biol. Chem. 241, 1569-1572, 1966
A:Title: The disulfide linkages in kallikrein inactivator of bovine lung.

A:Reference number: A92023; MUID:66171231; PMID:5296424
A:Contents: annotation; disulfide bonds
A:Accession: A92023
A:Molecule type: protein
A:Residues: 36-93 <AN2>
R:Chauvet, J.; Acher, R.
Bull. Soc. Chim. Biol. 49, 985-1000, 1967
A:Title: La structure covalente d'un inhibiteur polypeptidique de la trypsine (inhibiteu
A:Reference number: A90736; MUID:68012003; PMID:6053284
A:Contents: annotation; disulfide bonds
A:Accession: A90736
A:Molecule type: protein
A:Residues: 36-93 <CHA>
R:Diouha, V.; Pospisilova, D.; Meloun, B.; Sorm, F.
Collect. Czech. Chem. Commun. 33, 1363-1365, 1968
A:Title: Sequence of residues 18-20 in pancreatic trypsin inhibitor.
A:Reference number: A90927
A:Accession: A90927
A:Molecule type: protein
A:Residues: 36-93 <DLO>
R:Huber, R.; Kukla, D.; Ruhlmann, A.; Epp, O.; Formanek, H.
Naturwissenschaften 57, 389-392, 1970
A:Title: The basic trypsin inhibitor of bovine pancreas. I. Structure analysis and conf
A:Reference number: A3410; MUID:70255230; PMID:5447861
A:Contents: annotation; X-ray crystallography of basic protease inhibitor, 2.5 angstroms
R:Lewis, R.V.; Ray, P.; Cogull, R.; Kruggel, W.
Biochem. Biophys. Res. Commun. 167, 543-547, 1990
A:Title: Presence of pancreatic trypsin inhibitor in adrenal medullary chromaffin cells
A:Reference number: A34658; MUID:90211226; PMID:2322242
A:Accession: A34658
A:Molecule type: protein
A:Residues: 36-53,55-81 <LEW>
R:Anderson, S.; Kingston, I.B.
Proc. Natl. Acad. Sci. U.S.A. 80, 6838-6842, 1983
A:Title: Isolation of a genomic clone for bovine pancreatic trypsin inhibitor by using a
A:Reference number: A93977; MUID:84070725; PMID:6580617
A:Accession: A93977
A:Molecule type: DNA
A:Residues: 'PSLFNDPPIPA',34-97,'GKTGRAGEGKG' <AND>
A:Cross-references: GB:X03365; GB:K00966; NID:g142; PIDN:CAA27062.1; PID:g1364193
R:Siekman, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A:Title: Characterization and sequence determination of six aprotinin homologues from bo
A:Reference number: S00371; MUID:88221840; PMID:2453200
A:Accession: S10062
A:Molecule type: protein
A:Residues: 36-66,'p',68-82,'s',84-93 <SIE>
A:Experimental source: lung
A:Note: the authors designated this protein as isoprotinin 2
C:Comment: basic proteinase inhibitor is an intracellular polypeptide found in many tis
C:Genetics:
A:Introns: 34/1; 98/1
A:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-35/Domain: propeptide #status predicted <PRO>
F:36-100/Product: basic proteinase inhibitor #status experimental <MAT>
F:40-90/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:40-90,49-73,65-86/Disulfide bonds: #status experimental
F:50/inhibitory site: Lys (trypsin, chymotrypsin, kallikrein, plasmin) #status experime

Query Match 23.4%; Score 146; DB 1; Length 100;
Best Local Similarity 43.6%; Pred. No. 2.8e-06;
Matches 24; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

QY 48 RKDSCMPQEAAGPCLASIPHWYNNKTKCSFYGGCGGNNNNFQTEAICLVTC 102
DB 36 RPDFCLPEPYTGPKARIIRYFNAGKLCQTFVYGGCRKNPFKSAEDCMRTC 90

RESULT 40
S12143
lipoprotein-associated coagulation inhibitor precursor - rabbit

N;Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Accession: S12143; A61373
R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
Nucleic Acids Res. 18, 6440, 1990
A;Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
A;Reference number: S12143; MUID:91057146; PMID:2136251
A;Accession: S12143
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-300 <WES>
A;Cross-references: EMBL:X54708; NID:g1612; PIDN:CAA38515.1; PID:g1613
R;Colburn, P.; Crabb, J.W.; Buonassisi, V.
J. Cell. Physiol. 148, 320-326, 1991
A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell
A;Reference number: A61373; MUID:91349227; PMID:1880157
A;Accession: A61373
A;Molecule type: protein
A;Residues: 25-33,'X',35-46 <COL>
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; glycoprotein
F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match 23.4%; Score 146; DB 2; Length 300;
Best Local Similarity 33.0%; Pred. No. 6.7e-06;
Matches 36; Conservative 16; Mismatches 43; Indels 14; Gaps 4;

QY 3 ILGKPCPK-IKVECE-----VEEIQDCK--PRDCPENMKCCPFCGKKCLDFRDKICSM 54
DB 70 ILAHQCEFIYGGCGNGNRRFESLECKEKCARDPKMTTKLTFOKGR-----PDFCFL 123

QY 55 PQEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103
DB 124 EEDPGICRGYITRYFNQSKQCFERFYGGCLGNLNNFESLECKNTCE 172

RESULT 41
T34212
hypothetical protein F10E7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34212
R;Pauley, A.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F10E7.
A;Reference number: Z21489
A;Accession: T34212
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-805 <PAU>
A;Cross-references: UNIPROT:Q19305; EMBL:U41264; PIDN:AAA82427.1; CESP:F10E7.4
C;Genetics:
A;Gene: CESP:F10E7.4
A;Introns: 9/1; 34/3; 57/1; 90/3; 128/3; 162/1; 205/1; 285/2; 417/1; 475/1; 606/1; 745/1

Query Match 23.4%; Score 146; DB 2; Length 805;
Best Local Similarity 36.1%; Pred. No. 1.5e-05;
Matches 26; Conservative 11; Mismatches 35; Indels 0; Gaps 0;

QY 31 ENMKCCPFCGKKCLDFRDKICSMQEQAGPCLASIPHHWYNNKTKICSEFIYGGCGGN 90
DB 587 EKDTVMQSCRFFIENGSEIQEDKQACQAGNFRFYNNHEKTQCFRIFTGCKGNRN 646

QY 91 NFQTEAICLVTC 102
DB 647 QFTEECKQIC 658

RESULT 42
C89114

protein C37C3.6a [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89114
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele.
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: C89114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1558 <STO>
A;Cross-references: UNIPROT:Q81710; GB:chr_V; PIDN:AAC25867.1; PID:g3294501; GSPDB:GN000
C;Genetics:
A;Gene: C37C3.6a
A;Map position: 5

Query Match 23.4%; Score 146; DB 2; Length 1558;
Best Local Similarity 40.0%; Pred. No. 2.5e-05;
Matches 22; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

QY 51 ICSMPQEQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCKY 105
DB 1446 VCDEAKDTGPTCNFVTKYNNKADGTCNRRPHYGGCGTNNRFDNEQQCKAACQNH 1500

RESULT 43
T34395
hypothetical protein C37C3.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34395; T34394
R;Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C37C3.
A;Reference number: Z21518
A;Accession: T34395
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2167 <GEI>
A;Cross-references: UNIPROT:O76840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C
A;Experimental source: strain Bristol N2; clone C37C3
A;Accession: T34394
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1555,'SKF','GE2>
A;Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
A;Experimental source: strain Bristol N2; clone C37C3
C;Genetics:
A;Gene: CESP:C37C3.6b; CESP:C37C3.6a
A;Map position: 5
A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/3

Query Match 23.4%; Score 146; DB 2; Length 2167;
Best Local Similarity 40.0%; Pred. No. 3.2e-05;
Matches 22; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

QY 51 ICSMPQEQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCKY 105
DB 1446 VCDEAKDTGPTCNFVTKYNNKADGTCNRRPHYGGCGTNNRFDNEQQCKAACQNH 1500

RESULT 44
A55115
uterine plasmin/trypsin inhibitor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A55115
R;Stallings-Mann, M.L.; Burke, M.G.; Trout, W.E.; Roberts, R.M.
J. Biol. Chem. 269, 24090-24094, 1994
A;Title: Purification, characterization, and cDNA cloning of a Kunitz-type proteinase inhi

A:Reference number: A55115; MUID:95014140; PMID:7929061

A:Accession: A55115
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <STA>
A:Cross-references: UNIPROT:Q29100; GB:U14282; NID:G682652; PIDN:AAA62425.1; PID:G682653
A>Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Arg
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C:Keywords: serine proteinase inhibitor
F:38-88/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>

Query Match 23.2%; Score 145; DB 1; Length 122;
Best Local Similarity 47.1%; Pred. No. 4e-06;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 52 CSMPOBAGPCLASIPHHWYKTKICSEFYGGCGQNNNNFOTEAICLVTC 102

DB 38 CREPPYTGCSAHFVYFNATTLGCLQSFYGGCRGKQNNFWDKECLHTC 88

RESULT 45

I46937
tissue factor pathway inhibitor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I46937
R:Belaaouaj, A.; Kuppusewamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A:Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A:Reference number: I46937; MUID:93276427; PMID:8503123
A:Accession: I46937
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <BEL>

A:Cross-references: UNIPROT:P19761; GB:S61902; NID:G386015; PIDN:AAB26836.1; PID:G386016
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F:49-99/Domain: animal Kunitz-type proteinase inhibitor homolog <BPII>
F:120-170/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F:212-262/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI2>

Query Match 23.2%; Score 145; DB 2; Length 299;
Best Local Similarity 33.7%; Pred. No. 8.2e-06;
Matches 31; Conservative 15; Mismatches 38; Indels 8; Gaps 2;

QY 14 ECEVEIEDQCTK--PRDCPNMKCCPFSCGKCLDFKDKICSMPOBAGPCLASIPHHWYN 71

DB 86 ENRFESLECKEKCARDYPKWTKLTFQKGK-----PDFCFLEDPGICRGVITRYFN 139

QY 72 KTKICSEFYGGCGQNNNNFOTEAICLVTC 103

DB 140 NQSKQCFERFYGGCLGNLNNFESLECKNTCE 171

RESULT 46

B59399
short epsilon-dendrotoxin His55, subunit - Dendroaspis angusticeps
C:Species: Dendroaspis angusticeps
C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004
C:Accession: B59399
R:Sigle, R.; Hackett, M.; Aird, S.D.
Toxicol 40, 297-308, 2002
A:Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis

A:Reference number: A59399
A:Accession: B59399
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-57 <AIR>
A:Cross-references: UNIPROT:Q7LZE3
A>Note: trypsin inhibitor; K+ channel antagonist
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
F:5-55/Disulfide bonds: #status experimental
F:14-38/Disulfide bonds: #status experimental
F:30-51/Disulfide bonds: #status experimental

Query Match 23.0%; Score 144; DB 2; Length 57;
Best Local Similarity 48.1%; Pred. No. 2.7e-06;
Matches 26; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

QY 49 KDICSMPOBAGPCLASIPHHWYKTKICSEFYGGCGQNNNNFOTEAICLVTC 102

DB 2 RTFCLELPAEPGPKASIPAFYNNWAAKKQLPHYGGCKGNANRFTIEKCRHAC 55

RESULT 47

TIEPED
venom basic proteinase inhibitor E - black mamba
C:Species: Dendroaspis polylepsis polylepsis (black mamba)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C:Accession: A01215
R:Joubert, F.J.; Strydom, D.J.
Eur. J. Biochem. 87, 191-198, 1978
A:Title: Snake venoms. The amino-acid sequence of trypsin inhibitor E of Dendroaspis poly-

A:Reference number: A01215; MUID:78214615; PMID:668688
A:Accession: A01215
A:Molecule type: protein
A:Residues: 1-59 <JOU>
A:Cross-references: UNIPROT:P00984
A>Note: this protein inhibits trypsin and binds transition metal ions such as copper an-

Query Match 23.0%; Score 144; DB 1; Length 59;
Best Local Similarity 48.1%; Pred. No. 2.8e-06;
Matches 26; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

QY 49 KDICSMPOBAGPCLASIPHHWYKTKICSEFYGGCGQNNNNFOTEAICLVTC 102

DB 4 RTFCLELPAEPGPKASIPAFYNNWAAKKQLPHYGGCKGNANRFTIEKCRHAC 57

RESULT 48

S00371
isoaprotinin G1 - bovine hybrid
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S00371
R:Siekman, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A:Title: Characterization and sequence determination of six aprotinin homologues from b-

A:Reference number: S00371; MUID:882221840; PMID:2453200
A:Accession: S00371
A:Molecule type: protein
A:Residues: 1-59 <SIE>
A:Cross-references: UNIPROT:Q7M311
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor
C:Keywords: pyroglutamic acid; serine proteinase inhibitor
F:6-56/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:16/Inhibitory site: Lys (trypsin) #status predicted

Query Match 23.0%; Score 144; DB 2; Length 59;
Best Local Similarity 41.8%; Pred. No. 2.8e-06;
Matches 23; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 48 RKDICSMPBAGPCLASIPHHWYKTKICSEFYGGCGQNNNNFOTEAICLVTC 102

DB 2 RPDFCLEPPYTGPKARMIRYFNAGLQCFVYGGCRKSNFNFKSADCMRTC 56

RESULT 49

A59399
Long epsilon-dendrotoxin Arg55, subunit - Dendroaspis angusticeps
C:Species: Dendroaspis angusticeps
C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004

Search completed: September 21, 2005, 16:41:13
Job time : 16.3215 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 15:41:33 ; Search time 58.472 Seconds
(without alignments)
928.315 Million cell updates/sec

Title: US-10-807-204-2

Perfect score: 625

Sequence: 1 EGILGKPCPKIKVECEVEEI.....GNNNNFQTEAICLVTCCKYH 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	449	71.8	137	2 Q9BDL0	Q9bd06 oryctolagus
2	446	71.4	131	1 WFD6 HUMAN	Q9bgv6 homo sapien
3	408	65.3	182	2 Q6I1I9	Q6ie19 rattus norv
4	400	64.0	133	1 EPPI HUMAN	Q95925 homo sapien
5	400	64.0	143	2 Q86TF9	Q86cp9 homo sapien
6	393	62.9	133	2 Q8H245	Q8h245 papio papio
7	388	62.1	133	1 EPPI MACMU	Q9bd11 macaca mula
8	352	56.3	134	1 EPPI MOUSE	Q9da01 mus musculus
9	216	34.6	241	1 WFD8 HUMAN	Q8iaa0 homo sapien
10	197	31.5	759	2 Q8IT91	Q8it91 ancylostoma
11	187	29.9	2772	2 Q9VAV4	Q9vav4 drosophila
12	187	29.9	2776	2 Q869A0	Q869a0 drosophila
13	187	29.9	2894	2 Q7KEX2	Q7krx2 drosophila
14	187	29.9	2898	2 Q868Z9	Q868z9 drosophila
15	186	29.8	110	1 IBP CARCR	P00993 caretta car
16	184.5	29.5	988	2 Q2Z565	Q22565 caenorhabdi
17	182.5	29.2	571	2 Q7TQK3	Q7tqn3 mus musculus
18	182	29.1	2419	2 Q7PXZ1	Q7pxz1 anopheles g
19	173.5	27.8	576	2 Q8TU8	Q8teu8 homo sapien
20	173.5	27.8	576	2 Q6UXZ9	Q6uxz9 homo sapien
21	173.5	27.8	3198	2 Q9UXG8	Q9uxg8 manduca sex
22	173	27.7	587	2 Q6AX20	Q6ax20 xenopus lae
23	173	27.7	751	2 Q708Z0	Q708z0 xenopus lae
24	172.5	27.6	1599	2 Q09983	Q09983 caenorhabdi
25	172	27.5	67	1 IBPC BOVIN	P00976 bos taurus
26	172	27.5	750	2 Q6DJB6	Q6djbe xenopus tro
27	171	27.4	1416	1 YN81 CAEEL	Q03610 caenorhabdi
28	170.5	27.3	122	1 BTIA_BOOMI	P83609 boophilus m
29	170	27.2	83	2 Q6ITB9	Q6itb9 pseudechis
30	169	27.0	83	2 Q6ITB5	Q6itb5 oxyuranus m
31	169	27.0	169	2 Q9N0X7	Q9n0x7 bos taurus

RESULT 1

Q9BDL0 ID Q9BDL0 PRELIMINARY; PRT; 137 AA.
AC Q9BDL0; (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of mouse Eppin and a gene cluster of similar
RT protease inhibitors on mouse chromosome 2.";
RL Gene 312:125-134(2003).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF345415; RAK31337.1; -.
DR HSP; Q16039; IAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;

Query Match 71.8%; Score 449; DB 2; Length 137;

Best Local Similarity 70.9%; Pred. No. 7.3e-36;

Matches 73; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEI DQTKPRDCPENKCCPFSCGKKCLDFRDKICSMPOEAGP 60

Db 26 EGGFIKTCPIKVKVEEVESECTRRHRCPCDKMKCLFNCCKCLDLRDKVCSMPKETGP 85

QY 61 CLASIPHWYWKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103

Db 86 CLAFIPRWYDKEREICTEFYGGCGGNNNNFQTEAICLVICQ 128


```
RESULT 2
WFD6 HUMAN
ID WFD6 HUMAN STANDARD; PRT; 131 AA.
AC Q9BQY6; Q9NFV6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WAP four-disulfide core domain protein 6 precursor (Putative protease
DE inhibitor WAP6).
GN Name=WFD6; Synonyms=C20orf171, WAP6;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RA Clauss A., Lilja H., Lundwall A.;
RT "A locus on human chromosome 20 contains several genes expressing
RT protease inhibitor domains with homology to whey acidic protein.";
RL Biochem. J. 368:233-242(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.B.,
RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark A.P., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaeslao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.D., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaubin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BQY6-1; Sequences=Displayed;
CC Name=2;
CC IsoId=Q9BQY6-2; Sequences=VSP_007550, VSP_007551;
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels
CC are found in epididymis, testis and trachea.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC
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CC
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DR EMBL; AF411861; AAN03684.1; -.
DR EMBL; AL031663; CAC36264.1; -.
DR HSSP; P02760; 1B1K.
DR Genew; HGNC:16164; WFD6.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; FALSE_NEG.
DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 131 WAP four-disulfide core domain protein 6.
FT DOMAIN 31 69 WAP.
FT DOMAIN 70 128 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT VARSPLIC 75 86 IYAVCHRRLLAPA -> VSLTLYHKEELE (in isoform 2).
FT /FTId=VSP_007550.
FT VARSPLIC 87 131 Missing (in isoform 2).
FT /FTId=VSP_007551.
SQ SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;
Query Match 71.4%; Score 446; DB 1; Length 131;
Best Local Similarity 78.3%; Pred. No. 1.4e-35;
Matches 83; Conservative 1; Mismatches 22; Indels 0; Gaps 0;
QY 1 EGILGKPCPKIKVECEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKYAVCHRRLLAP 60
Db 26 EGILGKPCPKIKVECEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKYAVCHRRLLAP 85
QY 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 106
Db 86 AWPPYHTGGTITKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 131
RESULT 3
Q9IE19
ID Q9IE19 PRELIMINARY; PRT; 182 AA.
AC Q6IE19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WAP four-disulfide core 6-like 1.
GN Name=wfd6l1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15060002; DOI=10.1101/gr.1946304;
RT Puentes X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DDJB third party annotation (TPA) entry.
DR EMBL; BN000374; CAES1900.1; -.
DR HSSP; P00974; 1K6U.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
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DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EB12D7BFF756707E CRC64;

Query Match 65.3%; Score 408; DB 2; Length 182;
Best Local Similarity 58.5%; Pred. No. 8.9e-32;
Matches 62; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVBIIDQTRDCPENKCKPSCGKKCLDFKIDICSMPEQACG 60
DB 26 EGLFETCKPKYIKCDFERSQCRHKQCPKQRCMEACGKKCLDLNEDICSLPQDAGP 85
QY 61 CLASTPHWYNYKTKICSEFYICGCGNNNFOTEAICLVTKCKYH 106
DB 86 CLAYLPRWYNYKTNLTQFIYCGCGNTNFLSKDICTSICTRKH 131

RESULT 4
EPTI_HUMAN
ID EPTI_HUMAN STANDARD; PRT; 133 AA.
AC O95925; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINLW1; Synonyms=WAP7, WFDC7;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RX [1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=epididymis, and Testis;
RX MEDLINE=21297193; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French P.S., O'Rand M.G.;
RT "Cloning and sequencing of human Eppin: a novel family of protease
inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 1).
RP Stavrides G.S., Huckle E.J., Deloukas P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharvestaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko K.L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O95925-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O95925-2; Sequence=VSP_006755;
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
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CC -----
DR EMBL; AF286370; AAG00548.1; -;
DR EMBL; AF286369; AAG00547.1; -;
DR EMBL; AF286368; AAG00546.1; -;
DR EMBL; AL118493; CAB56343.1; -;
DR EMBL; AL031663; CAB37635.1; -;
DR EMBL; AL031663; CAC36265.1; -;
DR EMBL; BC053663; AAH53369.1; -;
DR HSP; P00974; 1BPTI.
DR Genew; HGNC:15932; SPINLW1.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 21
FT CHAIN 22 133
FT Eppin.


```
FT DOMAIN 29 73 WAP.
FT BPTI 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
FT VARSPIC 1 31 MSSGLLSLLVFLVLANVQGLTDWLPFR -> MLSKAH
FT GCKTALSUG (in isoform 2).
FT /FTIG-VSP 006755.
SQ SEQUENCE 133 AA; 15284 MW; 17831B203366D9DC CRC64;

Query Match 64.0%; Score 400; DB 1; Length 133;
Best Local Similarity 66.7%; Pred. No. 3.9e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 8 CPKIKVEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKICSMFQEQAGPCLASIPH 67
Db 33 CPKIRECEFERDVCTKRDQCQDNKKCCVFCGKKCLDLKQDVCCEMPKETGPGCLAYFLH 92

Qy 68 WYNNKTKICSEFYGGCGNNNNFQTEAICLVTC 103
Db 93 WYDKDKNTCSMFVYGGCGNNNNFQSKANCLNTCK 128

RESULT 5
Q86TP9 ID Q86TP9 PRELIMINARY; PRT; 143 AA.
AC Q86TP9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SPINLWI protein (fragment).
GN Name=SPINLWI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Colling E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH44829.1; -.
DR HSSP; P00974; 1UUA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;

Query Match 64.0%; Score 400; DB 2; Length 143;
Best Local Similarity 66.7%; Pred. No. 4.2e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 8 CPKIKVEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKICSMFQEQAGPCLASIPH 67
Db 43 CPKIRECEFERDVCTKRDQCQDNKKCCVFCGKKCLDLKQDVCCEMPKETGPGCLAYFLH 102

Qy 68 WYNNKTKICSEFYGGCGNNNNFQTEAICLVTC 103
Db 103 WYDKDKNTCSMFVYGGCGNNNNFQSKANCLNTCK 138

RESULT 6
Q8HZ45 ID Q8HZ45 PRELIMINARY; PRT; 133 AA.
AC Q8HZ45;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epididymal protease inhibitor 1.
GN Name=Eppin;
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinæ; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sivashanmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY141973; AA08507.1; -.
DR HSSP; P00974; 1UUA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 133 AA; 15277 MW; B33AE57ECBBE84 CRC64;

Query Match 62.9%; Score 393; DB 2; Length 133;
Best Local Similarity 65.6%; Pred. No. 1.9e-30;
Matches 63; Conservative 9; Mismatches 24; Indels 0; Gaps 0;

Qy 8 CPKIKVEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKICSMFQEQAGPCLASIPH 67
Db 33 CPKIRECEFERDVCTKRDQCQDNKKCCVFCGKKCLDLKQDVCCEMPKETGPGCLAFIR 92
```


Qy 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
|||:| | | : ||| ||| ||| : ||| |||
Db 93 WYVDKKNNTCSTFYGGCGNNNNFQSEANCLVTK 128

RESULT 7	EPPI_MACMU	STANDARD;	PMT; 133 AA.
ID	EPPI_MACMU		
AC	Q9BDL1;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Eppin precursor (Epididymal protease inhibitor) (Serine protease inhibitor-like with Kunitz and WAP domains 1).		
DE	Name=SPINLW;		
OS	Macaca mulatta (Rhesus macaque).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopithecinae; Macaca.		
OX	NCBI_TaxID=9544;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Epididymis, and Testis;		
RA	Rivichandran P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,		
RA	Richardson R.T.;		
RT	"Characterization of monkey and mouse Eppin, a protease inhibitor from epididymis and testis.";		
RT	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
RL	-1- SUBCELLULAR LOCATION: Secreted (Potential).		
CC	-1- TISSUE SPECIFICITY: Expressed in epididymis and testis.		
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.		
CC	-1- SIMILARITY: Contains 1 WAP-type domain.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	EMBL; AF346414; AAK31336.1; -.		
DR	HSP; P00974; 1BPI.		
DR	InterPro; IPR002223; Prot_Inh_Kunz-m.		
DR	InterPro; IPR008197; WAP.		
DR	Pfam; PF00014; Kunitz_BPTI; 1.		
DR	Pfam; PF00095; WAP; 1.		
DR	PRINTS; PR00759; BASICPTASE.		
DR	ProDom; PD00022; Prot_Inh_Kunz-m; 1.		
DR	SMART; SM00131; KU; 1.		
DR	SMART; SM00217; WAP; 1.		
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.		
DR	PROSITE; PS02079; BPTI_KUNITZ_2; 1.		
KW	Serine protease inhibitor; Signal.		
FT	SIGNAL 1 21 Potential.		
FT	CHAIN 22 133 Eppin.		
FT	DOMAIN 29 73 WAP.		
FT	DOMAIN 77 127 BPTI/Kunitz inhibitor.		
FT	DISULFID 33 61 By similarity.		
FT	DISULFID 40 65 By similarity.		
FT	DISULFID 48 60 By similarity.		
FT	DISULFID 54 69 By similarity.		
FT	DISULFID 77 127 By similarity.		
FT	DISULFID 86 110 By similarity.		
FT	DISULFID 102 123 By similarity.		
SO	SEQUENCE 133 AA; 15279 MW; 433AE946B39A35E9 CRC64;		

Db	33	CTTIRECEFRBDVCTRRQC	PDNKKCCVFCGKKCLDLQDVC	MPNETGPCLAFIR	92
Qy	68	WYNYKTKICSFYIGGCG	NNNNNQTBAILVTCK	103	
Db	93	WYDKNNNTCSFVHGGCG	NNNNNQSEANCLNTCK	128	

RESULT 8				
ID	EPPI_MOUSE	STANDARD;	PRT;	134 AA.
AC	09DA01;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Eppin precursor (Epididymal protease inhibitor) (Serine protease inhibitor-like with Kunitz and WAP domains 1).			
GN	Name=Spinlwi;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
SEQUENCE FROM N.A.				
RC	STRAIN=BALB/c; TISSUE=Epididymis, and Testis;			
RC	Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,			
RA	Richardson R.T.;			
RA	"Characterization of monkey and mouse Eppin, a protease inhibitor from			
RT	epididymis and testis."			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RC	MEDLINE=22354693; PubMed=12466951; DOI=10.1038/nature01266;			
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,			
RA	Yegi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schriml L.M., Knapin A., Matsuda H., Batalov S., Beisel K.W.,			
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,			
RA	Kanal A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,			
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,			
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,			
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,			
RA	Petrovskaya N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,			
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,			
RA	Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,			
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,			
RA	Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,			
RA	Wilming L.G., Wyngshaw-Boris A., Yanagisawa M., Yang I., Yang L.,			
RA	Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,			
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,			
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,			
RA	Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,			
RA	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,			
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,			
RA	Birney E., Hayashizaki Y.;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573 (2002).			
RN	[3]			
SEQUENCE FROM N.A.				
RC	TISSUE=Testis;			
RC	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haigh F.,			
RA	Datchenko L., Marudina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			


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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SURCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; AF346413; AAK31335.1; -.
DR EMBL; AK006296; BAB24514.1; -.
DR EMBL; BC048637; AAH48637.1; -.
DR HSSP; P31713; 1SHP.
DR MGD; MGI:1922776; Spinlwl.
DR GO; GO:0001669; C:acrosome; IDA.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 134 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 134 AA; 15470 MW; DFEB63D4D4C427F CRC64;

Query Match 56.3%; Score 352; DB 1; Length 134;
Best Local Similarity 55.7%; Pred. No. 1.8e-26;
Matches 54; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

QY 8 CPKIVCEVEIDICTPRDCPENMKCCPFSCGKKCLDFRDKICSMPOEAGPCIASIPH 67
Db 33 CPFRFEECHQHRDLCTRDRCPKKCCVFCNGKKCLNFPQDICSPLPKSGYCNAYFR 92
QY 68 WYNNKTKICSFYIGCGCGNNNNNFQTEAICLVCKK 104
Db 93 WNFENKSNSTCQFYIGCGCGNNNNNFQSQICQACNEK 129

RESULT 9
WFD8_HUMAN STANDARD; PRT; 241 AA.
ID WFD8_HUMAN
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AC Q8IUAO; Q96A34;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WAP four-disulfide core domain protein 8 precursor (Putative protease
DE inhibitor WAP8).
GN Name=WFD8; Synonyms=C20orf170, WAP8;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RT "A locus on human chromosome 20 contains several genes expressing
RT protease inhibitor domains with homology to whey acidic protein.";
RL Biochem. J. 368:233-242(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaio M.H., Leversha M.A., Lloyd K., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Senra H.K., Shownkeen R., Sims S.,
RA Skuce R.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SURCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed ubiquitously, the highest levels are
CC found in the epididymis followed by testis and trachea.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 3 WAP-type domains.
CC -----
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CC -----
DR EMBL; AF492015; AAN70997.1; -.
DR EMBL; AF492016; AAN70998.1; -.
DR EMBL; AL031663; CAB37634.2; -.
DR EMBL; AL591715; CAC39449.1; -.
DR HSSP; P31713; 1SHP.
DR Genew; HGNC:16163; WFD8.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 3.
DR PRINTS; PR00003; 4DISULPHCORE.
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DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 3.
DR PROSITE; PS00317; 4; DISULFIDE CORE; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Repeat; Serine protease inhibitor; Signal.
FT SIGNAL 1 38 Potential.
FT CHAIN 39 241 WAP four-disulfide core domain protein 8.
FT DOMAIN 47 90 WAP 1.
FT DOMAIN 95 145 BPTI/Kunitz inhibitor.
FT DOMAIN 150 193 WAP 2.
FT DOMAIN 197 239 WAP 3.
FT DISULFID 51 79 By similarity.
FT DISULFID 58 83 By similarity.
FT DISULFID 66 78 By similarity.
FT DISULFID 95 145 By similarity.
FT DISULFID 104 128 By similarity.
FT DISULFID 120 141 By similarity.
FT DISULFID 72 87 By similarity.
FT DISULFID 154 182 By similarity.
FT DISULFID 165 186 By similarity.
FT DISULFID 169 181 By similarity.
FT DISULFID 175 190 By similarity.
FT DISULFID 201 229 By similarity.
FT DISULFID 208 232 By similarity.
FT DISULFID 216 228 By similarity.
FT DISULFID 222 236 By similarity.
SQ SEQUENCE 241 AA; 27797 MW; 2566BS4AF4BDC57B CRG64;

Query Match 34.6%; Score 216; DB 1; Length 241;
Best Local Similarity 40.4%; Pred. No. 4.6e-13;
Matches 40; Conservative 12; Mismatches 45; Indels 2; Gaps 1;

QY 6 KP-CPKIKVEVEIDCTKPRDCPENKCKPSCGKKCLDFRKIDICSMPOEAGPCL 63
DB 47 KPGLCPKRLTCTTELPDSCNTDFDCKEYKQCFACQKCKMDPFPQPCWLPVRHGCN 106

QY 64 SIPHWYNNKTKICSEFYGGCGNNNFQTEAICLVTC 102
DB 107 EAQRWHDFKNVRCYTPFKYRGCEGNANFLSEDACTAC 145

RESULT 10
Q8IT91 PRELIMINARY; PRT; 759 AA.
ID Q8IT91
AC Q8IT91;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kunitz-like protease inhibitor precursor.
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatinae; Ancylostominae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Baltimore;
RX MEDLINE=22645137; PubMed=12760667;
RA Hawdon J.M., Datu B., Crowell M.;
RT "Molecular cloning of a novel multidomain Kunitz-type proteinase
inhibitor from the hookworm Ancylostoma caninum.";
RL J. Parasitol. 99:402-407(2003).
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR ENBL; AFS33590; AAN10061.1; -
DR HSP; P31713; 1SHP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR PRINTS; PR00759; BASICTPTASE.
DR SMART; SM00131; KU; 12.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 12.
KW Protease; Signal.
FT SIGNAL 1 16 Potential.
SQ SEQUENCE 759 AA; 84886 MW; C431A3C3F418F40A CRG64;

Query Match 31.5%; Score 197; DB 2; Length 759;
Best Local Similarity 46.1%; Pred. No. 9.3e-11;
Matches 35; Conservative 13; Mismatches 26; Indels 2; Gaps 1;

QY 31 ENMKCCPSCGKKCL--DFRKIDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCG 88
DB 560 ETMEDCTCFEORLAKPLEKDVCSQIPITAGCRASIPRYGVDSKKRCKVFTYSGCKGN 619

QY 89 NNNFQTEAICLVTCCK 104
DB 620 GNRFPKNECEKTKCR 635

RESULT 11
Q9VAV4 PRELIMINARY; PRT; 2772 AA.
ID Q9VAV4
AC Q9VAV4; Q9VAV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG33103-PB.
GN Name=Ppt; ORFNames=CG331103;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Spheroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolehakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fessler C., Gabrielian A.E., Gaig N.S., Galbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moehref A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapieton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
```



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DR PROSITE; PSS00092; TSP1; 5.
KW Matrix protein.
SQ SEQUENCE 2776 AA; 299741 MW; 92D38A17360D2D42 CRC64;

Query Match          29.9%; Score 187; DB 2; Length 2776;
Best Local Similarity 33.3%; Pred. No. 2.9e-09;
Matches 38; Conservative 13; Mismatches 33; Indels 30; Gaps 5;

QY 21 DOCTPR---DCPENN-----KCCPF---SCG-----KKCLD-----FRKD 50
DB 1788 DRCALPKQTGDCSEKLAHWFSESEKRCVPFYSGGKNNFPTLESCEDHCPQVAKD 1847

QY 51 ICSMPQAPCIASPHWYKTKICSEFYVGGCGGNNNTQTAEICLVTKK 104
DB 1848 ICEIPAEGECANYTSTWYTDQACRQFYVGGCGGNNRFTTEESCLARCDR 1901

RESULT 13
Q7KRX2 PRELIMINARY; PRT; 2894 AA.
AC Q7KRX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG33103-PA.
GN Name=Ppn; ORFNames=CG331103;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=2019606; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benton P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodagel, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RN Science 287:2185-2195(2000).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
SEQUENCE FROM N.A.
RX FLYBASE;
RG FlyBase;
RN Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
[6]
SEQUENCE FROM N.A.
RG FLYBASE;
RN Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF003765; AAF56795.3; -.
DR HSSP; P10646; IAD2.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; IG; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; ADISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4-DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00900; PLAC; 1.

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DR PROSITE; PS00092; TSP1; 5.  
SQ SEQUENCE 2894 AA; 312663 MW; A1BFE1BAD9B214BC CRC64;  
  
Query Match      29.9%; Score 187; DB 2; Length 2894;  
Best Local Similarity 33.3%; Pred.No. 3.1e-09;  
Matches 38; Conservative 13; Mismatches 33; Indels 30; Gaps 5;  
  
QY 21 DOCTKPR---DCPENM-----KCCPF---SCG-----KKCLD----FRKD 50  
|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |  
Db 1788 DRCALPQTGDGSEKLAKWHFSESEKRCVPFYVSGCGGNKNFPPTLSECDHCPQVAKD 1847  
  
QY 51 ICSMPQAGCGLASIPHWNNKTKICSEFTYGGCGQNINNFQTEATCLVTCKK 104  
|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |  
Db 1848 ICRIPASVGECANVTGWYDTDOACROFYFGCGGNENRFPTEESCLARCDR 1901
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RESULT 14	
ID	Q86829
AC	PRELIMINARY; PRT; 2898 AA.
CD	Q86829;
DT	01-JUN-2003 (TrEMBLrel. 24, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Extracellular matrix protein papilin 3.
DE	Names=Ppn;
GN	Drosophila melanogaster (Fruit fly).
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_Taxid=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=22552133; PubMed=12666201; DOI=10.1002/dvdy.10265;
RP	Kramerova I.A., Kramerov A.A., Fessler J.H.;
RT	"Alternative splicing of papilin and the diversity of Drosophila
RT	extracellular matrix during embryonic morphogenesis.";
RL	Dev. Dyn. 226:634-642(2003).
RL	[2]
RP	SEQUENCE FROM N.A.
RP	Kramerova I., Fessler J.H.;
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ database.
CC	-1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
EMBL	AF529180; AAO84908.1; -.
DR	HSSP; Pf12111; 1KTH.
DR	FlyBase; FBgn0003137; Ppn.
DR	GO; GO:0005604; C:basement membrane, IDA.
DR	InterPro; IPR010294; ADAM spacer1.
DR	InterPro; IPR006309; EGF Like.
DR	InterPro; IPR007110; Ig-Like.
DR	InterPro; IPR003598; Ig c2.
DR	InterPro; IPR010909; PLAC.
DR	InterPro; IPR002223; Prot_Inh_Kunz-m.
DR	InterPro; IPR000884; TSP1.
DR	InterPro; IPR008197; WAP.
DR	Pfam; PF05586; ADAM_spacer1; 1.
DR	Pfam; PF00047; Ig; 2.
DR	Pfam; PF00014; Kunitz_BPTI; 12.
DR	Pfam; PF00090; TSP 1; 5.
DR	Pfam; PF00095; WAP; 1.
DR	PRINTS; PR00003; ADISULPHCORE.
DR	PRINTS; PR00759; BASICPTASE.
DR	ProDom; PD000222; Prot_Inh_Kunz-m; 12.
DR	SMART; SM00408; IgC2; 3.
DR	SMART; SM00131; KU; 12.
DR	SMART; SM00209; TSP1; 7.
DR	SMART; SM00217; WAP; 1.
DR	PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 12.
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR	PROSITE; PS50835; IG_LIKE; 3.
DR	PROSITE; PS50900; PLAC; 1.
DR	PROSITE; PS50092; TSP1; 5.

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KW Matrix protein.  
SQ SEQUENCE 2898 AA; 313250 MW; 2F992742F2D64A00 CRC64;  
  
Query Match      29.9%; Score 187; DB 2; Length 2898;  
Best Local Similarity 33.3%; Pred. No. 3.le-09;  
Matches 36; Conservative 13; Mismatches 33; Indels 30; Gaps 5;  
  
Qy 21 DOCTKPR-----DCPENM-----KCCPF---SCG-----KKCLD----FRKD 50  
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 1788 DRCALPKQTGDGCSEKLAKWHFSESEKRCVPFYISGGCGNKNFPPTLESCDHCPQVAKD 1847  
  
Qy 51 ICSMPQAEAGCLASIPHWYWNKTTKTCEFIYGGCQGQNNNFTEALCVTCCK 104  
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 1848 ICSPIAEIVGCAKNTVSYYDTDOACRQFYGGCGGNENRFTEESCLARCDR 1901
```

RESULT 15
IDP_CARCR IDP_CARCR STANDARD; PRT; 110 AA.
AC P00593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Chelonianin (Basic protease inhibitor) (RTPI).
OS Caretta caretta (Loggerhead).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Chelonioidae; Cheloniidae; Caretta.
OC NCBI_TaxID=8467;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg white;
RA Kato I., Tomioka N.;
RA "Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of
RT two tandem domains -- one Kunitz -- one of a new family.";
RL Fed. Proc. 38:832-832(1979).
CC -1- FUNCTION: The first domain inhibits trypsin; the second one
CC inhibits subtilisin.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -1- CAUTION: As the paper only indicates the species as "red sea
CC turtle", the species indicated here is therefore an inference.
DR PIR; A01224; TITTOR.
DR HSPP; P00974; IK09.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI KUNITZ 1; 1.
DR PROSITE; PS00279; BPTI KUNITZ 2; 1.
KW Direct protein sequencing; Pyroliidone carboxylic acid;
KW Serine protease inhibitor.
KW MOD_RES 1 Pyroliidone carboxylic acid.
FT DOMAIN 8 58 BPTI/Kunitz inhibitor.
FT DOMAIN 63 105 WAP.
FT SITE 18 19 Reactive bond for trypsin.
FT FT DISULFID 8 58 By similarity.
FT FT DISULFID 17 41 By similarity.
FT FT DISULFID 33 54 By similarity.
FT FT DISULFID 67 92 By similarity.
FT FT DISULFID 76 97 By similarity.
FT FT DISULFID 80 93 By similarity.
FT FT DISULFID 86 101 By similarity.
SQ SEQUENCE 110 AA; 269436243813418E CRC64;
Query Match 29.8%; Score 186; DB 1; Length 110;
Best Local Similarity 50.0%; Pred. No. 1.8e-10;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
QV 48 RKDICSNPQAGPCLASIPHWYKTKICSEFIYGCQGNNNNFQTEAICLVTK 103

	Query Match	29.5%	Score 184.5	DB 2	Length 988
	Best Local Similarity	34.3%	Pred. No. 1.9e-03		
	Matches 35	Conservative 14	Mismatches 44	Indels 9	Gaps 2
Qy	12 KVECE-----VBEIOCTKPRDCPENMKCCPFSCGKKCLDFDKDTCSMPQEAAGPCLAS	64			
Db	402 KLVCNGNPLRIGSEWORCETNADCPSSHSC--QGSHKVCCTPQASLCTQPKRLGDCTSA	459			
Qy	65 IPHWYNNKTKICEEFTYGGCGGNNNNFQTEAILCVTCCKKH	106			
Db	460 VRRVYVYNAATSCBMFOYTCGCGNDNNFNTLMACQOIKRGTH	501			

GN Name=gCG49342; ORFName=ENSGANG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAS01008987; EAA01339.1; -.
DR HSSP; PI0646; INH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS00092; TSP1; 5.
FT NON_TER 1
SQ SEQUENCE 2419 AA; 260249 MW; 58078660983946 CRC64;

Query Match 29.1%; Score 182; DB 2; Length 2419;
Best Local Similarity 33.9%; Pred. No. 7.9e-09;
Matches 39; Conservative 12; Mismatches 32; Indels 32; Gaps 4;

Qy 21 DOCKTRP-----DCPENMKCCPFCSC-----KKC-----LDRPK 49
Db 1515 DVCHLPKISGPTGHHNMYDYDAERNM-CAQFTYGGCLGNMRFPSQECKALCSVDDSK 1573
Qy 50 DICSMPOAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCK 104
Db 1574 PPCQPMAGPCNGTFFERWYDYKTDACHPFYFGGCKGNKNYPTFASCGYHCKR 1628

RESULT 19
Q8TEU8 PRELIMINARY; PRT; 576 AA.
AC Q8TEU8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WFIKNRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyai L., Pathy L.;
RT "A human protein containing multiple types of protease-inhibitory
modules."

Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709 (2001).
[2]
SEQUENCE FROM N.A.
RA Trexler M., Banyai L., Pathy L.;
RP "Distinct expression pattern of two related human proteins containing
multiple types of protease-inhibitory modules."
RT Biol. Chem. 383:0-0 (2002).
RL -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC EMBL; AF468657; AAL77058.1; -.
DR HSSP; P00974; IKO9.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP-like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Query Match 27.8%; Score 173.5; DB 2; Length 576;
Best Local Similarity 31.8%; Pred. No. 1.4e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

Qy 22 QCTKP-----RDCPEN-----KCCPF-----SGKKCLDFRKDIC 52
Db 327 ECLPFPSEDCGEQTRHFDQAQNNCLTTFGCHRNHNHFYEAACMLACGSLAAC 386
Qy 53 SMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
Db 387 SLPALQGPCKAYAPWAYNSQTGQCFSFYGGCGGNGNPFESRACBESC 436

RESULT 20
Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bikunin hlg.
GN ORFNames=UNQ9235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.,
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.",
RL Genome Res. 13:2265-2270(2003).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAO88509.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG C2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match 27.8%; Score 173.5; DB 2; Length 576;
Best Local Similarity 31.8%; Pred. No. 1.4e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKE---RDCPENM-----KCCPF-----SQGKCLDFRKDIC 52
DB 327 ECLKPPDSDEGEEQTRWFDAQANNCLFTTGHCHRNLNHFETAEACMLACMSGPLAAC 386

QY 53 SMPQAGPCPLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 102
DB 387 SLPALQGPCKAYAPWAYNSQTGCQSFYVGCGEGNNGNFESREACEESC 436

RESULT 21
Q9U8G8 PRELIMINARY; PRT; 3198 AA.
AC Q9U8G8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE Lacunin precursor.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99457716; PubMed=10528409; DOI=10.1016/S0965-1748(99)00064-8;
RA Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
RT "Expression of lacunin, a large multidomain extracellular matrix
RT protein, accompanies morphogenesis of epithelial monolayers in Manduca
RT sexta.";
RL Insect Biochem. Mol. Biol. 29:893-897(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Nardi J., Martos R., Walden K., Lampe D., Robertson H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.

DR EMBL; AF078161; AAF04457.1; -.
DR HSSP; P12111; 1KTH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG C2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR004094; Prot_inh_antistn.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF02822; Anticstasin; 4.
DR Pfam; PF00014; Kunitz_BPTI; 10.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00131; KU; 10.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 5.
KW Signal.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 3198 AA; 349366 MW; AB4ACD459C0D9134 CRC64;

Query Match 27.8%; Score 173.5; DB 2; Length 3198;
Best Local Similarity 34.4%; Pred. No. 6.8e-08;
Matches 31; Conservative 15; Mismatches 33; Indels 5; Gaps 1;

QY 14 BCEVEIDQCTKPRDCPENMKCCPFSCGKCLDFRKDICSHMPQAGPCPLASIPHWYNNK 73
DB 2230 KCVTFEYGGCGGNRNPNPTTEBYCQYVCGT-----AQDICQLPMRSGPCTSLMRWFYDPS 2284

QY 74 TKICSEFYGGCGQNNNNFQTEAICLVTC 103
DB 2285 SDSCSQFTYGGCGDGNDRFTRDDCESRCR 2314

RESULT 22
Q6AX20 PRELIMINARY; PRT; 587 AA.
ID Q6AX20
AC Q6AX20;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE APlp2 A protein.
GN Name=aplp2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoides; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Derge J.G.,


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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR EMBL; U290936; AAG68408.1; -.
DR PIR; T16210; T16210.
DR HSSP; P10646; IAD2.
DR IntAct; Q09983; -.
DR WormBase; WBGene00017937; F30H5.3.
DR WormPep; F30H5.3; CE01927.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR006149; EB region.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 3.
DR Pfam; PF00014; Kunitz BPTI; 5.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WRI; 15.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 5.
KW Hypothetical protein.
SQ SEQUENCE 1599 AA; 171658 MW; AB5E6A1D86E9880D CRC64;

Query Match 27.6%; Score 172.5; DB 2; Length 1599;
Best Local Similarity 35.4%; Pred. NO. 4.4e-08;
Matches 35; Conservative 13; Mismatches 42; Indels 9; Gaps 2;

QY 12 KVECEV-----EEIDQCTKPRDCPNMKCFPGCGKKLDFRDXICSMWQEGPCLAS 64
DB 518 KLQCKYGTPLKIGSSNQRCASADCFSTHEC--QSDHNVCCPRQAICSGPLRLGDCQKS 575

QY 65 IPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 103
DB 576 VRYWYNATRACEFDYTGCGQNDNNFETLLEQNTCE 614

RESULT 25
IBPC BOVIN STANDARD; PRT; 67 AA.
AC P00976;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Colostrum trypsin inhibitor (Colostrum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Cechova D., Jonakova V., Sorm F.;
RT "Primary structure of trypsin inhibitor from cow colostrum (component B2).";
RL Collect. Czech. Chem. Commun. 36:3342-3357(1971).
RN [2]
RP DISULFIDE BONDS.
RA Cechova D., Ber E.;
RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
RL Collect. Czech. Chem. Commun. 39:680-688(1974).
RN [3]
RP CHARACTERIZATION.
RX PubMed=11947537;
RA Cechova D., Muszynska G.;
RT "Role of lysine 18 in active center of cow colostrum trypsin inhibitor.";
RT Inhibitor."
RL FEBS Lett. 8:84-86(1970).
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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01207; TIBOC.
DR HSSP; P02760; 1BIK.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Glycoprotein; Serine protease inhibitor.
FT SITE 18 19 Reactive bond for trypsin.
FT DISULFID 8 58
FT DISULFID 17 41
FT DISULFID 33 54
FT CARBOHYD 27 27 N-linked (GlcNAc...).
SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;

Query Match 27.5%; Score 172; DB 1; Length 67;
Best Local Similarity 48.1%; Pred. NO. 2.5e-09;
Matches 26; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMWQEGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 103
DB 6 DLQQLPQARGPKAALLRYFNSTSNACEPFTYGGCGGNBNFETEMCLRCIE 59

RESULT 26
QSDJB6 PRELIMINARY; PRT; 750 AA.
AC Q6DJB6;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE App-prov prov.
GN Name=app-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
TX TISSUE=Whole body;
RC Klein S., Gerhard D.S.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC075266; AAH75266.1; -.
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CC kallikrein. May play a role in blocking blood coagulation during
CC the larvae fixation on cattle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR InterPro: IPR002223; Kunitz_BPTI.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
KW Direct protein sequencing; Repeat; Serine protease inhibitor.
FT DOMAIN 10 60
FT DISULFID 62 112 BPTI/Kunitz inhibitor 1.
FT DISULFID 10 60 BPTI/Kunitz inhibitor 2.
FT DISULFID 35 56 By similarity.
FT NON CONS 69 70 By similarity.
FT DISULFID 71 121 By similarity.
FT DISULFID 80 104 By similarity.
FT DISULFID 96 117 By similarity.
FT SITE 19 20 Reactive bond (By similarity).
FT SITE 71 72 Reactive bond (By similarity).
FT NON TER 122 122
SQ SEQUENCE 122 AA; 13736 MW; 8F5B1F48E10C566F CRC64;

Query Match 27.3%; Score 170.5; DB 1; Length 122;
Best Local Similarity 46.7%; Pred. No. 6.1e-09;
Matches 35; Conservative 7; Mismatches 18; Indels 15; Gaps 3;

QY 36 CFPSC-----GKKCLDFRKDCSMPQAGCLASIPHWYNNKTKICSEFYGGCGQN 88
DB 56 CKASCKPETYEAKKCL-----ARP-ESGPCLAYMPWGYDLSKQCQCFEYGGCDGN 107
QY 89 NNNFQTEAICLVTK 103
DB 108 DNKYTTEEBCLSKCK 122

RESULT 29
Q6ITB9 PRELIMINARY; PRT; 83 AA.
AC Q6ITB9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mulgin-3.
OS Pseudechis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Pseudechis.
OX NCBI_TaxID=8670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626926; AAT45402.1; -.
DR HSP; Q16019; IAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9103 MW; 315C361D8EC89221 CRC64;

Query Match 27.28%; Score 170; DB 2; Length 83;
Best Local Similarity 52.74%; Pred. No. 4.8e-09;
Matches 29; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGCLASIPHWYNNKTKICSEFYGGCGQNNTFQTEAICLVTC 102
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DB 27 RPDFCELPAATGTCRVGFPSFYNDPEKKCLEFYGGCGGNANFTKCEESTC 81

RESULT 30
Q6ITB5 PRELIMINARY; PRT; 83 AA.
AC Q6ITB5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-1.
OS Oxyuranus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Oxyuranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626930; AAT45406.1; -.
DR HSP; F10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9040 MW; CB4F5E17570CF94C CRC64;

Query Match 27.0%; Score 169; DB 2; Length 83;
Best Local Similarity 50.9%; Pred. No. 6e-09;
Matches 28; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGCLASIPHWYNNKTKICSEFYGGCGQNNTFQTEAICLVTC 102
DB 27 RPDFCELPAATGTCRVGFPSFYNDPEKKCLEFYGGCGGNANFTKCEESTC 81

RESULT 31
Q9NOX7 PRELIMINARY; PRT; 169 AA.
AC Q9NOX7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Trophoblast Kunitz domain protein 2.
GN Name=TKDPI;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed Simmental X Hereford;
RA Green J.A., Maclean J.A. II, Gan X., Xie S., Roberts R.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF241777; AAF61248.1; -.
DR HSP; P00974; IKO9.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 169 AA; 18855 MW; B65C16F4DF0BA3D CRC64;

Query Match 27.0%; Score 169; DB 2; Length 169;
Best Local Similarity 47.3%; Pred. No. 1.2e-08;
Matches 26; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 48 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db 108 KPFCMEPELGGPKQDMTRIFYNAKTRICFPFYVGCGEGNNKNNFQTLUSHCIVTC 162

RESULT 32
Q7T363 PRELIMINARY; PRT; 516 AA.
AC Q7T363
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Zgc:64075.
GN ORFNames=zgc:64075;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; BC053239; AAH53239.1; -.
DR HSSP; F10846; 1ADZ.
DR ZFIN; ZDB-GENE-040426-2169; zgc:64075.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002172; LDL receptor_A.
DR InterPro; IPR011106; MAN5C_N.
DR InterPro; IPR000601; PKD.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MAN5C; 1.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS50069; LDLRA_2; 1.
SQ SEQUENCE 516 AA; 57695 MW; 20B0A4CSB270DE16 CRC64;

Query Match 27.0%; Score 169; DB 2; Length 516;
Best Local Similarity 26.6%; Pred. No. 3.3e-08;
Matches 37; Conservative 13; Mismatches 41; Indels 48; Gaps 4;

Qy 4 LGKPCPKIKVEC-EVEIDIOCTKPRDCPENKKCCP--FSGKKKCL----- 45
Db 297 IGSAPHPSGRIGIDAVEQCDRP-----CSPEHFTCDNKKCCIGKDLVCDKEKQCS 348

Qy 46 -----DPRKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGG 83
Db 349 GSDEKECDKWDYDLVKLRGISPDVSKARCVKPVVTGTCPSQTKWYNPNKRLCYRFNYG 408

Qy 84 GCGGNNNNFQTEAICLVTC 102
Db 409 GCEGNQRFETEAGCMTCF 427

RESULT 33
Q9GPI5 PRELIMINARY; PRT; 86 AA.
AC Q9GPI5
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Ixodes ricinus (Sheep tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
OX NCBI_TaxID=34613;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary glands;
RX MEDLINE=22134277; PubMed=12139212;
RA Lebouille G., Rochez C., Louahed J., Rutti B., Brossard M., Bollen A.,
RA Godfroid E.;
RT "Isolation of Ixodes ricinus salivary gland mRNA encoding factors
induced during the blood feeding process.";
RL Am. J. Trop. Med. Hyg. 66:225-233(2002).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ269641; CA955816.1; -.
DR HSSP; P12111; INKT.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 86 AA; 9727 MW; 9473B1794A055F0 CRC64;

Query Match 26.9%; Score 168; DB 2; Length 86;
Best Local Similarity 48.1%; Pred. No. 7.7e-09;
Matches 25; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 52 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 103
Db 31 CKLPDDGPCNARIPSYFDKTKTCFMYGCGEGNNNFENITTCQECR 82

RESULT 34
Q21418 PRELIMINARY; PRT; 922 AA.
AC Q21418
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
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RL Submitted (SEP-2004) to the EMBL/GenBank/DBSJ databases.
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 4 BPTI/Kunitz inhibitor domains.
DR EMBL; AC024830; AAF59608.3; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
KW Hypothetical protein.
SQ SEQUENCE 1297 AA; 142370 MW; 7C8FAA75CE07ED8C CRC64;

Query Match      26.8%; Score 167.5; DB 2; Length 1297;
Best Local Similarity 28.0%; Pred. No. 1.1e-07;
Matches 35; Conservative 13; Mismatches 34; Indels 43; Gaps 3;

Qy 22 QCTPRDCP-----ENMKCCPFs-----CGKKCLDFR----- 48
Db 673 RCARDTDCPSTHTCAMEHQVCCPTPPHREIQFKYKHDLVSSSLKIVGSRHENYRPRGFV 732
Qy 49 -----KDISCMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAIC 98
Db 733 ARPMLFLIEETKLTCTLEPLRVGDKQSVRFQWYNAETKTCESFLYTGCGGNNRFLNSEC 792
Qy 99 LVTCK 103
Db 793 QSYCK 797

RESULT 36
Q8T3S7 PRELIMINARY; PRT; 80 AA.
AC Q8T3S7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Toxin 1.
OS Araneus ventricosus.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Araneidae; Araneus.
OX NCBI_TaxID=182803;
RN [1]
RP SEQUENCE FROM N.A.
RA Jung E.H., Lee K.S., Han J.H., Je Y.H., Chang J.H., Roh J.Y.,
RA Sohn H.D., Jin B.R.;
RT "Molecular cloning of two cDNAs encoding an insecticidal toxin from
RT the spider, Araneus ventricosus, and construction of a recombinant
RT baculovirus expressing a spider toxin.";
RL Int. J. Ind. Entomol. 4:43-49(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Chung E.H., Lee K.S., Han J.H., Sohn H.D., Jin B.R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY091482; AAM14403.1; -.
DR HSSP; P12111; 1KTH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 80 AA; 9275 MW; D07F5F9AC6B7BC10 CRC64;

Query Match      26.7%; Score 167; DB 2; Length 80;
Best Local Similarity 51.9%; Pred. No. 9e-09;
Matches 28; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 24 KDRCLLPKVTGCKASLTRYTYDKTKACVEFYGGCGGNNRNFKRKDECEKAC 77
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RESULT 37
Q6ITB4 PRELIMINARY; PRT; 83 AA.
ID Q6ITB4;
AC Q6ITB4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-2.
OS Oxyuranus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626931; AAT45407.1; -.
DR HSSP; P10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Query Match      26.7%; Score 167; DB 2; Length 83;
Best Local Similarity 50.9%; Pred. No. 9.3e-09;
Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 48 RKDICSMPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 27 RPDFCELPADTGPCRVGFPSFYFNPDEKKCLEFYGGCGGNNNNFITKECESTC 81

RESULT 38
Q6ITB6 PRELIMINARY; PRT; 83 AA.
ID Q6ITB6;
AC Q6ITB6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scutellin-2.
OS Oxyuranus scutellatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=8668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626929; AAT45405.1; -.
DR HSSP; P10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Query Match      26.7%; Score 167; DB 2; Length 83;
```


Best Local Similarity 50.9%; Pred. No. 9.3e-09; Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 48 RXDICMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 102
DB 27 RPDFCLPADTGPCRVGFPSFYNDPKKLEFIYGGCGGNNNNFITECESTC 81

RESULT 39
Q6T6S5 PRELIMINARY; PRT; 90 AA.

AC Q6T6S5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kunitz protease inhibitor 2.
OS Bitis gabonica (Gaboon adder) (Gaboon viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OX NCBI_TaxID=8694;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15276202; DOI=10.1016/j.gene.2004.03.024;
RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
RA Ribeiro J.M.;
RT "Bitis gabonica (Gaboon viper) snake venom gland; toward a catalog for
RT the full-length transcripts (cDNA) and proteins.";
RL Gene 337:55-69(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY430413; AAK24535.1; -.
DR HSSP; Q16019; 1AAP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR KQ SEQUENCE 90 AA; 10006 MW; 2BEDCID2020852AF CRC64;

Query Match 26.7%; Score 167; DB 2; Length 90;
Best Local Similarity 45.2%; Pred. No. 1e-08;
Matches 28; Conservative 10; Mismatches 20; Indels 4; Gaps 1;

QY 41 GKCLDFRDKICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLV 100
DB 24 GK- - - - - RPDFCLPADTGPCRVGFPSFYNDPKKLEFIYGGCGGNNNNFITECESTC 79

QY 101 TC 102
DB 80 KC 81

RESULT 40
Q6DRJ1 PRELIMINARY; PRT; 515 AA.

AC Q6DRJ1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Serine protease inhibitor HGFAI.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15256591; DOI=10.1073/pnas.040329101;
RA Amsterdam A., Nissen R.M., Sun Z., Swindell E.C., Farrington S.,
RA Hopkins N.;
RT "Identification of 315 genes essential for early zebrafish
RT development";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY648768; AAT68086.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR000601; PKD.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MANSC; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLA; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00668; LDLRA_2; 1.
DR PROSITE; PS50093; PKD; 1.
DR Protease.
SQ SEQUENCE 515 AA; 57579 MW; AF948A7B0EE46DB4 CRC64;

Query Match 26.6%; Score 166.5; DB 2; Length 515;
Best Local Similarity 27.2%; Pred. No. 5.8e-08;
Matches 34; Conservative 12; Mismatches 32; Indels 47; Gaps 3;

QY 17 VEEIQCTKPRDCPENMKCCP--FSCGKKCL-----FSCGKKCL----- 45
DB 311 IDAVEQCDRP-----CSPEHFTCDNKKCKGLVCDKEKQCSGDSKECKWDYDL 362

QY 46 -----DFRKDICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEAL 97
DB 363 IKLRGISPDVSKARCVCVKPPVTGTCGSGTQKMYNPNKRLCYRPNYGGCGGNNRRFETAG 422

QY 98 CLVTC 102
DB 423 CMTFC 427

RESULT 41
Q90WAI PRELIMINARY; PRT; 83 AA.

AC Q90WAI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textlinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland.
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;

Flippovich I.V., Sorokina N.I., Masci P.P., de Jersey J., Whitaker A.N., Gaffney P.J., Lavin M.F.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -(- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; AF02324; AAK95519.1; --
DR HSPG_P25660; LJUC6
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PD00759; BASICPTASE.
DR PRODOM; PD00022; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0278; BPTI_KUNITZ_2; 1.
DR SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;
SQ

Query Match 26.6%; Score 166; DB 2; Length 83;
Best Local Similarity 50.9%; Pred. No. 1.2e-08;
Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDICSMPOBAGPCLASIPHHWNKTKICSEFIYGGCGGNNNFOTFAICLVTC 102
DB 27 RPDCELPADTGPCRVFRFPSPYPNPDEKKCLEFIYGCENANNFITKECESTC 81

RESULT 42

Q61750 PRELIMINARY; PRT; 507 AA.
ID Q61750 AC
DT 05-JUL-2004 (TrEMBIrel. 27, Created)
DT 05-JUL-2004 (TrEMBIrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBIrel. 27, Last annotation update)
DN Hepatocyte growth factor activator inhibitor-1.
GN Name=HAI-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RA Tezuka S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -(- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
EMBL; AB154834; BAB23971.1; --
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPRO02172; LDL receptor_A.
DR InterPro; IPRO11106; MANSC_N.
DR InterPro; IPRO02223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MANSC; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD00223; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDla; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS50068; LDLRA_2; 1.
DR SEQUENCE 507 AA; 56469 MW; 810043AE28CA7AF3 CRC64;
SQ

Query Match 26.6%; Score 166; DB 2; Length 507;
Best Local Similarity 34.0%; Pred. No. 6.4e-08;
Matches 33; Conservative 17; Mismatches 39; Indels 8; Gaps 3;

QY 15 CEVEIEDQCTKPRDCP---ENNKCPCPSG---KKCLDFRKD--ICSMPOBAGPCLASIP 66
DB 324 CCIDGFLECDTPCPDGSDTEATCEKYSSSGFDQLQSIFLSDXGYCAELPDTGFCENIP 383

QY 67 HWNYNKTTKICSEFIYGGCGGNNNFOTFAICLVTC 103
DB 384 RWYNPFSERCARTYGGCYGNKNFNFEQQOCLSCR 420

Q7YRQ8
ID Q7YRQ8 PRELIMINARY; PRT; 234 AA.
AC Q7YRQ8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos
OC NCBI_TaxID=9913;
OX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;
RA Du X., Deng F.M., Chand H.S., Kisiel W.;
RT "Molecular cloning, expression, and characterization of bovine tissue
factor pathway inhibitor-2.";
RL Arch. Biochem. Biophys. 417:96-104 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Deng F.-M., Kisiel W., Sun T.-T.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AY234861; AA084035.1; -;
DR HSSP; P00981; 1DTK.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26575 MW; 401EEC84D599B422 CRC64;

Query Match 26.4%; Score 165; DB 2; Length 234;
Best Local Similarity 49.1%; Pred. No. 3.9e-08;
Matches 27; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMQEQAGPCLASIPHWYKTKICSEFIYGGCGGNNNFTEAICLVTCCK 104
DB 34 EICLLPDDGFCRAPISYYIDRYTOSCFREMYGGCGGNANFTEACNEACWK 88

RESULT 45
ID Q6ZNI4 PRELIMINARY; PRT; 283 AA.
AC Q6ZNI4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16032.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamiyama K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai T.,
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AK131196; BA018391.1; -;
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin_C.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 86206E7309866D30 CRC64;

Query Match 26.4%; Score 165; DB 2; Length 283;
Best Local Similarity 42.2%; Pred. No. 4.6e-08;
Matches 27; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 39 SCGKCLDFRDKICSMQEQAGPCLASIPHWYKTKICSEFIYGGCGGNNNFTEAIC 98
DB 80 ACWLACMSGLAACSLPALQFCVAPRWAYNSGTQCSQSFYGGCGGNNFESREAC 139

QY 99 LVTC 102
DB 140 EESC 143

RESULT 46
Q7SZ46
ID Q7SZ46 PRELIMINARY; PRT; 342 AA.
AC Q7SZ46;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ambp-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
OX [1]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;

[illegible]


```

Qy 45 LDFRKICSPQAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 2 VFEDKQ-CVETADPGCKGFMFWWYNIFTSQCEFIYGGCGGNNDNRYRTKECDKTC 58

RESULT 50
Q708Y9 PRELIMINARY; PRT; 750 AA.
AC Q708Y9;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Amyloid-beta-like protein B precursor.
GN Name=aplp2 B;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
      [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Collin R.W.J., van Strien D., Leunissen J.A., Martens G.J.M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DE EMBL; AJ089333; CAS75663.1; -.
DR HSP; Q16019; IAAp.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR002223; Prot. Inh. Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00759; BASICPTASE.
DR ProDom; PD000222; Prot. Inh. Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 750 amyloid-beta-like protein B.
SQ SEQUENCE 750 AA; 85363 MW; 7118763E7A763689 CRC64;

Query Match 26.2%; Score 163.5; DB 2; Length 750;
Best Local Similarity 34.6%; Pred. No. 1.6e-07;
Matches 36; Conservative 12; Mismatches 37; Indels 19; Gaps 3

Qy 16 EVEBI-DQCTKPRDC-----PENMKCCPFSCGKCLDPRKDKICSPQAG 59
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 242 EEEIEDEVEDRYYYDNDENDNPTPEPNERQL---SGKDIITDKSVCSQEA VTG 298

Qy 60 PCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 299 PCRAMPRWYFDLQKKCVRFYGGCGGNRNPFSADYCMVACK 342

Search completed: September 21, 2005, 16:40:10
Job time : 59.472 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 14:52:13 ; Search time 31.8938 Seconds
(without alignments)
618.452 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127

Perfect score: 302

Sequence: 1 CSMFQAGPCIASIPHWYN.....GGCQGNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

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1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	302	100.0	106	7	ADAL19801 Mature fo
2	302	100.0	131	7	ADAL19800 Engineere
3	302	100.0	131	7	ADAL19811 Engineere
4	292	96.7	131	7	ADAL19814 Human DJ1
5	224	74.2	136	7	ADAL19815 Mouse DJ1
6	219	72.5	51	2	Aaw75257 Fragment
7	219	72.5	51	5	Aae27025 Human gen
8	219	72.5	51	5	Aae27163 Human gen
9	219	72.5	51	8	ADG89845 Human sec
10	219	72.5	58	4	ADG89848 Human sec
11	219	72.5	58	4	Aae13084 Human ser
12	219	72.5	58	7	ADFL1997 Human CAB
13	219	72.5	58	8	ADL16838 Human Kun
14	219	72.5	58	8	ADR89980 Human CAB
15	219	72.5	64	4	Aae13093 Human eer
16	219	72.5	102	5	Aae27095 Human sec
17	219	72.5	102	5	Aae28009 Human gen
18	219	72.5	102	6	ABU65039 Human sec
19	219	72.5	102	8	ADG89848 Human sec
20	219	72.5	117	5	Aae27094 Human sec
21	219	72.5	117	5	Aae27165 Human gen
22	219	72.5	117	6	ABU65038 Human sec
23	219	72.5	117	8	ADG89847 Human sec
24	219	72.5	133	2	Aaw75219 Human sec
25	219	72.5	133	5	Aae26982 Human gen

26	219	72.5	133	5	AAE27120	Human gen
27	219	72.5	133	6	ABU64993	Human sec
28	219	72.5	133	7	ADAL19812	Human EPP
29	219	72.5	133	8	ADG89802	Human Pro
30	219	72.5	164	3	AA70010	Human Pro
31	219	72.5	179	8	ABM85103	Human dia
32	188	62.3	134	7	ADAL19813	Mouse EPP
33	170	56.3	43	4	AAE13096	Human ser
34	169	56.0	571	7	AAE39498	Cloned mo
35	169	56.0	571	7	AAE39459	Mouse GDF
36	169	56.0	571	7	ADD93670	Mouse GDF
37	167	55.3	58	2	AAE99146	Aprotinin
38	166	55.0	54	4	AAE13092	Trypsin i
39	166	55.0	86	4	AAW48380	I. ricinu
40	161	53.3	51	2	AAW25929	Anti-tryp
41	161	53.3	55	2	AAW25931	RPDF-Kun1
42	161	53.3	58	2	AAW27402	Human neu
43	161	53.3	58	2	AAE99160	Genetical
44	161	53.3	58	2	AAE99159	Genetical
45	161	53.3	58	2	AAE99158	Genetical
46	161	53.3	58	8	ADF71964	Kallikrei
47	161	53.3	58	8	ADF71963	Kallikrei
48	161	53.3	58	8	ADF71962	Kallikrei
49	161	53.3	124	2	AAW25933	New prote
50	161	53.3	124	2	AAW25932	New prote

ALIGNMENTS

RESULT 1

ADAL19801

ID ADAL19801 standard; protein; 106 AA.

AC ADAL19801;

DT 20-NOV-2003 (first entry)

DE Mature form of engineered human DJ11 protein SEQ ID NO:2.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;

XX anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;

XX antibacterial; immunosuppressive; antirheumatic; antithrptic;

XX nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;

XX acute pancreatitis; pulmonary injury; allergy-induced protease release;

XX deep vein thrombosis; myocardial infarction; shock; septic shock;

XX hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;

XX idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;

XX chronic inflammatory bowel disease; psoriasis.

XX Synthetic.

XX Homo sapiens.

XX Key

XX Disulfide-bond 8..36

XX Disulfide-bond /note = predicted disulfide bond

XX Disulfide-bond 15..40

XX Disulfide-bond /note = predicted disulfide bond

XX Disulfide-bond 23..35

XX Disulfide-bond /note = predicted disulfide bond

XX Disulfide-bond 29..44

XX Disulfide-bond /note = predicted disulfide bond

XX Domain 52..102

XX Disulfide-bond /note = Kunitz domain predicted by pfacan

XX Disulfide-bond 52..102

XX Disulfide-bond /note = predicted disulfide bond

XX Disulfide-bond 61..85

XX Disulfide-bond /note = predicted disulfide bond

XX Disulfide-bond 77..98

XX Disulfide-bond /note = predicted disulfide bond

XX WO2003070770-A2.

PD 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 DR New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 FT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 FT hemorrhage.
 XX Claim 5; Page 71; 87pp; English.
 PS The present invention describes an isolated, purified or recombinant DJ11
 XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents the mature form of an engineered human
 CC DJ11 protein from the present invention.
 XX SQ Sequence 106 AA;
 Query Match 100.08; Score 302; DB 7; Length 106;
 Best Local Similarity 100.08; Pred. No. 3.2e-30;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CSMPQAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
 Db 52 CSMPQAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 102
 RESULT 2
 ADA19800
 ID ADA19800 standard; protein; 131 AA.
 XX ADA19800;
 AC ADA19800;
 XX 20-NOV-2003 (first entry)
 DT Engineered human DJ11 protein SEQ ID NO:1.
 DE DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 XX antiallergic; thrombolytic; anticoagulant; cardiatic; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 1..131
 FT /note= "eppin-like precursor"
 FT Peptide 1..25
 FT /label= signal
 FT Protein 26..131
 FT /note= "mature DJ11 protein"
 FT Disulfide-bond 33..61
 FT /note = predicted disulfide bond
 FT Disulfide-bond 40..65
 FT /note = predicted disulfide bond
 FT Disulfide-bond 48..60
 FT /note = predicted disulfide bond
 FT Disulfide-bond 54..69
 FT /note = predicted disulfide bond
 FT Domain 77..127
 FT /note = Kunitz domain predicted by pfscan
 FT Disulfide-bond 77..127
 FT /note = predicted disulfide bond
 FT Disulfide-bond 86..110
 FT /note = predicted disulfide bond
 FT Disulfide-bond 102..123
 FT /note = predicted disulfide bond
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 DR N-PSDB; ADA19810.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 FT hemorrhage.
 XX Claim 5; Page 69-70; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 302; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.1e-30;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 |||||
 DB 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127

RESULT 3
 ADA19811
 ID ADA19811 standard; protein; 131 AA.
 XX AC ADA19811;
 XX DT 20-NOV-2003 (first entry)
 XX DE Engineered human DJ11 protein SEQ ID NO:12.
 XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 OS WO2003070770-A2.
 XX PN 28-AUG-2003.
 XX PD 18-FEB-2003; 2003WO-EP001629.
 XX PF 21-FEB-2002; 2002US-0358683P.
 XX PR (GENE-) GENEPROT INC.
 XX PA Bougueleret L, Bairoch A, Niknejad A;
 XX PI WPI; 2003-663849/G2.
 XX DR New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX PT preventing or treating conditions associated with excessive proteinase
 XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX PT hemorrhage.
 XX PS Disclosure; Page 84; 87pp; English.

CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, immunosuppressive,
 CC anticoagulant, cardiant, vasotropic, antirheumatic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may

CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 302; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.1e-30;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 |||||
 DB 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127

RESULT 4

ADA19814
 ID ADA19814 standard; protein; 131 AA.

XX AC ADA19814;

XX DT 20-NOV-2003 (first entry)

XX DE Human DJ11 protein SEQ ID NO:15.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX OS Homo sapiens.

XX PN WO2003070770-A2.

XX PD 28-AUG-2003.

XX PF 18-FEB-2003; 2003WO-EP001629.

XX PR 21-FEB-2002; 2002US-0358683P.

XX PA (GENE-) GENEPROT INC.

XX PI Bougueleret L, Bairoch A, Niknejad A;

XX DR WPI; 2003-663849/G2.

XX PT New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX PT preventing or treating conditions associated with excessive proteinase
 XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX PT hemorrhage.

XX PS Disclosure; Fig 1; 87pp; English.

CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, immunosuppressive,
 CC anticoagulant, cardiant, vasotropic, antirheumatic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may

CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a human DJ11 protein given in comparison
CC with DJ11 proteins in the exemplification of the present invention.
XX
SQ Sequence 131 AA;

Query Match 96.7%; Score 292; DB 7; Length 131;
Best Local Similarity 98.0%; Pred. No. 7.5e-29;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 77 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127

RESULT 5
ADA19815
ID ADA19815 standard; protein; 136 AA.

XX ADA19815;

XX 20-NOV-2003 (first entry)

DE Mouse DJ11 protein SEQ ID NO:16.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoptic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

OS Mus musculus.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,

CC antirheumatic, antiarthritic, nephrotropic, antipsoptic and vulnery
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a mouse DJ11 protein given in comparison
CC with DJ11 proteins in the exemplification of the present invention.
XX
SQ Sequence 136 AA;

Query Match 74.2%; Score 224; DB 7; Length 136;

Best Local Similarity 66.7%; Pred. No. 3.2e-20;

Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Oy 1 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 77 CSLPQDFGCLAYLPRWYNNQETDLCTEFIYGGCGGNNNFSEGITCTVVC 127

RESULT 6

AAW75257

ID AAW75257 standard; protein; 51 AA.

XX AAW75257;

XX 29-JAN-1999 (first entry)

XX Fragment of human secreted protein encoded by gene 24.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX OS

XX WO9840483-A2.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US004858.

XX 14-MAR-1997; 97US-0040710P.

XX 14-MAR-1997; 97US-0040762P.

XX 30-MAY-1997; 97US-0048100P.

XX 30-MAY-1997; 97US-0048189P.

XX 30-MAY-1997; 97US-0048357P.

XX 30-MAY-1997; 97US-0050934P.

XX 06-JUN-1997; 97US-0048970P.

XX 05-SEP-1997; 97US-0057765P.

XX 19-DEC-1997; 97US-0068368P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Rosen CA, Li Y, zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz R, Wei YF, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX WPI; 1998-520811/44.
DR N-PSDB; AAV34309.

PT New polypeptides and nucleic acid molecules for diagnosing, preventing or
 PT treating diseases associated with aberrant expression or activity of the
 PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
 XX
 PS Disclosure; SEQ ID NO 118; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridisable to the nucleotide sequences, a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
 CC or epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the specification, a polynucleotide which
 CC encodes a species homologue of the above amino acid sequences, a
 CC polynucleotide capable of hybridising under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridise
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant host
 CC comprising the above nucleic acid molecule, making a recombinant host
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC comprising a sequence that is at least 95% identical to the polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosing or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular
 CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
 CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
 CC allergies, nephritis, Parkinson's disease, Alzheimer's disease, the methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a protein from
 CC one of the 28 disclosed secreted protein genes, it is not clear whether
 CC this is an alternative expressed protein or a fragment of one of the
 CC claimed proteins.

XX Sequence 51 AA;

SQ Query Match 72.5%; Score 219; DB 8; Length 51;
 Best Local Similarity 68.6%; Pred. No. 4.7e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
 DB 1 CEMPKEGTCLAYFLHWYDKDNTCSMFVYGGCGNNNNFQSKANCLNTC 51

RESULT 10

AAE13084

ID AAE13084 standard; peptide; 58 AA.

XX AAE13084;

XX 28-JAN-2002 (first entry)

DE Human serine proteinase inhibitor BTL.009 peptide.

XX Human, BTL.009 protein; serine proteinase inhibitor; cytostatic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angioedema;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;

KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.

XX Homo sapiens.

XX US6294648-B1.

XX 25-SEP-2001.

XX 20-JUL-1999; 99US-00358569.

XX 20-JUL-1999; 99US-00358569.

XX (FARB) BAYER CORP.

XX Delaria K, Roczniak S, Davies C;

XX WPI; 2001-662224/76.

XX New isolated protein for inhibiting human serine protease activity in the
 PT treatment of e.g. emphysema and adult respiratory distress syndrome.

XX Claim 1; Col 15-16; 16pp; English.

XX The invention relates to human BTL.009 protein, a serine proteinase
 CC inhibitor of the Kunitz family that exhibits greater potency towards
 CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
 CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
 CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid diseases
 CC and diseases involving lung and vascular injury. BTL.009 is also useful
 CC for preventing neutrophil and monocyte activation and formation of active
 CC oxygen species during the oxidative burst of stimulated granulocytes.
 CC BTL.009 is useful for reducing platelet activation and blood coagulation
 CC and for the prophylactic or therapeutic treatment of patients undergoing
 CC angioplasty. The present sequence is human serine proteinase inhibitor
 CC BTL.009 peptide corresponding to Kunitz domain used in the
 CC exemplification of the invention. Note: The present sequence shown in
 CC column 14 and sequence listing of the specification lacks 3 amino acid
 CC residues at the C-terminal end

XX Sequence 58 AA;

SQ Query Match 72.5%; Score 219; DB 4; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
 DB 5 CEMPKEGTCLAYFLHWYDKDNTCSMFVYGGCGNNNNFQSKANCLNTC 55

RESULT 11

AAE60630

ID AAE60630 standard; protein; 58 AA.

XX AAE60630;

XX 27-APR-2001 (first entry)

DE Kunitz domain, SEQ ID NO:8, used to identify BTL.010 protein.

XX Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;
 KW proteinase-3 inhibitor; Kunitz domain; emphysema;
 KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 KW platelet activation; blood coagulation; neutrophil activation;
 KW monocyte activation; angioedema; inflammatory disease; lung injury;
 KW vascular injury; nephrotropic; anti-rheumatic; antiarthritic.

XX Unidentified.

XX US6180607-B1.
 XX 30-JAN-2001.
 XX
 PD
 XX
 PF 05-AUG-1999; 99US-00369494.
 XX
 PR 05-AUG-1999; 99US-00369494.
 XX
 XX (DAVI/) DAVIES C.
 PA (CHEN/) CHEN D.
 PA (ROCZ/) ROCZNIK S.
 XX
 XX Davies C, Chen D, Rocznik S;
 XX WPI; 2001-190860/19.
 DR
 XX
 PT Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful
 PT for treating emphysema, cystic fibrosis, adult respiratory distress
 PT syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
 XX
 PS Disclosure; Col 6; 17pp; English.
 XX
 CC The invention relates to a novel human serine protease inhibitor of the
 CC Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and
 CC AAB60634). The BTL.010 protein is thought to preferentially inhibit
 CC neutral serine proteases such as elastase and proteinase-3, relative to
 CC trypsin-like and chymotrypsin-like proteases. A substantial proportion of
 CC the BTL.010 protein Kunitz domain (AAB60631) was identified via homology
 CC searching in the GenBank high throughput genomic (HTG) DNA sequence
 CC database using the Kunitz domain sequences AAB60630, and was confirmed as
 CC being novel using the Kunitz domain sequences AAB60632, and AAB60633.
 CC This sequence information was extended to provide a larger region of
 CC BTL.010 protein sequence data (AAB60634) by identifying an open reading
 CC frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain
 CC fragment in a 399 bp fragment of human genomic DNA (AAF59750),
 CC corresponding to bases 16016-16414 of GenBank accession number AC004846.
 CC The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from
 CC the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical
 CC compositions comprising it, may be used for inhibiting protease activity,
 CC particularly that of leukocyte elastase, in the prevention, treatment or
 CC amelioration of medical conditions such as emphysema, idiopathic
 CC pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,
 CC rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010
 CC compositions of the invention modulate at least one physiological
 CC condition such as platelet activation, blood coagulation, neutrophil
 CC activation, or monocyte activation. BTL.010 is also useful for the
 CC prophylactic or therapeutic treatment of patients undergoing angioplasty,
 CC and for the treatment of inflammatory diseases and diseases involving
 CC lung and vascular injury. The present sequence represents a Kunitz domain
 CC sequence used to identify the BTL.010 protein
 XX
 SQ Sequence 58 AA;
 Query Match 72.5%; Score 219; DB 4; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 Qy 1 CSMPEQAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 |||:||||| |||:| |||:|||||:|:|
 Db 5 CEMPKETGPCLAYFLHWWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55
 |||:||||| |||:| |||:|||||:|:|
 RESULT 12
 ADP41997
 ID ADP41997 standard; protein; 58 AA.
 XX
 AC ADP41997;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human CAB37 Kunitz domain peptide.
 XX

KW albumin fusion; Kunitz domain; cytostatic; haemostatic;
 KW hereditary angioedema; cancer; bleeding; gene therapy; human; CAB37.
 XX
 OS Homo sapiens.
 PN WO2003066824-A2.
 XX
 PD 14-AUG-2003.
 XX
 XX 07-FEB-2003; 2003WO-US003616.
 PF
 XX 07-FEB-2002; 2002US-0355547P.
 PR
 XX (AVET) AVENTIS BEHRING GMBH.
 PA (AVET) AVENTIS BEHRING LLC.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA (DYAX-) DYAX CORP.
 XX
 XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
 PI Ley AC;
 XX
 DR WPI; 2003-731497/69.
 XX
 CC Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
 CC useful for preparing a composition for treating a patient with hereditary
 CC angioedema or angioedema-related disease, cancer or bleeding disorder.
 PT
 XX
 PS Disclosure; Page 20; 110pp; English.
 CC
 CC The invention relates to a novel albumin fusion protein comprising a
 CC Kunitz domain peptide or its fragment or variant and an albumin or its
 CC fragment or variant. The fusion protein of the invention demonstrates a
 CC cycostatic and haemostatic activities and may be useful for preparing a
 CC composition for treating a patient with hereditary angioedema, an
 CC angioedema-related disease, cancer, a cancer-related disease or a
 CC bleeding disorder, as well as during gene therapy procedures. The current
 CC sequence is that of the human Kunitz domain peptide of the invention.
 XX
 SQ Sequence 58 AA;
 Query Match 72.5%; Score 219; DB 7; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 Qy 1 CSMPEQAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 |||:||||| |||:| |||:|||||:|:|
 Db 5 CEMPKETGPCLAYFLHWWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55
 |||:||||| |||:| |||:|||||:|:|
 RESULT 13
 ADL16838
 ID ADL16838 standard; peptide; 58 AA.
 XX
 AC ADL16838;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human Kunitz domain (KD) peptide.
 XX
 XX BTL.010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;
 KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 KW inflammatory disease; oxidative burst; platelet activation;
 KW blood coagulation; gene therapy; human; KD.
 XX
 OS Homo sapiens.
 XX
 XX US6689582-B1.
 PN
 XX
 PD 10-FEB-2004.
 XX
 PF 12-MAY-2000; 2000US-00569670.
 XX

PR 05-AUG-1999; 99US-00369494.
 XX (FARB) BAYER PHARM CORP.
 PA Davies C, Chen D, Rocznia S;
 PI WPI; 2004-141424/14.
 XX New isolated polynucleotide encoding BTL.010 serine proteinase, useful
 XX for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
 PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
 PT glomerulonephritis.
 XX
 PS Disclosure; SEQ ID NO 8; 17pp; English.
 XX
 CC The invention relates to BTL.010, a human serine proteinase inhibitor of
 CC the Kunitz family and its corresponding nucleic acid sequence. The
 CC sequences of the invention are useful for treating diseases, e.g.
 CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
 CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
 CC glomerulonephritis or inflammatory diseases. The BTL.010 protein is also
 CC useful for preventing neutrophil and monocyte activation and formation of
 CC active oxygen species during the oxidative burst of stimulated
 CC granulocytes. It is also useful for reducing platelet activation and
 CC blood coagulation. BTL.010 DNA is useful in gene therapy. The present
 CC sequence is human Kunitz domain (KD) peptide.
 XX
 SQ Sequence 58 AA;

 Query Match 72.5%; Score 219; DB 8; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

 QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 DB 5 CEMPKEGTCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

 RESULT 14
 ADR89980
 ID ADR89980 standard; peptide; 58 AA.
 XX
 AC ADR89980;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human CAB37 protein kunitz domain peptide.
 XX
 KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
 KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
 KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
 KW cytostatic; haemostatic; CAB37 protein; human.
 XX
 OS Homo sapiens.
 XX
 PN US200417194-A1.
 XX
 PD 02-SEP-2004.
 XX
 PF 07-FEB-2003; 2003US-00361997.
 XX
 PR 07-FEB-2003; 2003US-00361997.
 XX
 PA (LADN/) LADNER R C.
 PA (LEYA/) LEY A C.
 XX
 PI Ladner RC, Ley AC;
 XX
 DR WPI; 2004-625120/60.
 XX
 CC New kunitz domain peptide useful as human neutrophil elastase inhibitor
 PT for the treatment of e.g. cystic fibrosis and related disease.
 XX

PS Disclosure; SEQ ID NO 5; 123pp; English.
 XX
 CC The invention relates to proteins comprising kunitz domain peptide,
 CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angioedema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cytostatic and haemostatic agent. The present sequence is the human CAB37
 CC protein (A4) kunitz domain peptide. This sequence is used in the
 CC invention.
 XX
 SQ Sequence 58 AA;

 Query Match 72.5%; Score 219; DB 8; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

 QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 DB 5 CEMPKEGTCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

 RESULT 15
 AAE13093
 ID AAE13093 standard; peptide; 64 AA.
 XX
 AC AAE13093;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Human serine proteinase inhibitor BTL.009 C-terminal peptide.
 XX
 KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angioedema;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6294648-B1.
 XX
 PD 25-SEP-2001.
 XX
 PF 20-JUL-1999; 99US-00358569.
 XX
 PR 20-JUL-1999; 99US-00358569.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Delaria K, Rocznia S, Davies C;
 XX
 DR WPI; 2001-662224/76.
 XX
 PT New isolated protein for inhibiting human serine protease activity in the
 PT treatment of e.g. emphysema and adult respiratory distress syndrome.
 XX
 PS Disclosure; Col 6; 16pp; English.
 XX
 CC The invention relates to human BTL.009 protein, a serine proteinase
 CC inhibitor of the Kunitz family that exhibits greater potency towards
 CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
 CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
 CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
 CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
 CC and diseases involving lung and vascular injury. BTL.009 is also useful
 CC for preventing neutrophil and monocyte activation and formation of active
 CC oxygen species during the oxidative burst of stimulated granulocytes.
 CC BTL.009 is useful for reducing platelet activation and blood coagulation

CC and for the prophylactic or therapeutic treatment of patients undergoing
 CC angioplasty. The present sequence is human serine proteinase inhibitor
 CC BTL-009 C-terminal peptide containing Kunitz domain which is used in the
 CC exemplification of the invention

XX Sequence 64 AA;

Query Match 72.5%; Score 219; DB 4; Length 64;
 Best Local Similarity 68.6%; Pred. No. 6e-20; Indels 0; Gaps 0;
 Matches 35; Conservative 5; Mismatches 11;

Qy 1 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 |||:||||| |||:|| | :||||| |||:| |||
 Db 7 CEMPKEGPCLAYFLHWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 57

RESULT 16
 AAE27095

ID AAE27095 standard; protein; 102 AA.

XX AAE27095;

AC AAE27095;

DT 13-DEC-2002 (first entry)

XX Human secreted protein #2.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotrophic; vulnery; cytostatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.

XX Homo sapiens.

XX OS

XX US2002077287-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00852659.

XX 11-SEP-1998; 98US-00152060.

XX (RUBE/) RUBEN S M.

XX (ROSE/) ROSEN C A.

XX (LIYY/) LI Y.

XX (ZENG/) ZENG Z.

XX (KYAW/) KYAW H.

XX (FISC/) FISCHER C L.

XX (LTH/) LI H.

XX (SOPP/) SOPPET D R.

XX (GENT/) GENTZ R L.

XX (WEIY/) WEI Y.

XX (MOOR/) MOORE P A.

XX (YOUN/) YOUNG P E.

XX (GREE/) GREENE J M.

XX (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

XX AAD4636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogenic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders. e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperparathyroidism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention

XX Sequence 102 AA;

Query Match 72.5%; Score 219; DB 5; Length 102;

Best Local Similarity 68.6%; Pred. No. 1e-19;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 |||:||||| |||:|| | :||||| |||:| |||

Db 46 CEMPKEGPCLAYFLHWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 96

RESULT 17

AAE28009

ID AAE28009 standard; protein; 102 AA.

XX AAE28009;

XX 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein fragment #2.

XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotrophic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;

XX Homo sapiens.

XX OS

XX US2002076756-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00853161.

XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of

XX 02-FEB-2001; 2001US-0265583P.
 PR (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX
 PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 XX WPI; 2002-574454/61.
 DR
 XX New nucleic acid molecules encoding 28 human secreted proteins, useful
 PT for diagnosing, preventing, treating or ameliorating medical conditions
 PT and as food additives or preservatives.
 PT
 XX
 XX Disclosure; Page 17; 209pp; English.
 XX
 CC AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
 CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Secreted protein sequences of the invention are useful for the
 CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
 CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
 CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
 CC angioneurosis), cardiovascular disorders (e.g. cardiac arrest), nervous
 CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
 CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
 CC polypeptides can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues and in chemotaxis. They can also be used as food
 CC additives or preservative to increase or decrease storage capabilities,
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
 CC and other nutritional components. The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention
 XX
 XX Sequence 102 AA;
 SQ
 Query Match 72.5%; Score 219; DB 5; Length 102;
 Best Local Similarity 68.6%; Pred. No. 1e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMQEGAGCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEALCLVTC 51
 DB 46 CEMPKEGPCLAYFLHWYDKDNTCSMFVYGGCGQNNNNFQSKANCLNTC 96
 RESULT 18
 ABU65039
 ID ABU65039 standard; peptide; 102 AA.
 XX
 AC ABU65039;
 XX
 DT 15-MAY-2003 (first entry)
 XX
 DE Human secreted protein gene 24, protein #3.
 XX
 KW Secreted protein; immunodeficiency; multiple sclerosis;

KW severe combined immunodeficiency; autoimmune disorder; cancer;
 KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
 KW inflammatory condition; septic shock; inflammatory bowel disease;
 KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
 KW gastrointestinal disorder; central nervous system disorder;
 KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
 KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
 KW blood-related disorder; thrombosis; acute glomerulonephritis;
 KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
 KW endocrine disorder; liver disease; reproductive system disorder;
 KW endometriosis; infectious disease; pancreatic disorder; vaccine;
 KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
 KW body height; hair colour; human.
 XX Homo sapiens.
 OS
 XX US2002172994-A1.
 PN
 XX 21-NOV-2002.
 PD
 XX 11-MAY-2001; 2001US-00852797.
 PF
 XX 14-MAR-1997; 97US-0040710P.
 PR 14-MAR-1997; 97US-0040762P.
 PR 30-MAY-1997; 97US-0048100P.
 PR 30-MAY-1997; 97US-0048189P.
 PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0050934P.
 PR 06-JUN-1997; 97US-0048970P.
 PR 05-SEP-1997; 97US-0057765P.
 PR 19-DEC-1997; 97US-0068368P.
 PR 12-MAR-1998; 98WO-US004858.
 PR 11-SEP-1998; 98US-0015206P.
 PR 02-FEB-2001; 2001US-0265583P.
 XX (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX
 PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 XX WPI; 2003-310989/30.
 DR
 XX New human secreted polypeptides and polynucleotides for diagnosing,
 PT prognosing, preventing and treating immune, hyperproliferative, liver,
 PT kidney, reproductive disorders and for identifying modulators of
 PT therapeutic use.
 XX
 PS Disclosure; Page 16; 209pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising an amino acid
 CC sequence at least 95% identical to sequence of 28 human secreted
 CC proteins, their fragment, polypeptide domain, epitope, secreted form,
 CC variant, allelic variant, or species homologue, or the encoded sequence
 CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
 CC acids, recombinant vectors, host cells, antibodies, and genes. The
 CC proteins and nucleic acids are useful for diagnosing, preventing,
 CC treating, prognosing or ameliorating a medical condition e.g.
 CC immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell
 CC immunodeficiencies, severe combined immunodeficiencies), autoimmune

disorders (e.g. systemic erythematosis, rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis), haematopoietic disorders, inflammatory conditions (e.g. septic shock, sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease), respiratory disorders (e.g. asthma and allergy), gastrointestinal disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and breast), central nervous system (CNS) disorders (e.g. ischaemic brain injury and/or stroke, traumatic brain injury), neurodegenerative disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related dementia, and prion disease), cardiovascular disorders (e.g. atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary bypass complications), inflammation (e.g. hepatitis, gout, trauma, pancreatitis, sarcoidosis, dermatitis, allogenic transplant rejection), blood-related disorders (thrombosis, arterial thrombosis), hyperproliferative disorders, renal disorders (e.g. acute glomerulonephritis), endocrine disorders (e.g. Addison's disease, hyperthyroidism, hypothyroidism, liver diseases and disorders, reproductive system disorders (e.g. endometriosis), infectious diseases, and pancreatic disorders. Many other diseases and disorders are listed in the specification. They also useful as a vaccine adjuvant. Further they are useful to enhance or inhibit complement mediated cell lysis, for stimulating wound and tissue repair, angiogenesis, and the repair of vascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreted protein of the invention

SQ Sequence 102 AA;

Query Match 72.5%; Score 219; DB 6; Length 102;

Best Local Similarity 68.6%; Pred. No. 1e-19;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPQAGPCPLASIPHWYNNKTKICSEFIYGGCGNNNNFQTRAILCVTC 51

Db 46 CEMPRTGPCLAYFLHWWYDKDKTCSFVYGGCGNNNNFQSKANCLNTC 96

RESULT 19

ADG89848

ID ADG89848 standard; protein; 102 AA.

XX AC ADG89848;

XX DT

XX 11-MAR-2004 (first entry)

XX Human secreted protein gene 24 protein #6.

XX Secreted protein; gene therapy; neural disorder; immune system disorders; muscular disorder; reproductive disorder; gastrointestinal disorder; muscular disorder; cardiovascular disorder; renal disorder; proliferative disorder; cancer; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia; Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis; Parkinson's disease; Alzheimer's disease; atherosclerosis; myocardial infarction; AIDS; infection; human.

OS Homo sapiens.

XX US2003225009-A1.

XX 04-DEC-2003.

XX 30-JAN-2002; 2002US-00058993.

XX 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US0004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
PR 11-MAY-2001; 2001US-00852659.
PR 11-MAY-2001; 2001US-00852797.
PR 11-MAY-2001; 2001US-00853161.

XX (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (LIYU/) LI Y.

PA (ZENG/) ZENG Z.

PA (KIYAW/) KIYAW H.

PA (FISC/) FISCHER C L.

PA (LIHH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEIY/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

PA (HAST/) HASTINGS G A.

XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM, Hastings GA;

XX WPI; 2004-042167/04.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or

treating diseases associated with aberrant expression or activity of the polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

Disclosure; SEQ ID NO 121; 320pp; English.

The invention relates to an isolated nucleic acid molecule encoding a secreted protein that is at least 95% identical to a polynucleotide fragment of any of the nucleotide sequences listed in table 1A of the specification, which is hybridisable to the nucleotide sequences, a polynucleotide encoding a polypeptide (or a polypeptide fragment, domain or epitope of any of the amino acid sequences) listed in table 1A of the specification, a polynucleotide which is an (allelic) variant of the nucleotide sequences listed in the specification, a polynucleotide which encodes a species homologue of the above amino acid sequences, a polynucleotide capable of hybridising under stringent conditions to any of the above polynucleotides, where the polynucleotide does not hybridise of the above polynucleotides, where the polynucleotide having a nucleotide sequence of only A or T residues. Also included are a recombinant vector comprising the above nucleic acid molecule, making a recombinant host cell comprising the above nucleic acid molecule, an isolated polypeptide comprising a sequence that is at least 95% identical to the polypeptide (or its fragment, domain, epitope, secreted form, (allelic) variant or homologue) encoded by the above nucleic acid molecule, an isolated antibody that binds specifically to the above polypeptide, a recombinant host cell produced by the above method and that expresses the above polypeptide, making an isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnosing a pathological condition or a binding partner to the above polypeptide, the gene corresponding to the cDNA sequence given in the specification, and identifying an activity in a biological assay. The nucleic acid molecule and polypeptide are useful in diagnosing, preventing, prognosing or treating diseases or disorders associated with aberrant expression and/or activity of the above polypeptide, such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders and/or cancers. In particular, these diseases are systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis,

CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
 CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
 CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a protein from
 CC one of the 28 disclosed secreted protein genes, it is not clear whether
 CC this is an alternative expressed protein or a fragment of one of the
 CC claimed proteins.

XX
 SQ Sequence 102 AA;
 Query Match 72.5%; Score 219; DB 8; Length 102;
 Best Local Similarity 68.6%; Pred. No. 1e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSBFIYGGCGGNNNNFQTEAICLVTC 51
 DB 46 CEMPXETGPCLAYFLHWYDKDNTCSMFYGGCGGNNNNFQSKANCLNTC 96

RESULT 20
 AAE27094
 ID AAE27094 standard; protein; 117 AA.
 AC AAE27094;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human secreted protein #1.
 XX
 KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotrophic; vulnerary; cytostatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.

XX
 OS Homo sapiens.
 XX
 XX US2002077287-A1.
 XX
 XX 20-JUN-2002.
 XX
 XX 11-MAY-2001; 2001US-00852659.
 XX
 XX 11-SEP-1998; 98US-00152060.
 XX
 XX (RUBE/) RUBEN S M.
 XX (ROSE/) ROSEN C A.
 XX (LIYY/) LI Y.
 XX (ZENG/) ZENG Z.
 XX (KYAW/) KYAW H.
 XX (FISC/) FISCHER C L.
 XX (LIHH/) LI H.
 XX (SOPP/) SOPPET D R.
 XX (GENT/) GENTZ R L.
 XX (WEIY/) WEI Y.
 XX (MOOR/) MOORE P A.
 XX (YOUN/) YOUNG P E.
 XX (GREE/) GREENE J M.
 XX (FERR/) FERRIE A M.
 XX
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 XX Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 XX Ferrie AM;
 XX WPI; 2002-598780/64.

XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular, PT
 PT neurological, reproductive disorders and identifying modulators of
 XX therapeutic use.
 XX
 PS Disclosure; Page 16; 209pp; English.
 XX
 AA044636-AA044676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogenic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders, e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 XX The present sequence represents a human secreted protein of the invention
 SQ Sequence 117 AA;
 Query Match 72.5%; Score 219; DB 5; Length 117;
 Best Local Similarity 68.6%; Pred. No. 1.2e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSBFIYGGCGGNNNNFQTEAICLVTC 51
 DB 61 CEMPXETGPCLAYFLHWYDKDNTCSMFYGGCGGNNNNFQSKANCLNTC 111

RESULT 21
 AAE27165
 ID AAE27165 standard; protein; 117 AA.
 AC AAE27165;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human gene 24 encoded secreted protein fragment #1.
 XX
 KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiodenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotrophic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 KW vulnerary.
 XX
 XX Homo sapiens.
 XX
 XX US2002076756-A1.


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XX PD 20-JUN-2002.
XX PF 11-MAY-2001; 2001US-00853161.
XX PR 02-FEB-2001; 2001US-0265583P.
XX PA (RUBE//) RUBEN S M.
XX PA (ROSE//) ROSEN C A.
XX PA (LIYY//) LI Y.
XX PA (ZENG//) ZENG Z.
XX PA (KYAW//) KYAW H.
XX PA (FISC//) FISCHER C L.
XX PA (LIHH//) LI H.
XX PA (SOPP//) SOPPET D R.
XX PA (GENT//) GENTZ R L.
XX PA (WEIY//) WEI Y.
XX PA (MOOR//) MOORE P A.
XX PA (YOUN//) YOUNG P E.
XX PA (GREE//) GREENE J M.
XX PA (FERR//) FERRIE A M.
XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
XX PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
XX PI Ferrie AM;
XX DR WPI; 2002-574454/61.
XX PR New nucleic acid molecules encoding 28 human secreted proteins, useful
XX PT for diagnosing, preventing, treating or ameliorating medical conditions
XX PT and as food additives or preservatives.
XX PS Disclosure; Page 17; 209pp; English.
XX CC AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
XX CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
XX CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
XX CC and their corresponding secreted proteins are useful for preventing,
XX CC treating or ameliorating medical conditions, e.g., by protein or gene
XX CC therapy. Secreted protein sequences of the invention are useful for the
XX CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
XX CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
XX CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
XX CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
XX CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
XX CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
XX CC polypeptides can also be used to aid wound healing and epithelial cell
XX CC proliferation, to prevent skin aging due to sunburn, to maintain organs
XX CC before transplantation, for supporting cell culture of primary tissues,
XX CC to regenerate tissues and in chemotaxis. They can also be used as food
XX CC additives or preservative to increase or decrease storage capabilities,
XX CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
XX CC and other nutritional components. The present sequence represents a human
XX CC secreted protein fragment referred to in the disclosure of the invention
XX SQ Sequence 117 AA;
XX
XX Query Match 72.5%; Score 219; DB 5; Length 117;
XX Best Local Similarity 68.6%; Pred. NO. 1.2e-19;
XX Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX Qy 1 CSMPOEAGPCCLASIPHHVYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX Db 61 CEMPKEITGCLAYFLHWDYDKDNTCSMPVYVYGGCGGNNNNFQSKANCLNTC 111
XX
XX RESULT 22
XX ABU65038
XX ID ABU65038 standard; protein; 117 AA.
XX AC ABU65038;
XX DT 15-MAY-2003 (first entry)

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XX DE Human secreted protein gene 24, protein #4.
XX KW Secreted protein; immunodeficiency; multiple sclerosis;
XX KW severe combined immunodeficiency; autoimmune disorder; cancer;
XX KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
XX KW inflammatory condition; septic shock; inflammatory bowel disease;
XX KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
XX KW gastrointestinal disorder; central nervous system disorder;
XX KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
XX KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
XX KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
XX KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
XX KW endocrine disorder; liver disease; reproductive system disorder;
XX KW endometriosis; infectious disease; pancreatic disorder; vaccine;
XX KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
XX KW body height; hair colour; human.
XX OS Homo sapiens.
XX PN US2002172994-A1.
XX XX 21-NOV-2002.
XX PF 11-MAY-2001; 2001US-00852797.
XX XX 14-MAR-1997; 97US-0040710P.
XX PR 14-MAR-1997; 97US-0040762P.
XX PR 30-MAY-1997; 97US-0048100P.
XX PR 30-MAY-1997; 97US-0048189P.
XX PR 30-MAY-1997; 97US-0048357P.
XX PR 30-MAY-1997; 97US-0050934P.
XX PR 06-JUN-1997; 97US-0048970P.
XX PR 05-SEP-1997; 97US-0057765P.
XX PR 19-DEC-1997; 97US-0068368P.
XX PR 12-MAR-1998; 98WO-US004858.
XX PR 11-SEP-1998; 98US-00152060.
XX PR 02-FEB-2001; 2001US-0265583P.
XX (RUBE//) RUBEN S M.
XX PA (ROSE//) ROSEN C A.
XX PA (LIYY//) LI Y.
XX PA (ZENG//) ZENG Z.
XX PA (KYAW//) KYAW H.
XX PA (FISC//) FISCHER C L.
XX PA (LIHH//) LI H.
XX PA (SOPP//) SOPPET D R.
XX PA (GENT//) GENTZ R L.
XX PA (WEIY//) WEI Y.
XX PA (MOOR//) MOORE P A.
XX PA (YOUN//) YOUNG P E.
XX PA (GREE//) GREENE J M.
XX PA (FERR//) FERRIE A M.
XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
XX PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
XX PI Ferrie AM;
XX DR WPI; 2003-310989/30.
XX XX
XX PT New human secreted polypeptides and polynucleotides for diagnosing,
XX PT prognosing, preventing and treating immune, hyperproliferative, liver,
XX PT kidney, reproductive disorders and for identifying modulators of
XX PT therapeutic use.
XX PS Disclosure; Page 16; 209pp; English.
XX CC The invention relates to an isolated polypeptide comprising an amino acid
XX CC sequence at least 95% identical to sequence of 28 human secreted
XX CC proteins, their fragment, polypeptide domain, epitope, secreted form,
XX CC variant, allelic variant, or species homologue, or the encoded sequence
XX CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
XX CC acids, recombinant vectors, host cells, antibodies, and genes. The

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PA (LIHH//) LI H.
 PA (SOPP//) SOPPET D R.
 PA (GENTZ//) GENTZ R L.
 PA (WEIY//) WEI Y.
 PA (MOOR//) MOORE P A.
 PA (YOUN//) YOUNG P E.
 PA (GREE//) GREENE J M.
 PA (FERR//) FERRIE A M.
 XX
 PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 DR WPI: 2002-598780/64.
 DR N-PSDB; AAD44659.
 XX
 PT Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular, of
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 PT
 XX
 PS Claim 11; Page 185-186; 209pp; English.
 XX
 CC AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogeneic transplant rejection, blood related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders. e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention
 XX
 SQ Sequence 133 AA;
 Query Match 72.5%; Score 219; DB 5; Length 133;
 Best Local Similarity 68.6%; Pred. No. 1.3e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMQBPAGPCLASIPHWYNNKTKICSEFIYGCQGNNNFQTEATCLVTC 51
 DB 77 CEMPKETGCLAVFLHWYDKDNTCSMFYGCQGNNNFQSKANCLNTC 127
 RESULT 26
 AAE27120
 ID AAE27120 standard; protein; 133 AA.
 XX
 AC AAE27120;
 XX
 DT 13-DEC-2002 (first entry)
 XX

DE Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:75.
 XX
 XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= Signal_peptide
 FT Protein 22..133
 FT /note= "Mature human secreted protein"
 XX
 PN US2002076756-A1.
 XX
 XX 20-JUN-2002.
 XX
 PF 11-MAY-2001; 2001US-00853161.
 XX
 PR 02-FEB-2001; 2001US-0265583P.
 XX
 PA (RUBE//) RUBEN S M.
 PA (ROSE//) ROSEN C A.
 PA (LIYY//) LI Y.
 PA (ZENG//) ZENG Z.
 PA (KYAW//) KYAW H.
 PA (FISC//) FISCHER C L.
 PA (LIHH//) LI H.
 PA (SOPP//) SOPPET D R.
 PA (GENT//) GENTZ R L.
 PA (WEIY//) WEI Y.
 PA (MOOR//) MOORE P A.
 PA (YOUN//) YOUNG P E.
 PA (GREE//) GREENE J M.
 PA (FERR//) FERRIE A M.
 XX
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 XX WPI: 2002-574454/61.
 DR N-PSDB; AAD44877.
 XX
 PT New nucleic acid molecules encoding 28 human secreted proteins, useful
 PT for diagnosing, preventing, treating or ameliorating medical conditions
 PT and as food additives or preservatives.
 XX
 PS Claim 11; Page 185-186; 209pp; English.
 XX
 CC AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
 CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Secreted protein sequences of the invention are useful for the
 CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
 CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
 CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
 CC angiodysplasia), cardiovascular disorders (e.g. cardiac arrest), nervous
 CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
 CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
 CC polypeptides can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues and in chemotaxis. They can also be used as food
 CC additives or preservative to increase or decrease storage capabilities,

AC ADA19812;
XX
XX
XX 20-NOV-2003 (first entry)
XX
XX Human EPPIN protein SEQ ID NO:13.
XX
XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis; EPPIN.
XX
XX Homo sapiens.
XX WO2003070770-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Disclosure; Fig 1; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a human EPPIN protein given in comparison
CC with DJ11 proteins in the exemplification of the present invention.
XX
XX Sequence 133 AA;
XX
XX Query Match 72.5%; Score 219; DB 7; Length 133;
XX Best Local Similarity 68.6%; Pred. NO. 1.3e-19;
XX Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX 1 CSMQAGAGCLASIPHWNTNKKTKICSEFIYGCQGNNNFQTEAICLVTC 51
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 77 CEMPKETGCLAYFLHWYDKDNTCSMFYGCQGNNNFOSKNCVNTC 127

RESULT 29
ADG89802
ID ADG89802 standard; protein; 133 AA.
XX
XX AC ADG89802;
XX
XX 11-MAR-2004 (first entry)
XX Human protein from secreted protein gene 24 #1.
XX
XX Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.
XX
XX Homo sapiens.
XX OS
XX PN US2003225009-A1.
XX
XX 04-DEC-2003.
XX PD
XX
XX 30-JAN-2002; 2002US-00058993.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057765P.
XX 19-DEC-1997; 97US-0068368P.
XX 12-MAR-1998; 98WO-US004858.
XX 11-SEP-1998; 98US-00152060.
XX 02-FEB-2001; 2001US-0265583P.
XX 11-MAY-2001; 2001US-00852659.
XX 11-MAY-2001; 2001US-00852797.
XX 11-MAY-2001; 2001US-00853161.
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (LIY/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEI/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX (HAST/) HASTINGS G A.
XX
XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
XX WPI; 2004-042167/04.
XX N-PSDB; ADG89761.
XX
XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
XX Claim 11; SEQ ID NO 75; 320pp; English.
XX

XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marianovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Stuve EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Fatury S, Shi X, Suarez Cu;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN43755.
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX Claim 27; Page; 190pp; English.
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX Sequence 179 AA;
SQ
Query Match 72.5%; Score 219; DB 8; Length 179;
Best Local Similarity 68.6%; Pred. NO. 1.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 77 CEMPKETGCLAYFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 127
RESULT 32
ADA19813
ID ADA19813 standard; protein; 134 AA.
XX ADA19813;
XX 20-NOV-2003 (first entry)
DE Mouse EPPIN protein SEQ ID NO:14.
XX
XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis; EPPIN.
XX Mus musculus.
XX W02003070770-A2.
PN

XX 28-AUG-2003.
XX 18-FEB-2003; 2003WO-EP001629.
XX 21-FEB-2002; 2002US-0358683P.
XX (GENE-) GENEPROT INC.
XX Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX Disclosure; Fig 1; 87pp; English.
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a mouse EPPIN protein given in comparison
CC with DJ11 proteins in the exemplification of the present invention.
XX Sequence 134 AA;
SQ
Query Match 62.3%; Score 188; DB 7; Length 134;
Best Local Similarity 54.9%; Pred. NO. 1.1e-15;
Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY 1 CSMQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 77 CSLPKDSGYCMAYFRWWFKENSTCQVFIYGGCGNNNNFQSQICQAC 127
RESULT 33
AAE13096
ID AAE13096 standard; peptide; 43 AA.
XX AAE13096;
XX 28-JAN-2002 (first entry)
XX Human serine proteinase inhibitor BTL.009 peptide fragment #2.
XX Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX

OS Homo sapiens.
 PN US6294648-B1.
 XX
 PD 25-SEP-2001.
 XX
 PF 20-JUL-1999; 99US-00358569.
 XX
 PR 20-JUL-1999; 99US-00358569.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Delaria K, Rocznik S, Davies C;
 XX
 DR WPI; 2001-662224/76.
 XX
 PT New isolated protein for inhibiting human serine protease activity in the
 PT treatment of e.g. emphysema and adult respiratory distress syndrome.
 XX
 PS Disclosure; Col 5-6; 16pp; English.
 XX
 CC The invention relates to human BTL.009 protein, a serine proteinase
 CC inhibitor of the Kunitz family that exhibits greater potency towards
 CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
 CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
 CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
 CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
 CC and diseases involving lung and vascular injury. BTL.009 is also useful
 CC for preventing neutrophil and monocyte activation and formation of active
 CC oxygen species during the oxidative burst of stimulated granulocytes.
 CC BTL.009 is useful for reducing platelet activation and blood coagulation
 CC and for the prophylactic or therapeutic treatment of patients undergoing
 CC angioplasty. The present sequence is human serine proteinase inhibitor
 CC BTL.009 peptide fragment related to the invention
 XX
 SQ Sequence 43 AA;
 Query Match 56.3%; Score 170; DB 4; Length 43;
 Best Local Similarity 68.3%; Pred. No. 6.2e-14;
 Matches 28; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 QY 11 LASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
 DB 1 LAYELHWYDKNDTCSEFYGGCGGNNNNFQSKANCLNTC 41
 RESULT 34
 AAEE39498
 XX
 AC AAEE39498;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Cloned mouse GDF-associated serum protein (GASP)1.
 XX
 KW Mouse; GDF-associated serum protein; GASP; amyotrophic lateral sclerosis;
 KW growth and differentiation factor; GDF; chronic glucocorticoid therapy;
 KW familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
 KW progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
 KW bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
 KW muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
 KW carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
 KW nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;
 KW androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;
 KW metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
 KW myotonia; neuroprotective; obesity; immunomodulator; diabetes.
 XX
 OS Mus sp.
 XX
 FN US2003162714-A1.
 XX

PD 28-AUG-2003.
 XX
 PF 21-FEB-2003; 2003US-00369736.
 XX
 PR 21-FEB-2002; 2002US-0357845P.
 PR 20-DEC-2002; 2002US-0434644P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Hill JJ, Wolfman NM;
 XX
 DR WPI; 2003-756055/71.
 DR N-PSDB; RAD59931.
 XX
 PT Composition containing growth and differentiation factor-associated serum
 PT protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
 PT for diagnosis.
 XX
 PS Example 9; Fig 13; Opp; English.
 XX
 CC The present invention relates to the use of a protein GDF (growth and
 CC differentiation factor)-associated serum protein (GASP) 1 comprising
 CC at least one follistatin domain to modulate the level or activity of
 CC growth and differentiation factor (GDF) -8. Administration of GASP1 is
 CC used to modulate GDF-8 for treatment of muscular disorders such as
 CC muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
 CC myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
 CC progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
 CC congestive obstructive pulmonary disease, congenital myopathy (myotonia),
 CC familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
 CC Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
 CC carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
 CC and other muscle wasting syndromes such as traumatic or chronic injury to
 CC muscle, metabolic disorders such as diabetes types 1 or 2, impaired
 CC glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
 CC induced by trauma and obesity, adipose tissue disorder such as obesity,
 CC and bone degenerative conditions such as osteoporosis, osteopaenia,
 CC osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
 CC premature gonadal failure, vitamin D deficiency, androgen suppression,
 CC secondary hyperparathyroidism, nutritional deficiencies and anorexia
 CC nervosa. The present sequence is cloned mouse GDF (growth and
 CC differentiation factor)-associated serum protein (GASP)
 XX
 SQ Sequence 571 AA;
 Query Match 56.0%; Score 169; DB 7; Length 571;
 Best Local Similarity 49.0%; Pred. No. 1.4e-12;
 Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
 QY 1 CSMPQEGAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
 DB 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFYVGGCGGNNNFESREACEESC 431
 RESULT 35
 AAEE39459
 ID AAEE39459 standard; protein; 571 AA.
 XX
 AC AAEE39459;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Mouse GDF-associated serum protein (GASP)1 protein.
 XX
 KW Mouse; GDF-associated serum protein; GASP; amyotrophic lateral sclerosis;
 KW growth and differentiation factor; GDF; chronic glucocorticoid therapy;
 KW familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
 KW progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
 KW bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
 KW muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
 KW carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
 KW nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;
 KW androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;
 KW metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
 KW myotonia; neuroprotective; obesity; immunomodulator; diabetes.

KW metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
KW myotonia; neuroprotective; obesity; immunomodulator; diabetes.
OS Mus sp.

XX Key Location/Qualifiers
FH 105..170
FT Domain /note= "Follistatin domain"
XX US2003162714-A1.
XX 28-AUG-2003.
XX 21-FEB-2003; 2003US-00369736.
XX 21-FEB-2002; 2002US-0357845P.
PR 20-DEC-2002; 2002US-0434644P.
XX (AMHP) WYETH.
XX Hill JJ, Wolfman NM;
XX WPI; 2003-756055/71.
DR N-PSDB; AAD59923.
XX Composition containing growth and differentiation factor-associated serum
PT protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
PT for diagnosis.
XX Disclosure; Fig 6C; Opp; English.

XX The present invention relates to the use of a protein GDF (growth and
CC differentiation factor)-associated serum protein (GASP) 1 comprising
CC at least one follistatin domain to modulate the level or activity of
CC growth and differentiation factor (GDF) -8. Administration of GASP 1 is
CC used to modulate GDF-8 for treatment of muscular disorders such as
CC muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
CC myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
CC progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
CC congestive obstructive pulmonary disease, congenital myopathy (myotonia),
CC familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
CC Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
CC carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
CC and other muscle wasting syndromes such as traumatic or chronic injury to
CC muscle, metabolic disorders such as diabetes types 1 or 2, impaired
CC glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
CC induced by trauma and obesity, adipose tissue disorder such as obesity,
CC and bone degenerative conditions such as osteoporosis, osteopaenia,
CC osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
CC premature gonadal failure, vitamin D deficiency, androgen suppression,
CC secondary hyperparathyroidism, nutritional deficiencies and anorexia
CC nervosa. The present sequence is mouse GDF (growth and differentiation
CC factor)-associated serum protein (GASP)
XX
SQ Sequence 571 AA;

Query Match 56.0%; Score 169; DB 7; Length 571;
Best Local Similarity 49.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQBPAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNNFOTEATCLVTC 51
DB 381 CSLPALQGPCKAVPRWAYNSQTGLCQSFYVGCGEGNGNFFESRACESC 431

RESULT 36
ADD93670
ID ADD93670 standard; protein; 571 AA.
XX ADD93670;
XX
XX 29-JAN-2004 (first entry)
XX

DE Mouse GDF-associated serum protein 1 (GASPl).
XX Mouse; GDF-associated serum protein 1; GASPl; antidiabetic; anorectic;
KW osteopathic; gene therapy.
XX Mus sp.
XX Key Location/Qualifiers
FH Peptide 1..29
FT /note= "Signal peptide"
FT Protein 30..571
FT /note= "Mature protein"
FT Domain 105..170
FT /note = Follistatin domain
FT Modified-site 313
FT /note= "potential N-glycosylation site"
FT Modified-site 514
FT /note= "potential N-glycosylation site"

XX WO2003072714-A2.

XX 04-SEP-2003.

XX 21-FEB-2003; 2003WO-US005150.

XX 21-FEB-2002; 2002US-0357846P.

XX 20-DEC-2002; 2002US-0434645P.

XX (AMHP) WYETH.

XX Hill JJ, Wolfman NM;

XX WPI; 2003-812402/76.

XX N-PSDB; ADD93719, ADD93720.

XX New compositions comprising a protein containing at least one follistatin
PT domain, useful for treating muscular dystrophy (e.g. sarcopaenia, and
PT cachexia), metabolic disease (e.g. diabetes or obesity), or bone
PT degenerative diseases.

XX Example 9; Fig 6C; 113pp; English.

XX The present sequence is the protein sequence for mouse GDF-associated
CC serum protein 1 (GASPl), a protein which includes a follistatin domain
CC and which binds to growth and differentiation factor-8 (GDF-8 or
CC myostatin). The invention provides methods for modulating the effects of
CC GDF-8 on cells. These methods involve administering a protein comprising
CC at least one follistatin domain, or a nucleic acid encoding such a
CC protein. The methods are used to treat disorders relating to the level or
CC activity of GDF-8. These include a muscular disorder such as muscular
CC dystrophy (e.g. severe or benign X-linked muscular dystrophy, limb-girdle
CC dystrophy, facioscapulohumeral dystrophy, myotonic dystrophy, distal
CC muscular dystrophy, progressive dystrophic ophthalmoplegia,
CC oculopharyngeal dystrophy, Fukuyama-type congenital muscular dystrophy,
CC congenital myopathy, myotonia congenita, familial periodic paralysis,
CC paroxysmal myoglobinuria, myasthenia gravis, Eaton-Lambert syndrome,
CC secondary myasthenia, denervation atrophy, paroxysmal muscle atrophy,
CC muscle wasting syndrome, sarcopaenia, and cachexia), traumatic or chronic
CC injury to muscle tissue, metabolic disease or disorder (e.g. type 2
CC diabetes, non-insulin-dependent diabetes mellitus, hyperglycaemia, or
CC obesity), adipose tissue disorder (e.g. obesity), and bone degenerative
CC disease (e.g. osteoporosis) (all claimed).

XX Sequence 571 AA;

Query Match 56.0%; Score 169; DB 7; Length 571;
Best Local Similarity 49.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQBPAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNNFOTEATCLVTC 51
DB 381 CSLPALQGPCKAVPRWAYNSQTGLCQSFYVGCGEGNGNFFESRACESC 431


```
RESULT 37
AAR99146
ID AAR99146 standard; protein; 58 AA.
XX
XX AAR99146;
AC
XX
XX 12-FEB-1997 (first entry)
DT
XX
XX Aprotinin-like Kunitz domain.
DE
XX
XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW algal antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX
XX Synthetic.
OS
XX WO9620278-A2.
PN
XX
XX 04-JUL-1996.
PD
XX
XX 15-DEC-1995; 95WO-US016349.
PF
XX
XX 16-DEC-1994; 94US-00358160.
PR
XX
XX (PROT-) PROTEIN ENG CORP.
PA
XX
XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
PI
XX
XX WPI; 1996-321851/32.
DR
XX
XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX
XX Example 23; Page 47; 105pp; English.
PS
XX
XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211
XX
XX Sequence 58 AA;
SQ
Query Match 55.3%; Score 167; DB 2; Length 58;
Best Local Similarity 56.9%; Pred. No. 2.1e-13;
Matches 29; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : | | | | | | | | | | : | | | | | | | | | | | | | |
Db 5 CLLPAETGPCRAMIPRFYNNAKSGKCEPFYIYGGCGGNNNFQTEECRRTC 55
RESULT 38
AAE13092
ID AAE13092 standard; peptide; 54 AA.
XX
XX AAE13092;
AC
XX
XX 28-JAN-2002 (first entry)
DT
XX
XX Trypsin inhibitor peptide.
DE
XX
XX BTL.009 protein; serine proteinase inhibitor; cytostatic; therapeutic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW
```

```
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW trypsin inhibitor.
XX
XX Unidentified.
OS
XX US6294648-B1.
PN
XX
XX 25-SEP-2001.
PD
XX
XX 20-JUL-1999; 99US-00358569.
PF
XX
XX 20-JUL-1999; 99US-00358569.
PR
XX
XX (FARB ) BAYER CORP.
PA
XX
XX Delaria K, Roczniak S, Davies C;
PI
XX
XX WPI; 2001-662224/76.
DR
XX
XX New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
XX Disclosure; Col 5-6; 16pp; English.
PS
XX
XX The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is trypsin inhibitor peptide related to
CC the invention
XX
XX Sequence 54 AA;
SQ
Query Match 55.0%; Score 166; DB 4; Length 54;
Best Local Similarity 51.0%; Pred. No. 2.6e-13;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : | | | | | | | | | | : | | | | | | | | | | | | | |
Db 3 CQLPQARGPCAKALLRYFNSTNACEPFYIYGGCGGNNNFQTEMCRLIC 53
RESULT 39
AAB48380
ID AAB48380 standard; protein; 86 AA.
XX
XX AAB48380;
AC
XX
XX 20-APR-2001 (first entry)
DT
XX
XX I. ricinus salivary gland polypeptide.
DE
XX
XX Salivary gland; arthropod; tick; therapeutic; anticoagulant; vaccine;
KW medicinal agent; hematology; transplantation; rheumatology; Lyme disease;
KW tick encephalitis virus disease; antibacterial; antirheumatic; antiviral.
XX
XX Ixodes ricinus.
OS
XX
XX WO200077198-A2.
PN
XX
XX 21-DEC-2000.
PD
XX
XX
```



```
XX PD 18-DEC-2003.
XX PF 06-JUN-2003; 2003WO-US017665.
XX PR 07-JUN-2002; 2002US-0387239P.
XX PR 28-AUG-2002; 2002US-0407003P.
XX PA (DYAX-) DYAX CORP.
XX PI Ladner RC, Ley AC, Hirani S, Williams A;
XX DR WPI; 2004-062190/06.
XX PT Preventing or reducing ischemia in patient involves administering to
XX PT patient composition comprising a kallikrein inhibitory polypeptide.
XX PS Disclosure; SEQ ID NO 44; 46pp; English.
XX CC The present invention describes a method (M1) for preventing or reducing
XX CC ischaemia in a patient. M1 involves administering to the patient a
XX CC composition comprising a polypeptide (I) having an amino acid sequence of
XX CC ADF71926 and inhibiting kallikrein. (I) has vasotrophic activity, and can
XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
XX CC reducing ischaemia in a patient such as perioperative blood loss due to a
XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
XX CC is also useful for preventing or reducing the onset of systemic
XX CC inflammatory response associated with a surgical procedure in a patient
XX CC which involves administering (I) to a patient. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 58 AA;

Query Match 53.3%; Score 161; DB 8; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Oy 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRPYFYNGASMACOTFYGGCGMGNNFVTEKDLQTC 55

RESULT 47
ADF71963
ID ADF71963 standard; protein; 58 AA.
XX AC ADF71963;
XX DT 11-MAR-2004 (first entry)
XX DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:43.
XX KW ischaemia; vasotrophic; kallikrein inhibitor; blood loss;
XX KW systemic inflammatory response.
XX OS Homo sapiens.
XX PN WO2003103475-A2.
XX PD 18-DEC-2003.
XX PF 06-JUN-2003; 2003WO-US017665.
XX PR 07-JUN-2002; 2002US-0387239P.
XX PR 28-AUG-2002; 2002US-0407003P.
XX PA (DYAX-) DYAX CORP.
XX PI Ladner RC, Ley AC, Hirani S, Williams A;
XX DR WPI; 2004-062190/06.
XX PT Preventing or reducing ischemia in patient involves administering to
XX PT patient composition comprising a kallikrein inhibitory polypeptide.
XX PS Disclosure; SEQ ID NO 42; 46pp; English.
XX CC The present invention describes a method (M1) for preventing or reducing
XX CC ischaemia in a patient. M1 involves administering to the patient a
XX CC composition comprising a polypeptide (I) having an amino acid sequence of
XX CC ADF71926 and inhibiting kallikrein. (I) has vasotrophic activity, and can
XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
XX CC reducing ischaemia in a patient such as perioperative blood loss due to a
XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
XX CC is also useful for preventing or reducing the onset of systemic
XX CC inflammatory response associated with a surgical procedure in a patient
XX CC which involves administering (I) to a patient. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 58 AA;

Query Match 53.3%; Score 161; DB 8; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Oy 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRPYFYNGASMACOTFYGGCGMGNNFVTEKDLQTC 55

RESULT 48
ADF71962
ID ADF71962 standard; protein; 58 AA.
XX AC ADF71962;
XX DT 11-MAR-2004 (first entry)
XX DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:42.
XX KW ischaemia; vasotrophic; kallikrein inhibitor; blood loss;
XX KW systemic inflammatory response.
XX OS Homo sapiens.
XX PN WO2003103475-A2.
XX PD 18-DEC-2003.
XX PF 06-JUN-2003; 2003WO-US017665.
XX PR 07-JUN-2002; 2002US-0387239P.
XX PR 28-AUG-2002; 2002US-0407003P.
XX PA (DYAX-) DYAX CORP.
XX PI Ladner RC, Ley AC, Hirani S, Williams A;
XX DR WPI; 2004-062190/06.
XX PT Preventing or reducing ischemia in patient involves administering to
XX PT patient composition comprising a kallikrein inhibitory polypeptide.
XX PS Disclosure; SEQ ID NO 42; 46pp; English.
XX CC The present invention describes a method (M1) for preventing or reducing
XX CC ischaemia in a patient. M1 involves administering to the patient a
XX CC composition comprising a polypeptide (I) having an amino acid sequence of
XX CC ADF71926 and inhibiting kallikrein. (I) has vasotrophic activity, and can
XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
XX CC reducing ischaemia in a patient such as perioperative blood loss due to a
XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
XX CC is also useful for preventing or reducing the onset of systemic
```


DR N-PSDB; AAT79080.
XX
PT New protease inhibitor - useful for treating diseases involving elastase.
XX
PS Claim 5; Page 3; 37pp; Japanese.
XX
CC This is the amino acid sequence of a novel protease inhibitor based on
CC the sequence of the anti-trypsin inhibitor UTI. The protein comprises
CC Kunitz domains 1 and 2 of UTI, but lacks amino acids 1-21. Of the
CC remaining amino acids, residues 1-4 (22-26 of the native sequence) are
CC replaced by the peptide Arg-Pro-Asp-Phe. The construct also has the
CC sequence encoding the active site residue and the adjacent amino acids
CC (amino acids 36-40 of the wild type sequence) and amino acids 52 and 55
CC substituted. The modified protease inhibitors are targeted to the
CC protease elastase, especially from neutrophils and can be used to treat
CC diseases associated with elastase. Modifications of the active site were
CC done by site directed mutagenesis
XX
SQ Sequence 124 AA;
Query Match 53.3%; Score 161; DB 2; Length 124;
Best Local Similarity 51.0%; Pred. No. 2.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
Qy 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : ||||: | :
Db 5 COLGYSAGPCIAFPFRYPYNGTSMACQTFVYGGCGNGNFFVTEKECLQTC 55
Search completed: September 21, 2005, 16:36:49
Job time : 32.8938 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:27:13 ; Search time 9.32743 Seconds
(without alignments)
408.162 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127
Perfect score: 302
Sequence: 1 CSMPOEAGPCLASIPHHWYN.....GCGCGNNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	72.5	54	US-09-358-569D-8	Sequence 8, Appli
2	219	72.5	55	US-09-358-569D-1	Sequence 1, Appli
3	219	72.5	58	US-09-369-494-8	Sequence 8, Appli
4	219	72.5	58	US-09-569-670-8	Sequence 8, Appli
5	219	72.5	64	US-09-358-569D-10	Sequence 10, Appli
6	219	72.5	133	US-09-152-060-75	Sequence 75, Appli
7	170	56.3	43	US-09-358-569D-13	Sequence 13, Appli
8	170	56.3	66	US-08-358-160-113	Sequence 113, Appli
9	170	56.3	79	5466783-7	Patent No. 5466783
10	170	56.3	79	5466783-7	Patent No. 5466783
11	167	55.3	58	US-08-358-160-71	Sequence 71, Appli
12	166	55.0	54	US-09-358-569D-9	Sequence 9, Appli
13	166	55.0	67	US-08-358-160-123	Sequence 123, Appli
14	166	55.0	86	US-09-910-430-8	Sequence 8, Appli
15	161	53.3	58	US-08-358-160-17	Sequence 17, Appli
16	161	53.3	58	US-08-358-160-18	Sequence 18, Appli
17	160	53.0	77	5466783-4	Patent No. 5466783
18	160	53.0	77	5466783-4	Patent No. 5466783
19	157	52.0	61	US-08-829-876-211	Sequence 211, App
20	157	52.0	61	US-08-829-876-214	Sequence 214, App
21	157	52.0	61	US-09-234-874A-211	Sequence 211, App
22	157	52.0	61	US-09-234-874A-214	Sequence 214, App
23	157	52.0	61	US-09-234-873A-211	Sequence 211, App
24	157	52.0	61	US-09-234-873A-214	Sequence 214, App
25	156	51.7	58	US-07-664-989B-48	Sequence 48, Appli
26	156	51.7	58	US-07-664-989B-51	Sequence 51, Appli
27	156	51.7	58	US-08-358-160-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-358-569D-8
; Sequence 8, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-8
Query Match 72.5%; Score 219; DB 3; Length 54;
Best Local Similarity 68.6%; Pred. No. 3.1e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNKTKTCSBFIYGGCGNNNNFQTEAICLVTC 51
DB 3 CEMPKEGPECLAYFLHWYDKDNTCSMFVYGGCGNNNNFQSKANCLNTC 53

RESULT 2

US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match          72.5%; Score 219; DB 3; Length 55;
Best Local Similarity 68.6%; Pred. No. 3.2e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
Db 5 CEMPKEGTGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 3
US-09-369-494-8
; Sequence 8, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-8

Query Match          72.5%; Score 219; DB 3; Length 58;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
Db 5 CEMPKEGTGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 4
US-09-569-670-8
; Sequence 8, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8
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```
Query Match          72.5%; Score 219; DB 4; Length 58;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
Db 5 CEMPKEGTGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 5
US-09-358-569D-10
; Sequence 10, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Extension of
; OTHER INFORMATION: Seq Id 1
US-09-358-569D-10

Query Match          72.5%; Score 219; DB 3; Length 64;
Best Local Similarity 68.6%; Pred. No. 3.7e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
Db 7 CEMPKEGTGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 57

RESULT 6
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match      72.5%; Score 219; DB 4; Length 133;
Best Local Similarity 68.6%; Pred. No. 8.2e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      1  CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      77  CEMPKEGTGCLAYFLHWYDKKONTCSMFYVGGCGGNNNNFQSKANCLNTC 127

RESULT 7
US-09-358-569D-13
; Sequence 13, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: sequence derived from EST database
US-09-358-569D-13

Query Match      56.3%; Score 170; DB 3; Length 43;
Best Local Similarity 68.3%; Pred. No. 5.3e-15;
Matches 28; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY      11  LASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
      |||:|||||:|||||:|||||:|||||:|||||:|||||
DB      1  LAYELHWYDKKONTCSMFYVGGCGGNNNNFQSKANCLNTC 41

RESULT 8
US-08-358-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; City: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```



```

; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEV=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-123

Query Match 55.0%; Score 166; DB 1; Length 67;
Best Local Similarity 51.0%; Pred. No. 2.8e-14;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 8 CQLPQARGPCKAALLRYFNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 14
US-09-910-430-8
; Sequence 8, Application US/09910430
; Patent No. 6794166
; GENERAL INFORMATION:
; APPLICANT: Bollen, Alex
; APPLICANT: Godfroi, Edmond
; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALLIARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CP1

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; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
; US-09-910-430-8

Query Match 55.0%; Score 166; DB 4; Length 86;
Best Local Similarity 49.0%; Pred. No. 3.7e-14;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 31 CKLPDDGFCRARIPSYFYDRKTKCKEFMYGGCGEGNNNFENITTCQEEC 81

RESULT 15
US-08-358-160-17
; Sequence 17, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEV, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEV=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-123

```



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; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-17

Query Match 53.3%; Score 161; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQEQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 5 CQLGYSAGPCVAMPFRYPFYNGTSMACETFYVGGCMGNGNMFVTEKDCIQTC 55

RESULT 16
US-08-358-160-18
; Patent No. 5663143
; Application US/08358160
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
```

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; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-18

Query Match 53.3%; Score 161; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQEQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 5 CQLGYSAGPCVAMPFRYPFYNGASMACOTFYVGGCMGNGNMFVTEKDCIQTC 55

RESULT 17
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain; Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 4
; LENGTH: 77
5466783-4

Query Match 53.0%; Score 160; DB 6; Length 77;
Best Local Similarity 47.1%; Pred. No. 1.9e-13;
Matches 24; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQEQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 8 CQLPQARGPCVKAALRYFYBSTSNACEPFTYVGGCGGNNNFETTEMCLRIC 58

RESULT 18
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain; Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 4
; LENGTH: 77
5466783-4

Query Match 53.0%; Score 160; DB 6; Length 77;
Best Local Similarity 47.1%; Pred. No. 1.9e-13;
Matches 24; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
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;
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-234-874A-211

Query Match 52.0%; Score 157; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRAAIQHWYFDVTEGKCAPFFYGGCGGNNRNNFDTTEYCMAVC 57

RESULT 22
US-09-234-874A-214
; Sequence 214, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-234-874A-211

Query Match 52.0%; Score 157; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRAAIQHWYFDVTEGKCAPFFYGGCGGNNRNNFDTTEYCMAVC 57
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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-234-874A-214

Query Match 52.0%; Score 157; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRAAIQHWYFDVTEGKCAPFFYGGCGGNNRNNFDTTEYCMAVC 57

RESULT 23
US-09-234-873A-211
; Sequence 211, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-234-873A-211

Query Match 52.0%; Score 157; DB 4; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRAAIQHWYFDVTEGKCAPFFYGGCGGNNRNNFDTTEYCMAVC 57
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RESULT 24
US-09-234-873A-214
; Sequence 214, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-234-873A-214

Query Match 52.0%; Score 157; DB 4; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQATGTCRALIPRWYFDVTEGKCAPFFYGGCGRNNNFDEEYCMVAVC 57

RESULT 25
US-07-664-989B-48
; Sequence 48, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; TITLE OF INVENTION: Binding Proteins

; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-48
Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 CLEPPYTGTCVAMFPFYNNAKAGLCQTFYGGCGNGNNGNFKASAECDMRTC 55
RESULT 26
US-07-664-989B-51
; Sequence 51, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004


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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 01-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 51:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-664-989B-51

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCIASIPHHWYKTKICSEFYGGCGNNNFQTEAICLVTC 51
Db 5 CLEPPTGCIAPFRYFYNAKAGLCQTFVYGGCGNGNFKSAEDCMRTC 55

RESULT 27
US-08-358-160-1
; Sequence 1, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-1

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCIASIPHHWYKTKICSEFYGGCGNNNFQTEAICLVTC 51
Db 5 CLEPPTGPCVAMPFRYFYNAKAGLCQTFVYGGCGNGNFKSAEDCMRTC 55

RESULT 28
US-08-358-160-26
; Sequence 26, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
```


PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEV=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-26

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQAEAGCLASIPHWYNNKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
DB 5 CLEPPYTGPCIAFFPRFYNAKGLCQTFVYGGCMGNNFKSAEDCMTC 55

RESULT 29
US-08-463-155A-56
Sequence 56, Application US/08463155A
Patent No. 5780265
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,155A
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-155A-56

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 4.7e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMQAEAGCLASIPHWYNNKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
DB 5 CSEQAEDGPCRAAIPRWYFDVTGKCAPFIYGGCGNNRNFDTTEYCAAVC 55

RESULT 30
US-08-463-432B-56
Sequence 56, Application US/08463432B
Patent No. 5786328
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,432B
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944-2
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-432B-56

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 4.7e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMQAEAGCLASIPHWYNNKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
DB 5 CSEQAEDGPCRAAIPRWYFDVTGKCAPFIYGGCGNNRNFDTTEYCAAVC 55

RESULT 31
US-08-829-876-180
Sequence 180, Application US/08829876
Patent No. 5962266
GENERAL INFORMATION:
APPLICANT: White, Tyler R.
APPLICANT: Damm, Deborah
APPLICANT: Lesikar, David D.
APPLICANT: McFadden, Kathleen
APPLICANT: Garrick, Brett L.


```
;
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-829-876-180
;
; Query Match 51.7%; Score 156; DB 2; Length 61;
; Best Local Similarity 49.0%; Pred. NO. 5e-13;
; Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
;
; Qy 1 CSMQEQAGPCLASIPHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
; Db 7 CSEQAETGCRAGIPRWYFDVTEGKCAPPFFYGGCGNNRNFDTBEYCMVAVC 57
;
; RESULT 32
; US-08-829-876-218
; Sequence 218, Application US/08829876
; Patent No. 5962266
;
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
;
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
;
; US/08/829,876
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;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-829-876-218
;
; Query Match 51.7%; Score 156; DB 2; Length 61;
; Best Local Similarity 49.0%; Pred. NO. 5e-13;
; Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
;
; Qy 1 CSMQEQAGPCLASIPHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
; Db 7 CSEQAESGPCRAAIYHWYFDVTEGKCAPPFFYGGCGNNRNFDTBEYCMVAVC 57
;
; RESULT 33
; US-09-234-874A-180
; Sequence 180, Application US/09234874A
; Patent No. 6376648
;
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
;
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
;
; US-08-829-876-218
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US-09-234-873A-180
; Sequence 180, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-873A-180
Query Match 51.7%; Score 156; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
DB 7 CSEQAETGCRAGIPRWYFDVTEGKCAPFFYGGCGNNRNNFDTBYCMAVC 57
RESULT 34
US-09-234-874A-218
; Sequence 218, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-874A-218
Query Match 51.7%; Score 156; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
DB 7 CSEQAEGPCRAAIYHWYFDVTEGKCAPFFYGGCGNNRNNFDTBYCMAVC 57
RESULT 35

US-09-234-873A-180
; Sequence 180, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-873A-180
Query Match 51.7%; Score 156; DB 4; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
DB 7 CSEQAETGCRAGIPRWYFDVTEGKCAPFFYGGCGNNRNNFDTBYCMAVC 57
RESULT 36
US-09-234-873A-218
; Sequence 218, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500

Query Match 51.7%: Score 156: DB 1: Length 62:

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Query Match      51.7%; Score 156; DB 1; Length 62;
Best Local Similarity 47.1%; Pred.No. 5.le-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

1 CSMQEQAGPCILASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
  ||| | | | | | | | | | | | | | | | | | | | | | | | | |
9 CLEPPYTGCIAFFPRFYNAKGLCOTFIYGGCMGNNGNFKGAEDCMRTC 59
  ||| | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 38
US-07-664-989B-49
; Sequence 49, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Rosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409a
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; STREET: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530

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Thu Sep 22 07:16:45 2005

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US89/03731
;; FILING DATE: 01-SEP-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/487,063
;; FILING DATE: 02-MAR-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/240,160
;; FILING DATE: 02-SEP-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cooper, Iver P.
;; REGISTRATION NUMBER: 28005
;; REFERENCE/DOCKET NUMBER: LADNER 7
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 49:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 58 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-07-664-989B-49

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 6.4e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMQAGAGCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGPCVAIFRYFYNAKAGLCQTFYGGCGGNGNFKSABDCMRTC 55

RESULT 39
US-08-358-160-9
; Sequence 9, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEV, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/487,063
;; FILING DATE: 02-MAR-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/240,160
;; FILING DATE: 02-SEP-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cooper, Iver P.
;; REGISTRATION NUMBER: 28,005
;; REFERENCE/DOCKET NUMBER: LEY=1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 58 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-358-160-9
Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
QY 1 CSMQAGAGCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 COLGYSAGPCVAMFPRFYNGTSMACETFYGGCGGNGNPFVTEKDCLOTC 55
RESULT 40
US-08-358-160-10
; Sequence 10, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990


```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-10

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMQEAGPCLASIPHWYKTKICSEFYGGCGNNNFQTEAICLVTC 51
   : |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 5 CQLGYSAGPCVAMPFRYFNGTSMACETFOYGGCMGNGNMFVTEKDCQTC 55

RESULT 41
US-08-358-160-11
; Sequence 11, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: GUTERMAN, Bruce L.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-11

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMQEAGPCLASIPHWYKTKICSEFYGGCGNNNFQTEAICLVTC 51
   : |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 5 CQLGYSAGPCVAMPFRYFNGTSMACETFOYGGCMGNGNMFVTEKDCQTC 55

RESULT 42
US-08-358-160-15
; Sequence 15, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: GUTERMAN, Bruce L.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
```


TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-829-876-129

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 6.4e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 5 CLEPPYTGPCVAIPRPYFNKAGLCQTFFYGGCGNGNFKSADCMRTC 55

RESULT 45

US-08-829-876-129
Sequence 129, Application US/08829876
Patent No. 5962266

GENERAL INFORMATION:
APPLICANT: White, Tyler R.

APPLICANT: Damm, Deborah
APPLICANT: Lesikar, David D.
APPLICANT: McFadden, Kathleen
APPLICANT: Garrick, Brett L.

TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES

NUMBER OF SEQUENCES: 228

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/829,876

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/436,555

FILING DATE: 08-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Pelto, Don J.

REGISTRATION NUMBER: 33,754

REFERENCE/DOCKET NUMBER: 56324/106/SCNO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 129:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-829-876-129

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRAMIPRWYFDVTGKCAPFFYGGCGNNNFDTBEYCMAVC 57

RESULT 46

US-08-829-876-139

Sequence 139, Application US/08829876

Patent No. 5962266

GENERAL INFORMATION:

APPLICANT: White, Tyler R.

APPLICANT: Damm, Deborah

APPLICANT: Lesikar, David D.

APPLICANT: McFadden, Kathleen

APPLICANT: Garrick, Brett L.

TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES

NUMBER OF SEQUENCES: 228

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/829,876

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/436,555

FILING DATE: 08-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Pelto, Don J.

REGISTRATION NUMBER: 33,754

REFERENCE/DOCKET NUMBER: 56324/106/SCNO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 139:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-829-876-139

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRAMISHWYFDVTGKCAPFFYGGCGNNNFDTBEYCMAVC 57

RESULT 47

US-08-829-876-208

Sequence 208, Application US/08829876

Patent No. 5962266

GENERAL INFORMATION:

APPLICANT: White, Tyler R.

APPLICANT: Damm, Deborah

APPLICANT: Lesikar, David D.

APPLICANT: McFadden, Kathleen

APPLICANT: Garrick, Brett L.

TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES


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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-222

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Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMQEGAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQAETGPGCRGSRHWYFDVTEGKCAPFFYGGCGGNRNNFDTSEYCNVAVC 57

RESULT 50

US-09-234-874A-129
; Sequence 129, Application US/09234874A
; Patent No. 6376648

; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.

; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234, 874A
; FILING DATE: 11-Jun-2001

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-09-234-874A-129

Query Match 51.3%; Score 155; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMQEGAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQAETGPGCRGSRHWYFDVTEGKCAPFFYGGCGGNRNNFDTSEYCNVAVC 57

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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:33:14 ; Search time 31.8938 Seconds
(without alignments)
650.835 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127
Perfect score: 302
Sequence: 1 CSMPOEAGFCLASIPHWYN.....GCGQGNNNFQTEAICLVTC 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues
Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Published Applications AA:*

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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302	100.0	106	16	US-10-807-204-2
2	302	100.0	131	16	US-10-807-204-1
3	302	100.0	131	16	US-10-807-204-12
4	292	96.7	131	16	US-10-807-204-15
5	224	74.2	136	16	US-10-807-204-16
6	219	72.5	51	15	US-10-058-993-118
7	219	72.5	58	16	US-10-361-997-5
8	219	72.5	58	17	US-10-931-153-21
9	219	72.5	102	9	US-09-852-659A-120
10	219	72.5	102	15	US-10-058-993-121
11	219	72.5	117	9	US-09-852-659A-119
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 12, Appl
					Sequence 15, Appl
					Sequence 16, Appl
					Sequence 118, App
					Sequence 5, Appli
					Sequence 21, Appl
					Sequence 120, App
					Sequence 121, App
					Sequence 119, App

12	219	72.5	117	15	US-10-058-993-120	Sequence 120, App
13	219	72.5	133	9	US-09-853-161-75	Sequence 75, Appl
14	219	72.5	133	9	US-09-852-659A-75	Sequence 75, Appl
15	219	72.5	133	9	US-09-852-797-75	Sequence 75, Appl
16	219	72.5	133	15	US-10-058-993-75	Sequence 75, Appl
17	219	72.5	133	16	US-10-807-204-13	Sequence 13, Appl
18	188	62.3	134	16	US-10-807-204-14	Sequence 14, Appl
19	169	56.0	571	14	US-10-369-736-3	Sequence 3, Appli
20	169	56.0	571	14	US-10-369-736-49	Sequence 49, Appl
21	169	56.0	571	14	US-10-369-738-3	Sequence 3, Appli
22	169	56.0	571	14	US-10-369-738-49	Sequence 49, Appl
23	169	56.0	571	19	US-11-028-058-3	Sequence 3, Appli
24	169	56.0	571	19	US-11-028-058-49	Sequence 49, Appl
25	168	55.6	64	10	US-09-856-095-160	Sequence 160, App
26	168	55.6	64	14	US-10-038-722-103	Sequence 103, App
27	168	55.6	64	15	US-10-115-134-17	Sequence 17, Appl
28	167	55.3	58	14	US-10-038-722-5	Sequence 5, Appli
29	166	55.0	67	10	US-09-896-095-147	Sequence 147, App
30	166	55.0	67	14	US-10-038-722-90	Sequence 90, Appl
31	166	55.0	67	15	US-10-115-134-4	Sequence 4, Appli
32	166	55.0	86	9	US-09-910-430-8	Sequence 8, Appli
33	166	55.0	86	14	US-10-165-605A-8	Sequence 8, Appli
34	161	53.3	58	14	US-10-038-722-17	Sequence 17, Appl
35	161	53.3	58	14	US-10-038-722-18	Sequence 18, Appl
36	161	53.3	58	14	US-10-038-722-19	Sequence 19, Appl
37	161	53.3	58	15	US-10-115-134-88	Sequence 88, Appl
38	161	53.3	58	15	US-10-115-134-89	Sequence 89, Appl
39	161	53.3	58	15	US-10-115-134-90	Sequence 90, Appl
40	161	53.3	58	15	US-10-456-986A-42	Sequence 42, Appl
41	161	53.3	58	15	US-10-456-986A-43	Sequence 43, Appl
42	161	53.3	58	15	US-10-456-986A-44	Sequence 44, Appl
43	161	53.3	58	18	US-10-953-902A-42	Sequence 42, Appl
44	161	53.3	58	18	US-10-953-902A-43	Sequence 43, Appl
45	161	53.3	58	18	US-10-953-902A-44	Sequence 44, Appl
46	160	53.0	503	14	US-10-007-580A-233	Sequence 233, App
47	160	53.0	576	9	US-09-794-589-2	Sequence 2, Appli
48	160	53.0	576	14	US-10-315-380-2	Sequence 2, Appli
49	160	53.0	576	14	US-10-369-736-7	Sequence 7, Appli
50	160	53.0	576	14	US-10-369-738-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US2004022912A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015-US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN

; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (23)...(35)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-2

Query Match 100.0%; Score 302; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.1e-29;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
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Db 52 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 102
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RESULT 2
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(25)
; OTHER INFORMATION: predicted by SignalP 2.0
; FEATURE:

; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
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; OTHER INFORMATION: predicted disulfide bond
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; LOCATION: (54)...(69)
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; OTHER INFORMATION: predicted disulfide bond
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; NAME/KEY: DISULFID
; LOCATION: (102)...(123)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-1

Query Match 100.0%; Score 302; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
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Db 77 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 127
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RESULT 3
US-10-807-204-12
; Sequence 12, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-12

Query Match 100.0%; Score 302; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
|||||
Db 77 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
|||||

RESULT 4

US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Anos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-15

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Best Local Similarity 98.0%; Pred. No. 6.5e-28;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
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Db 77 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
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RESULT 5

US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Anos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-16

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Best Local Similarity 66.7%; Pred. No. 1.5e-19;
Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
|||||
Db 77 CSLPQDPGCLAYLPRWYNNQETDLCTEFIYGGCGGNNPFPSEGICTVVC 127
|||||

RESULT 6

US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-118

Query Match 72.5%; Score 219; DB 15; Length 51;
Best Local Similarity 68.6%; Pred. No. 2.5e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
|||||
Db 1 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 51
|||||

RESULT 7

US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84


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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5

Query Match          72.5%; Score 219; DB 16; Length 58;
Best Local Similarity 68.6%; Pred. No. 2.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| ||||:||| ||:||||| ||||:|:| |||
Db 5 CEMPKEIGPCLAYFLHWWYDKKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 8
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-PEGYLATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match          72.5%; Score 219; DB 17; Length 58;
Best Local Similarity 68.6%; Pred. No. 2.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| ||||:||| ||:||||| ||||:|:| |||
Db 5 CEMPKEIGPCLAYFLHWWYDKKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 9
US-09-852-659A-120
; Sequence 120, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120

Query Match          72.5%; Score 219; DB 9; Length 102;
Best Local Similarity 68.6%; Pred. No. 4.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| ||||:||| ||:||||| ||||:|:| |||
Db 46 CEMPKEIGPCLAYFLHWWYDKKNTCSMFVYGGCGGNNNNFQSKANCLNTC 96

RESULT 10
US-10-058-993-121
; Sequence 121, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 03/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120
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; ORGANISM: Homo sapiens
US-10-058-993-121

Query Match          72.5%; Score 219; DB 15; Length 102;
Best Local Similarity 68.6%; Pred. No. 4.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 46 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 96

RESULT 11
US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,762
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-120

Query Match          72.5%; Score 219; DB 15; Length 117;
Best Local Similarity 68.6%; Pred. No. 5.5e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 111

RESULT 13
US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 111

RESULT 12
US-10-058-993-120
; Sequence 120, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
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QY 1 CSM PQEAGPCLASIPHHWYNKTKICSEFIYGGCQGNNNFQTEAICLVTC 51

; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-75

Query Match 72.5%; Score 219; DB 15; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
DB 77 CEMPKEGPCLAYFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTC 127

RESULT 17

US-10-807-204-13
; Sequence 13, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-13

Query Match 72.5%; Score 219; DB 16; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
DB 77 CEMPKEGPCLAYFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTC 127

RESULT 18

US-10-807-204-14
; Sequence 14, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-14

Query Match 62.3%; Score 188; DB 16; Length 134;
Best Local Similarity 54.9%; Pred. No. 4e-15;
Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
DB 77 CSLPKDSGVCYAFYFRWFWNKENSICQVFIYGGCGQNNNNFQSQICQNAC 127

RESULT 19

US-10-369-736-3
; Sequence 3, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-736-3

Query Match 56.0%; Score 169; DB 14; Length 571;
Best Local Similarity 49.0%; Pred. No. 3.6e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
DB 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFYGGCGGNNGNPFESREACBESC 431

RESULT 20

US-10-369-736-49
; Sequence 49, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS


```

1  APPLICANT: WOLFMAN, NEIL M.
2  TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
3  FILE REFERENCE: 08702.0015-00
4  CURRENT APPLICATION NUMBER: US/11/028.058
5  CURRENT FILING DATE: 2005-01-04
6  PRIOR APPLICATION NUMBER: US/10/369,736
7  PRIOR FILING DATE: 2003-02-21
8  PRIOR APPLICATION NUMBER: 60/357,846
9  PRIOR FILING DATE: 2002-02-21
10 PRIOR APPLICATION NUMBER: 60/434,645
11 PRIOR FILING DATE: 2002-12-20
12 NUMBER OF SEQ ID NOS: 53
13 SOFTWARE: PatentIn Ver. 2.1
14 SEQ ID NO 49
15 LENGTH: 571
16 TYPE: PRT
17 ORGANISM: Mus sp.
18 US-11-028-058-49

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Query Match 56.0%; Score 169; DB 19; Length 571;
Best Local Similarity 49.0%; Pred. No. 3.6e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 381 CSLPALQGPCKAYVPRWAYNSQTGLCSFVYGGCEGNGNFKTKAECVRAC 431

RESULT 25
US-09-896-095-160
Sequence 160, Application US/09896095
Publication No. US20030219886A1
GENERAL INFORMATION:

APPLICANT: LADNER, Charles C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: LEY, Arthur C.
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
FILE REFERENCE: LADNER-7L
CURRENT APPLICATION NUMBER: US/09/896,095
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 08/415,922
PRIOR FILING DATE: 1995-03-04
PRIOR APPLICATION NUMBER: 08/009,319
PRIOR FILING DATE: 1993-01-26
PRIOR APPLICATION NUMBER: 07/864,989
PRIOR FILING DATE: 1991-03-01
PRIOR APPLICATION NUMBER: 08/993,776
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn version 3.2
SEQ ID NO 160
LENGTH: 64
TYPE: PRT
ORGANISM: Caretta sp.

US-09-896-095-160
Query Match 55.6%; Score 168; DB 10; Length 64;
Best Local Similarity 49.0%; Pred. No. 5.7e-13;
Matches 25; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 8 CRLPPEQGPCKGRLPRFYFNPASRMCESEFIYGGCKGNKNNFKTKAECVRAC 58

RESULT 26
US-10-038-722-103
Sequence 103, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY=1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1

SEQ ID NO 103
LENGTH: 64
TYPE: PRT
ORGANISM: Caretta sp.
US-10-038-722-103

Query Match 55.6%; Score 168; DB 14; Length 64;
Best Local Similarity 49.0%; Pred. No. 5.7e-13;
Matches 25; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 8 CRLPPEQGPCKGRLPRFYFNPASRMCESEFIYGGCKGNKNNFKTKAECVRAC 58

RESULT 27
US-10-115-134-17
Sequence 17, Application US/10115134
Publication No. US20030223977A1
GENERAL INFORMATION:

APPLICANT: LEY, Arthur Charles
APPLICANT: GUTERMAN, Sonia Kosow
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel Baribault
APPLICANT: ROBERTS, Bruce Lindsay
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
FILE REFERENCE: LEY=1C
CURRENT APPLICATION NUMBER: US/10/115,134
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 08/849,406
PRIOR FILING DATE: 2001-07-21
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 64
TYPE: PRT
ORGANISM: Caretta sp.
US-10-115-134-17

Query Match 55.6%; Score 168; DB 15; Length 64;
Best Local Similarity 49.0%; Pred. No. 5.7e-13;
Matches 25; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 8 CRLPPEQGPCKGRLPRFYFNPASRMCESEFIYGGCKGNKNNFKTKAECVRAC 58

RESULT 28
US-10-038-722-5
Sequence 5, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY=1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5


```
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5

Query Match      55.3%; Score 167; DB 14; Length 58;
Best Local Similarity 56.9%; Pred. No. 6.9e-13;
Matches 29; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 CLLPAETGCPAMIPRFYNNKSGKCEPFIYGGCGGNNNNFTEECRRTC 55

RESULT 29
US-09-896-095-147
; Sequence 147, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER=7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 147
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-896-095-147

Query Match      55.0%; Score 166; DB 10; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 CQLPQARGPCKAALLRYFYNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 30
US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
```

```
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/359,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Query Match      55.0%; Score 166; DB 14; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 CQLPQARGPCKAALLRYFYNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 31
US-10-115-134-4
; Sequence 4, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-115-134-4

Query Match      55.0%; Score 166; DB 15; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 CQLPQARGPCKAALLRYFYNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 32
US-09-910-430-8
; Sequence 8, Application US/09910430
; Patent No. US20020127235A1
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Leboulle, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CP1
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
```


Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Query Match	55.0%;	Score 166;	DB 9;	Length 86;			
Best Local Similarity	49.0%;	Pred. No. 1.3e-12;					
Mismatches	25;	Conservative	10;	Mismatches	16;	Indels	0;
Query	1	CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC	51				
Db	31	CKLPDDGPRARIPSYFDKTKCKEPMYGGCGGNNNNFENITTCQEEC	81				
RESULT 33							
US-10-165-605A-8							
Sequence 8,	Application US/10165605A						
Publication No.	US20030086937A1						
GENERAL INFORMATION:							
APPLICANT:	Godfroid, Edmond						
APPLICANT:	Bollen, Alex						
APPLICANT:	Lebouille, Gerard						
TITLE OF INVENTION:	IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF						
TITLE OF INVENTION:	PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY						
TITLE OF INVENTION:	GLANDS						
FILE REFERENCE:	VANM229.001CP2						
CURRENT APPLICATION NUMBER:	US/10/165,605A						
CURRENT FILING DATE:	2002-06-07						
PRIOR APPLICATION NUMBER:	09/910,430						
PRIOR FILING DATE:	2001-07-19						
PRIOR APPLICATION NUMBER:	PCT/BE00/00061						
PRIOR FILING DATE:	2000-06-06						
PRIOR APPLICATION NUMBER:	GB9913425.6						
PRIOR FILING DATE:	1999-06-09						
NUMBER OF SEQ ID NOS:	34						
SOFTWARE:	PatentIn Ver. 2.1						
SEQ ID NO 8							
LENGTH:	86						
TYPE:	PRT						
ORGANISM:	Ixodes ricinus						
US-10-165-605A-8							
Query Match	55.0%;	Score 166;	DB 14;	Length 86;			
Best Local Similarity	49.0%;	Pred. No. 1.3e-12;					
Mismatches	25;	Conservative	10;	Mismatches	16;	Indels	0;
Query	1	CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC	51				
Db	31	CKLPDDGPRARIPSYFDKTKCKEPMYGGCGGNNNNFENITTCQEEC	81				
RESULT 34							
US-10-038-722-17							
Sequence 17,	Application US/10038722						
Publication No.	US20030175919A1						
GENERAL INFORMATION:							
APPLICANT:	LEY, Arthur C.						
APPLICANT:	GUTERMAN, Sonia K.						
APPLICANT:	MARKLAND, William						
APPLICANT:	KENT, Rachel B.						
APPLICANT:	ROBERTS, Bruce L.						
APPLICANT:	LADNER, Robert C.						
TITLE OF INVENTION:	ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS						
FILE REFERENCE:	LEY-1B						
CURRENT APPLICATION NUMBER:	US/10/038,722						
CURRENT FILING DATE:	2002-01-08						
PRIOR APPLICATION NUMBER:	US 08/849,406						
PRIOR FILING DATE:	1999-07-21						
PRIOR APPLICATION NUMBER:	PCT/US95/16349						
PRIOR FILING DATE:	1995-12-15						


```
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-038-722-19

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
| : ||||| : : || : : ||||| : ||||| : ||||| : |||||
Db 5 CQLGYSAGPCVAMPFRYFYNGTSMACQTFVYGGCGGNGNNGNFVTEKDCIQC 55

RESULT 37
US-10-115-134-88
; Sequence 88, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 88
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-115-134-88

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
| : ||||| : : || : : ||||| : ||||| : ||||| : |||||
Db 5 CQLGYSAGPCVAMPFRYFYNGTSMACQTFVYGGCGGNGNNGNFVTEKDCIQC 55

RESULT 38
US-10-115-134-89
; Sequence 89, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
```

```
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 89
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-115-134-89

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
| : ||||| : : || : : ||||| : ||||| : ||||| : |||||
Db 5 CQLGYSAGPCVAMPFRYFYNGASMACQTFVYGGCGGNGNNGNFVTEKDCIQC 55

RESULT 39
US-10-115-134-90
; Sequence 90, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 90
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-115-134-90

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
| : ||||| : : || : : ||||| : ||||| : ||||| : |||||
Db 5 CQLGYSAGPCVAMPFRYFYNGTSMACQTFVYGGCGGNGNNGNFVTEKDCIQC 55

RESULT 40
US-10-456-986A-42
; Sequence 42, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
```



```

; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITI-E7-141 Sequence
; US-10-456-986A-42

```

```

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCILASIPHWYNNKTKICISFEFYIGGCGNNNNFQTEAICLVTC 51
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
nb 5 COLCVSAGPCVAMPEPRFYNGTCSMACOTEFVYGGCGMGNNGNFEVTEKDCLOT 55
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 41
US-10-456-986A-43
; Sequence 43, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A Sequence
US-10-456-986A-43

```

```
Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
```

RESULT 42
US-10-456-986A-44
; Sequence 44, Application US/10456986A
; Publication No. US2004003893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002

```

, CURRENT APPLICATION NUMBER: US/10/4556, 9866A
,
, CURRENT FILING DATE: 2003-06-06
,
, PRIOR APPLICATION NUMBER: 60/387,239
,
, PRIOR FILING DATE: 2002-06-07
,
, PRIOR APPLICATION NUMBER: 60/407,003
,
, PRIOR FILING DATE: 2002-08-28
,
, NUMBER OF SEQ ID NOS: 54
,
, SOFTWARE: FastSeq for Windows Version 4.0
,
, SEQ ID NO 44
,
, LENGTH: 58
,
, TYPE: PRT
,
, ORGANISM: Artificial Sequence
,
, FEATURE:
,
, OTHER INFORMATION: MUTOX Sequence
,
, US-10-4556-9866A-44

```

Query Match 53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

```

RESULT 43
US-10-953-902A-42
; Sequence 42, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-42

```

Query Match 53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNKKTKICEFIYGGCGGNNNFQTBAICLVTC 51
|||||
5 COLGSAGPCVAMEPFYNGTSCMACOTEVYGGCMGNNGNFFVTBKDCLOTC 55

RESULT 44
US-10-953-902A-43
; Sequence 43, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladhner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hixant, Shirish


```

; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953,902A-43

```

Query Match 53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

[illegible]

RESULT 45

```

US/10-953-902A-44
; Sequence 44, Application US/10953902A
; Publication NO. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALIKRIIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US/10-953-902A-44

```

```
Query Match      53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
```

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNGNFQTEAICLVTC 51
| : ||||| : || : | : ||||| ||||| |||||
Dd 5 COLGYSAGPCVAMFPRYFYNGTSMACETFYGGCMGNNGNVTEKDCLQC 55

RESULT 46

US-10-007-280A-233
; Sequence 233, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,640
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 233
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-007-280A-233

Query Match	53.0%;	Score 160;	DB 14;	Length 503;
Best Local Similarity	49.0%;	Pred. No. 4e-11;		
Matches 25; Conservative	7;	Mismatches 19;	Indels 0;	Gaps 0;

QY

1 CSMPQEAGPCLASIPHWYNKTKICSEFYGGCGGNNNFQTAEI CLVT C 51
||| ||| ||| | : ||| : ||| :: ||| :

Dd

317 CSLPALGCPCKAYAPRWAYSOTGCQC SFVYGGE GNGNPFREACEESC 367

RESULT 47

```

US-09-794-589-2
; Sequence 2, Application US/09794589
; Patent No. US20020004224A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/09/794,589
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-589-2

```

Query Match 53.0%; Score 160; DB 9; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy	1	CSMPQ	BAGP	CLAS	IPHH	WYNN	KKTK	ICSE	FYGG	QGN	NNNF	QTEA	ICLV	TC	51	
	:						:	:				:	:	:	:	
D _b	386	CSLP	ALQ	GPCK	KAY	PRW	AYNS	QTG	CCQ	CSF	YGG	CEG	NNNF	ESRE	ACEESC	436

RESULT 48

```

US-10-315-380-2
; Sequence 2, Application US/10315380
; Publication No. US20030129577A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/10/315,380
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/794,589
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069

```



```

; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-315-380-2

```

Query Match	53.0%	Score 160;	DB 14;	Length 576;
Best Local Similarity	49.0%;	Pred. NO. 4.6e-11;		
Matches 25: Conservative	7;	Mismatches 19;	Indels 0;	Gaps 0;

QY 1 CSMPQEAGPCLASIPHWYNKTKTICSEFIYGCGGNNNFQTEAICLVC 51
|||: ||| | | : | | : |||: |||: | :
db 385 CSLPALGPGCKAYAPWAYNSOTGCOSFYVGCGEGNNGNNFEREACEESC 436

```

RESULT 49
US-10-369-736-7
; Sequence 7, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-736-7

```

Query Match 53.0%; Score 160; DB 14; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25: Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQEAGPCIASIPHHWYNKTKICSEFIYGCQGNNNFQTEAICLVTC 51
|||: ||| | | | : | : |||: ||| :: | :
pb 186 CSI.PALOGPCXAYAPRWYNSTGOCSEFYGCQEGNNGFNESREACEESC 436

```

RESULT 50
US-10-369-738-7
; Sequence 7, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-738-7

```

Query Match 53.0%; Score 160; DB 14; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0;

Qy 1 CSMQBAGCLASIPHWYNNKTKICSFYVGGCGNNNFQTEAICLVTC 51
386 CSLPALQGGCKAYAPRWAYNSGTQCGSFVYGGCGNNNPFESRACEECS 436
Db

Search completed: September 21, 2005, 16:45:52
Job time : 32.8938 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:21:48 ; Search time 7.37168 Seconds
(without alignments)
665.663 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127

Perfect score: 302
Sequence: 1 CSMPOEAGPCLASIPHWYN.....GCGQGNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

PIR_79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	56.3	110	1 TITTOR	basic proteinase i
2	163	54.0	67	1 TIBOC	trypsin inhibitor,
3	160	53.0	252	2 JG0185	hepatocyte growth
4	158	52.3	62	2 A4180	taicotoxin serine
5	154	51.0	747	2 JH0773	Alzheimer's disease
6	153	50.7	58	1 TIRABK	isoalbinhibitor K (BP
7	153	50.7	62	2 S19127	proteinase inhibit
8	152	50.3	62	2 S07451	hypothetical prote
9	152	50.3	922	2 T23573	basic proteinase i
10	149	49.3	57	2 A59204	venom basic protei
11	148	49.0	65	1 TIVIVC	Alzheimer's disease
12	147	48.7	76	2 S06678	Alzheimer's disease
13	147	48.7	76	2 S03607	hypothetical Alzhe
14	147	48.7	484	4 A32761	Alzheimer's disease
15	147	48.7	770	1 QRHUA4	amyloid precursor
16	146	48.3	111	2 S41082	beta-amyloid precu
17	146	48.3	751	2 A49974	amyloid beta (A4)
18	146	48.3	763	2 A49321	amyloid precursor-
19	146	48.3	765	2 S42880	proteinase inhibit
20	145	48.0	57	1 TIFRBP	uterine plasmin/tr
21	145	48.0	122	1 A55115	hypothetical prote
22	145	48.0	1599	2 T16210	chymotrypsin inhib
23	144	47.7	62	2 S01802	Alzheimer's disease
24	144	47.7	76	2 S04855	Alzheimer's disease
25	144	47.7	100	2 A32282	short epsilon-dend
26	143	47.4	57	2 B59399	venom basic protei
27	143	47.4	59	1 TIEPED	Long epsilon-dendr
28	143	47.4	59	2 A59399	chymotrypsin inhib
29	143	47.4	62	2 S01803	

30	143	47.4	302	1 TIRCKK	tissue factor path
31	143	47.4	352	1 HCHU	alpha-1-microglobu
32	143	47.4	372	2 JC2556	alpha-1-microglobu
33	142	47.0	61	1 TIVIT1	venom basic protei
34	142	47.0	337	1 TIPGB1	alpha-1-microglobu
35	142	47.0	352	1 TIBOBI	alpha-1-microglobu
36	141	46.7	1522	2 H88380	inter-alpha-trypsi
37	140	46.4	123	2 A29652	hypothetical prote
38	140	46.4	1558	2 C89114	proteinase inhibit
39	140	46.4	2167	2 T34395	proteinase inhibit
40	138	45.7	61	1 TIRCBP	alpha-1-microglobu
41	138	45.7	125	1 TIRHBI	Kunitz-type protei
42	138	45.7	265	2 A53390	tissue factor path
43	137	45.4	235	2 A54951	basic proteinase i
44	136	45.0	100	1 TIBO	hypothetical prote
45	136	45.0	805	2 T34212	hypothetical prote
46	135	44.7	1743	2 T26859	isoprotinin G1 -
47	134	44.4	59	2 S00371	serum basic protei
48	134	44.4	60	1 TIBOR	protein ZC84.6 (im
49	134	44.4	1474	2 D88550	hypothetical prote
50	134	44.4	2844	2 S28291	

ALIGNMENTS

RESULT 1

TITTOR

basic proteinase inhibitor - loggerhead

C:Species: Caretta caretta (loggerhead)

C>Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A01224

R:Kato, I.; Tominega, N.

Fed. Proc. 38, 832, 1979

A:Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tand

A:Reference number: A01224

A:Accession: A01224

A:Molecule type: protein

A:Residues: 1-110 <KAT>

A:CROSS-references: UNIPROT:P00993

C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inhi

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:63-105/Domain: antileukoproteinase repeat homology <ALP>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8-58,17-41,33-54,67-93,76-97,80-92,86-101/disulfide bonds: #status predicted

F:18/inhibitory site: Lys (trypsin) #status predicted

Query Match 56.3%; Score 170; DB 1; Length 110;

Best Local Similarity 51.0%; Pred. No. 2e-13;

Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNKTKICSFYGGCGGNNNFQTEAICLVTC 51

DB 8 CRLPPEQGCGRIPRYFYNPASRMCSFIYGGCKGNKNFKYAEVCVRAC 58

RESULT 2

TIBOC

trypsin inhibitor, colostrum (BPI type) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A01207

R:Čechova, D.; Jonakova, V.; Sorm, F.

Collect. Czech. Chem. Commun. 36, 3342-3357, 1971

A:Title: Primary structure of trypsin inhibitor from cow colostrum (component B2).

A:Reference number: A90928

A:Accession: A01207

A:Molecule type: protein

A:Residues: 1-26, B' 28-67 <CEC>

A:CROSS-references: UNIPROT:P00976

A:Note: the residue identified as Asx is bound to carbohydrate; therefore, we have show

Query Match 49.0%; Score 148; DB 1; Length 65;
Best Local Similarity 49.0%; Pred. No. 5.3e-11;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
|||:||||:|::||:|||||:|||||:|||||:|
Db 7 CYLPADPRCLAYMPRFYINPASNKCKFIYGGCGNNNNFKTWDECRHTC 57
|||:||||:|::||:|||||:|||||:|||||:|

RESULT 12

S06678
Alzheimer's disease amyloid beta protein - rhesus macaque (fragment)
C/Species: Macaca mulatta (rhesus macaque)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C/Accession: S06678
R/Koo, E.H.; Sisodia, S.S.; Price, D.L.
submitted to the EMBL Data Library, July 1989
A/Reference number: S06678
A/Accession: S06678
A/Molecule type: mRNA
A/Residues: 1-76 <KOO>
A/Cross-references: UNIPROT:P29216; EMBL:X15985; NID:G38080; PIDN:CAA34116.1; PID:G93023
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C/Keywords: alternative splicing; serine proteinase inhibitor
F;3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.7%; Score 147; DB 2; Length 76;
Best Local Similarity 47.1%; Pred. No. 8.2e-11;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
|||:||||:|::||:|||||:|||||:|||||:|
Db 3 CSEAGETGPCRAMISRWYFDVTEGCKAPFFYGGCGNNNNFDTTEYCMVVC 53
|||:||||:|::||:|||||:|||||:|||||:|

RESULT 13

S03607
Alzheimer's disease amyloid A4 protein - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: S03607
R/Kang, J.; Mueller-Hill, B.
Nucleic Acids Res. 17, 2130, 1989
A/Title: The sequence of the two extra exons in rat preA4.
A/Reference number: S03607; MUID:89183625; PMID:2648331
A/Accession: S03607
A/Molecule type: mRNA
A/Residues: 1-76 <KAN>
A/Cross-references: UNIPROT:P08592; EMBL:X14066; NID:G56957; PIDN:CAA32229.1; PID:G93023
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C/Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F;3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.7%; Score 147; DB 2; Length 76;
Best Local Similarity 47.1%; Pred. No. 8.2e-11;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
|||:||||:|::||:|||||:|||||:|||||:|
Db 3 CSEAGETGPCRAMISRWYFDVTEGCKAPFFYGGCGNNNNFDTTEYCMVVC 53
|||:||||:|::||:|||||:|||||:|||||:|

RESULT 14

A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (fra
C/Species: Homo sapiens (man)
C/Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C/Accession: A32761
E/de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A/Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted ph
A/Reference number: A32761; MUID:89346754; PMID:2569763
A/Accession: A32761

A:Molecule type: mRNA
A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A>Note: the authors translated the codon ATG for residue 433 as Leu
C:Comment: This is the hypothetical translation of a sequence believed to contain cloning
C:Keywords: cloning artifact

Query Match 48.7%; Score 147; DB 4; Length 484;
Best Local Similarity 47.1%; Pred. No. 4.8e-10;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

Dy 1 CSMPQAGPCLASIPHWYNNKTKICSFYIGCGCGGNNFQTAEATCLVTC 51
||| :|::| |::| |::| |::| |:
Db 212 CSEQAETGPCRAMISRYFVDTEGRCAFPFYGGCGGNRNFPTEEYCMAYC 262

RESULT 15
ORHU44

Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIA inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 Sequence revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A33277; A33260; A35486; I39452; I39453; I59562; A44
4668; A28593; A29302; A60805; JI0038; S06321; A60355; A59011; A38384; S29076; S38252; S3
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A>Title: The PrA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288,'V',365-770 <LEM1>
A:Cross-references: EMBL:X13466
A>Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:g871360
A>Note: alternative splice form APP(695)
R:La Fauri, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A>Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24547; NID:G341202; PIDN:AAC13654.1; PID:G516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:gl78863; PIDN:AA51768.1; PID:gl78865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of i
A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A>Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, K.; Sakaki, Y.
Gene 87, 257-263, 1990
A>Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39452
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL

A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A:Accession: I39451
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-530, 'QWLMPVTPAFWEAKVGR' <YOS2>
A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R:Yoshiaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Contents: annotation; extractum
A>Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260663; PMID:2111584
A:Accession: I39453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LRV>
A:Cross-references: GB:M37896; NID:g178618; PIDN:AAAS1727.1; PID:g178620
A>Note: a mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R:Kamino, K.; Orr, H.T.; Payami, H.; Wljsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heaton, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A>Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A>Note: sequence extracted from NCBI backbone (NCBIP:115376)
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A>Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAAS1722.1; PID:g178540
A>Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584

A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAAS5540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15533; NID:g177957; PIDN:AAAS1564.1; PID:g177958
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A>Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A>Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A:Experimental source: glioblastoma cell line
A>Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtot
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three i
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-286, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAAS1726.1; PID:g178573
A>Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 60

RESULT 22
T16210
hypoetical protein F30H5.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*

A:Title: Sequence of the protease inhibitor domain of the M4 amyloid protein precursor
A:Reference number: S04855; MUID:89345111; PMID:2569710
A:Accession: S04855
A:Molecule type: mRNA
A:Residues: 1-76 <FUK>
A:Cross-references: UNIPROT:P12023; EMBL:X15210; NID:G49965; PIDN:CAA33280.1; PID:G930
A:Note: the authors translated the codon CAT for residue 74 as Val
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
E:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.7%; Score 144; DB 2; Length 76;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;

C;Comment: The amino acid at position p2' (228-Met) appears to determine the specificity
nd elastase; those with leucine interact strongly.
C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;20-173/Domain: lipocalin homology <Lip>
F;216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;216-266,225-249,241-262,272-322,281-305,297-316/Dissulfide bonds: #status predicted
F;226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F;235/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;282/Inhibitory site: Arg (trypsin) #status predicted

Query Match 47.0%; Score 142; DB 1; Length 337;
Best Local Similarity 47.1%; Pred. No. 1.4e-09;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPEAGCLASIPHHWYNKTKICSFYGGCGGNNNFOTEAICLVTC 51
: ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 216 COLGVSQGPLEGMKRYFYNGSMACETHYGGCMGNGNFVSEKECLQTC 266

RESULT 35

TISOB1

alpha-1-microglobulin / inter-alpha-trypsin inhibitor precursor [validated] - bovine
N/Alternate names: BI-14 (inhibitory fragment of ITI); bikunin; ITI
C/Species: Bos primigenius taurus (cattle)
C/Date: 25-Feb-1985 #sequence revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: S68149; A91717; A90685; S31219; A01209
R/Lindqvist, A.; Åkerström, B.
Biochim. Biophys. Acta 1306, 98-106, 1996
A/Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver
A/Reference number: S68149; MUID:96201710; PMID:8611630
A/Accession: S68149
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-352 <LIN>
A/Cross-references: UNIPROT:P00978; EMBL:U35642; NID:g1016297; PIDN:AAB07599.1; PID:g101
R/Hochrasser, K.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983
A/Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A/Reference number: A91717; MUID:84133807; PMID:6199275
A/Accession: A91717
A/Molecule type: protein
A/Residues: 327-267,'L',269-273,'Q',275-297,'AF',300-329,'Q',331-345,'R',347-348 <HOC>
R/Hochrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A/Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A/Reference number: A90685; MUID:85225967; PMID:2408637
A/Accession: A90685
A/Molecule type: protein
A/Residues: 347-349 <HOC2>
R/Hochrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983
A/Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A/Reference number: A91718; MUID:84133808; PMID:6199276
A/Contents: annotation; reactive sites
R/Castillo, G.M.; Templeton, D.M.
FEBS Lett. 319, 292-296, 1993
A/Title: Subunit structure of bovine ESF (extracellular-matrix stabilizing factor(s)). f
A/Reference number: S31219; MUID:93178646; PMID:7680011
A/Accession: S31219
A>Status: preliminary
A/Molecule type: protein
A/Residues: 206-214,'X',216,'X',218-220 <CAS>
C/Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
F;335-188/Domain: lipocalin homology <Lip>
F;231-281/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;241/inhibitory site: Leu (chymotrypsin, elastase) #status experimental
F;250/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;297/inhibitory site: Arg (trypsin) #status experimental

A:Molecule type: protein
A:Residues: 1-61 <NAK>
A:CROSS-references: UNIPROT:P16044
A:Experimental source: hemocytes
A:Comment: The inhibitory activity is similar to bovine basic proteinase inhibitor.
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C:Keywords: serine proteinase inhibitor
F:8-58/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F:18/Inhibitory site: Arg (chymotrypsin, elastase, trypsin, plasmin, plasma kallikrein)
Query Match 45.7%; Score 138; DB 1; Length 61;
Best Local Similarity 45.1%; Pred. No. 8e-10;
Matches 23; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
QY 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQEAICLVTC 51
DB 8 CTSPPVTGCRAGFRKYRNTYNTKQCEPFYGGCKGNRYKSEQDCLDAC 58
RESULT 41
TIHOBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
N:Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
C:Species: Equus caballus (domestic horse)
C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: A01210; A45653
R:Hochstrasser, K.; Wachtel, E.; Albrecht, G.J.; Reisinger, P.
Biochem. J. 1987; 223:473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-1-trypsin inhibitor
A:Reference number: A90685; UID:85225967; PMID:2408637
A:Accession: A01210
A:Molecule type: protein
A:Residues: 3-125 <HOC>
A:CROSS-references: UNIPROT:P04355
R:Veeraragavan, K.; Singh, K.; Wachtel, E.; Hochstrasser, K.
Biochem. Int. 26, 405-413, 1992
A:Title: Characterization of a trypsin inhibitor from equine urine.
A:Reference number: A45653; UID:92328813; PMID:1627153
A:Accession: A45653
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12, 'E', 14-33 <VEE>
A:CROSS-references: PIDN:AA22430.1; PID:G250858
A:Experimental source: urine
A:Note: sequence extracted from NCBI backbone (NCBI:P107966)
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis of the first domain interacts weakly with PMN-granulocytic elastase and not at all with pancreatic elastase. The amino acid at position P2' (19-Met) appears to determine the specificity of the fragment.
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precursor
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F:63-113/Domain: animal Kunitz-type proteinase inhibitor homolog <BP2>
F:7-57, 16-40, 32-53, 63-113, 72-96, 88-109/Diulfide bonds: #status predicted
F:17/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:26/Binding site: carbohydrate (asn) (covalent) #status experimental
F:73/Inhibitory site: Arg (trypsin) #status predicted
Query Match 45.7%; Score 138; DB 1; Length 125;
Best Local Similarity 45.1%; Pred. No. 1.6e-09;
Matches 23; Conservative 6; Mismatches 22; Indels 0; Gaps 0;
QY 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQEAICLVTC 51
DB 7 COLDHAQGPCLGIMISFYFNGTSMACETFOYGGCLGNNNFASQKELQTC 57
RESULT 42
AS3390
Kunitz-type proteinase inhibitor precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C:Accession: A53390
R:Kramer, K.K.; Duffy, J.Y.; Klemann, S.W.; Bixby, J.A.; Low, B.G.; Pope, W.F.; Roberts, J. Biol. Chem. 269, 7255-7261, 1994
A:Title: Selective cloning of cDNA for secretory proteins of early embryos. Identification of a novel proteinase inhibitor
A:Reference number: A53390; UID:94171738; PMID:7510284
A:Accession: A53390
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-265 <KRA>
A:CROSS-references: UNIPROT:Q29428; GB:U00165; NID:G501024; PIDN:AAA19108.1; PID:G9392040
C:Keywords: serine proteinase inhibitor
F:208-258/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
Query Match 45.7%; Score 138; DB 2; Length 265;
Best Local Similarity 41.2%; Pred. No. 3.3e-09;
Matches 21; Conservative 12; Mismatches 18; Indels 0; Gaps 0;
QY 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQEAICLVTC 51
DB 208 CLPEKVTGDCNATMYRFTYNTQTGLCEQFVYTGCGNGNFFENLEDCKMTC 258
RESULT 43
AS4951
Tissue factor pathway inhibitor-2 precursor - human
N:Alternate names: placental protein 5 (PF5)
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: A54951; I55185; A34029; B34029
R:Spröcher, C.A.; Kiesel, W.; Mathewes, S.; Foster, D.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3353-3357, 1994
A:Title: Molecular cloning, expression, and partial characterization of a second human tissue factor pathway inhibitor
A:Reference number: A54951; UID:94211862; PMID:8159751
A:Accession: A54951
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:CROSS-references: UNIPROT:P48307; GB:I27624; NID:G441149; PIDN:AAA20094.1; PID:G44115
A:Experimental source: placenta
R:Miyagi, Y.; Koshikawa, N.; Yasumitsu, H.; Miyagi, E.; Hirahara, F.; Aoki, I.; Muegi, J. Biochem. J. 1994, 303, 939-942, 1994
A:Title: CDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by human placental cells
A:Reference number: I55185; UID:95204397; PMID:7896752
A:Accession: I55185
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RE2>
A:CROSS-references: GB:D29992; NID:G484050; PIDN:BAA06272.1; PID:G484051
A:Note: parts of this sequence, including the amino end of the mature protein, were determined from the complementary DNA sequence of the mature protein.
R:Buetzow, R.; Huhtala, M.L.; Bohn, H.; Virtanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A:Title: Purification and characterization of placental protein 5.
A:Reference number: A34029; UID:88106628; PMID:3276312
A:Accession: A34029
A:Molecule type: protein
A:Residues: 'A', 24-33, 'X', 35 <BUB>
A:Accession: C34029
A:Molecule type: protein
A:Residues: 47-50, 'X', 52-53 <BU2>
A:Accession: B34029
A:Molecule type: protein
A:Residues: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>
C:Genetics:
A:Gene: GDB:TFPI2
A:CROSS-references: GDB:354485
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C:Keywords: anticoagulant; blood coagulation; duplication; predicted <SIG>
F:1-22/Domain: signal sequence #status predicted
F:23-235/Product: tissue factor pathway inhibitor-2 #status predicted
F:36-86/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F:96-149/Domain: animal Kunitz-type proteinase inhibitor homolog <BP2>
F:158-208/Domain: animal Kunitz-type proteinase inhibitor homolog <BP3>
F:36-86, 45-69, 61-82, 96-149, 106-130, 122-145, 158-208, 167-191, 183-204/Diulfide bonds: #at

Query Match 45.4%; Score 137; DB 2; Length 235;
Best Local Similarity 43.1%; Pred. No. 3.8e-09;
Matches 22; Conservative 11; Mismatches 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHHWYNKTKICSEFLYGCGGNNNNFQTEAICLVTC 51
DB 36 CLPLDYPGRALLRLYYDRYTQSCRFYGCCEGANNFYTWEACDDAC 86

RESULT 44

TIBO

N; basic proteinase inhibitor precursor - bovine
N/Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPTI; cationic kallikrein
C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Apr-1984 #sequence revision 22-Jul-1994 #text change 09-Jul-2004
C/Accession: S00277; A30333; S10546; S02486; S28197; A90162; A92023; A90736; A90927; A34
R/Creighton, T.E.; Charles, I.G.
J. Mol. Biol. 194, 11-22, 1987
A/Title: Sequences of the genes and polypeptide precursors for two bovine protease inhib
A/Reference number: S00274; UID:87283904; PMID:2441071
A/Acession: S00277
A/Molecule type: DNA; mRNA
A/Residues: 1-100 <CR2>
A/Cross-references: UNIPROT:P00974; GB:M20934; GB:X05274; NID:g162767; PIDN:AAD13685.1;
R/Creighton, T.E.; Charles, I.G.
Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987
A/Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.
A/Reference number: A90926; UID:88295740; PMID:2456884
A/Acession: A30333
A/Molecule type: DNA
A/Residues: 1-100 <CRE>
A/Cross-references: GB:M20934; GB:X05274; NID:g162767; PIDN:AAD13685.1; PID:g162769
R/Kington, I.B.; Anderson, S.
Biochem. J. 233, 443-450, 1986
A/Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic e
A/Reference number: S10546; UID:86158754; PMID:2420326
A/Acession: S10546
A/Molecule type: protein
A/Residues: 34-97 <KIN>
R/Fioretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
Biol. Chem. Hoppe-Seyler 369(Suppl.), 37-42, 1988
A/Title: Aprotinin-like isoforms in bovine organs.
A/Reference number: S02485; UID:89076531; PMID:2462435
A/Acession: S02486
A/Molecule type: protein
A/Residues: 36-93 <FIO>
R/Ikekita, M.; Jones, C.S.; Kamo, M.; Tsugita, A.; Kizuki, K.; Moriya, H.
Protein Seq. Data Anal. 5, 7-11, 1992
A/Title: Purification and characterization of the major cationic kallikrein inhibitor in
A/Reference number: S28197; UID:93150003; PMID:1283464
A/Acession: S28197
A/Molecule type: protein
A/Residues: 36-93 <IKX>
R/Kassell, B.; Laskowski, M.
Biochem. Biophys. Res. Commun. 20, 463-468, 1965
A/Title: The basic trypsin inhibitor of bovine pancreas. V. The disulfide linkages.
A/Reference number: A90162; UID:66083012; PMID:5860161
A/Contents: annotation; disulfide bonds
A/Acession: A90162
A/Molecule type: protein
A/Residues: 36-93 <KAS>
R/Anderson, F.A.; Hornle, S.
J. Biol. Chem. 241, 1569-1572, 1966
A/Title: The disulfide linkages in kallikrein inactivator of bovine lung.
A/Reference number: A92023; UID:66171231; PMID:5296424
A/Contents: annotation; disulfide bonds
A/Acession: A92023
A/Molecule type: protein
A/Residues: 36-93 <ANZ>
R/Chauvet, J.; Achet, R.
Bull. Soc. Chim. Biol. 49, 985-1000, 1967
A/Title: La structure covalente d'un inhibiteur polypeptidique de la trypsine (inhibiteu

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-805 <PAU>

A;Cross-references: UNIPROT:Q19305; EMBL:U41264; PIDN:AAA82427.1; CESP:F10E7.4

C;Genetics:

A;Gene: CESP:F10E7.4

A;Introns: 9/1; 34/3; 57/1; 90/3; 128/3; 162/1; 205/1; 285/2; 417/1; 475/1; 606/1; 745/1; 745/1

Query Match 45.0%; Score 136; DB 2; Length 805;
Best Local Similarity 41.2%; Pred. No. 1.6e-08;
Matches 21; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 608 QCEDKQACGAGNPPRYWYNHEKTQCERFTFTCKGNRNQFETEECKQIC 658

RESULT 46

T26859
hypothetical protein Y43F8B.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T26859

R;Ainscough, R.
submitted to the EMBL Data Library, October 1998

A;Reference number: Z20278

A;Accession: T26859

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-1743 <ML>

A;Cross-references: UNIPROT:Q9XWX5; EMBL:AL032623; PIDN:CAA21511.1; CESP:Y43F8B.3

A;Experimental source: clone Y43F8B

C;Genetics:

A;Gene: CESP:Y43F8B.3

A;Introns: 65/1; 92/2; 128/1; 229/1; 367/1; 422/1; 486/2; 523/1; 571/1; 628/1; 857/2; 947/2; 947/2

Query Match 44.7%; Score 135; DB 2; Length 1743;
Best Local Similarity 36.6%; Pred. No. 4.5e-08;
Matches 26; Conservative 6; Mismatches 19; Indels 20; Gaps 1;

Qy 1 CSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTE----- 44
| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1667 CLVRADPGPCNREIPRAYDKASGCKFFGGCGGNLNFDNQCVAFYTGCGGNLN 1726

Qy 45 ----AICLVTC 51

Db 1727 FVSIADCOATC 1737

RESULT 47

S00371
isoaprotinin G1 - bovine hybrid

C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C;Accession: S00371

R;Siekemann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988

A;Title: Characterization and sequence determination of six apertinin homologues from bovine

A;Reference number: S00371; MUID:88221840; PMID:2453200

A;Accession: S00371

A;Molecule type: protein

A;Residues: 1-59 <SIE>

A;Cross-references: UNIPROT:Q7M311

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C;Keywords: pyroglutamic acid; serine proteinase inhibitor

F;6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F;1/Inhibitory site: Lys (trypsin) #status predicted

Query Match 44.4%; Score 134; DB 2; Length 59;
Best Local Similarity 41.2%; Pred. No. 2.4e-09;
Matches 21; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 15:41:33 ; Search time 28.1327 Seconds
(without alignments)
928.315 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127

Perfect score: 302

Sequence: 1 CSMPEAGFCLASIPHWYN.....GCGQNNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247	81.8	137	Q9BDL0	Q9bdl0 oryctolagus
2	223	73.8	182	Q6IE19	Q6ie19 rattus norv
3	219	72.5	133	EPPI_HUMAN	Q95925 homo sapien
4	219	72.5	143	Q86TP9	Q86tp9 homo sapien
5	216	71.5	133	Q8HZ45	Q8hz45 papio papio
6	211	69.9	133	EPPI_MACMU	Q9bdl1 macaca mula
7	188	62.3	134	EPPI_MOUSE	Q9da01 mus musculus
8	170	56.3	110	IBP_CARCR	P00993 caretta car
9	169	56.0	571	Q7TQX3	Q7tqn3 mus musculus
10	166	55.0	86	Q9GP15	Q9gp15 ixodes ric
11	166	55.0	169	Q9N0X7	Q9n0x7 bos taurus
12	165	54.6	131	1_WFDB_HUMAN	Q9bqy6 homo sapien
13	163	54.6	750	Q6DJB6	Q6djb6 xenopus tro
14	163	54.0	67	IBPC_BOVIN	P00976 bos taurus
15	160	53.0	83	Q6ITB9	Q6itb9 pseudechis
16	160	53.0	252	1_SPT2_MOUSE	Q9wa03 mus musculus
17	160	53.0	283	Q6ZNI4	Q6zni4 homo sapien
18	160	53.0	576	Q8TEU8	Q8teu8 homo sapien
19	160	53.0	576	Q6UXZ9	Q6uxz9 homo sapien
20	159	53.0	2419	Q7PXZ1	Q7pxz1 anopheles g
21	159	52.6	80	Q8T3S7	Q8t3s7 araneus ven
22	159	52.6	2174	Q9GGR0	Q9gr0 drosophila
23	159	52.6	2772	Q9VAV4	Q9vav4 drosophila
24	159	52.6	2776	Q869A0	Q869a0 drosophila
25	159	52.6	2894	Q7KRX2	Q7krx2 drosophila
26	159	52.6	2898	Q86BZ9	Q86bz9 drosophila
27	158	52.3	62	1_IVBT_OXYSC	Q7lze4 oxyuranus s
28	158	52.3	69	1_CRPI_BOOMI	P81l62 boophilus m
29	158	52.3	142	Q6B8G1	Q6b8g1 ixodes paci
30	157	52.0	83	Q6ITB4	Q6itb4 oxyuranus m
31	157	52.0	83	Q6ITB5	Q6itb5 oxyuranus m

32	157	52.0	83	2	Q6ITB6	Q6itb6 oxyuranus s
33	157	52.0	122	1	BTIA_BOOMI	P3609 boophilus m
34	157	52.0	234	2	Q7YRQ8	Q7yrq8 bos taurus
35	157	52.0	759	2	Q8IT91	Q8it91 ancylostoma
36	156	51.7	83	2	Q90WA1	Q90wa1 pseudonaja
37	156	51.7	587	2	Q6AX20	Q6ax20 xenopus lae
38	156	51.7	751	2	Q708Z0	Q708z0 xenopus lae
39	154	51.0	747	2	Q91963	Q91963 xenopus. ap
40	154	51.0	749	2	Q6NRR1	Q6nrr1 xenopus lae
41	154	51.0	984	2	Q9GQN1	Q9gqn1 calliactis
42	154	51.0	984	2	Q9GQN2	Q9gqn2 calliactis
43	153	50.7	58	1	1S1K_HELP0	P09994 helix pomat
44	153	50.7	62	1	1VBT_ERIMA	P24541 eristocophi
45	153	50.7	90	2	Q6T6S5	Q6t6s5 bitis gabon
46	153	50.7	224	2	Q7T0Z5	Q7t0z5 xenopus lae
47	152	50.3	62	1	1P52_ANESU	P10280 anemonia eu
48	152	50.3	83	2	Q90WA0	Q90wa0 pseudonaja
49	152	50.3	83	2	Q6ITB7	Q6itb7 oxyuranus s
50	152	50.3	154	2	Q9N0X3	Q9n0x3 ovib aries

ALIGNMENTS

RESULT 1

Q9BDL0 PRELIMINARY; PRT; 137 AA.
AC Q9BDL0; DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of mouse Eppin and a gene cluster of similar
RT protease inhibitors on mouse chromosome 2.";
RL Gene 312:125-134(2003).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF346415; AAK31337.1; -.
DR HSSP; Q16019; IAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DSULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR PRODom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;

Query Match 81.8%; Score 247; DB 2; Length 137;

Best Local Similarity 78.4%; Pred. No. 1.1e-22;
Matches 40; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 CSMPEAGFCLASIPHWYNKKTKCSFIYGGCGGNNNNFQTEAICLVTC 51

Db 77 CSMPEKGTGCLAPIPRWYDKEREICTEFTYGGCGNNNNFQTEAICLVIC 127

RESULT 2

Q6IE19


```

ID Q6IE19 PRELIMINARY; PRT; 182 AA.
AC Q6IE19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WAP four-disulfide core 6-like 1.
GN Name=wfd6c11;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15660002; DOI=10.1101/gr.1946304;
RA Puente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ third party annotation (TPA) entry.
DR EMBL; BN000374; CAES1900.1; -.
DR HSP; P00974; Ix6U.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EBI207BFF756707E CRC64;

Query Match 73.8%; Score 223; DB 2; Length 182;
Best Local Similarity 66.7%; Pred. No. 1.3e-19;
Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFYVGGCGNNNFQTRAILVTC 51
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 77 CSLPDQAGPCLAYLPRWYNNKTNLTQFIYGGCGNTNLFSLKDICTISIC 127

RESULT 3
EPPI HUMAN STANDARD; PRT; 133 AA.
AC O95925; O96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE EpPin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
DE domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINLW1; Synonyms=WAP7, WFDC7;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnithini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epididymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Silvasanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French F.S., O'Rand M.G.;
RT "Cloning and sequencing of human EpPin: a novel family of protease
RT inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stavrides G.S., Huckle E.J., Deloukas P.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21639749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaealho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Senra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilmings L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Nadeau A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O95925-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O95925-2; Sequence=VSP_006755;
CC -1- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.; and initial analysis of more than 15,000 full-length human
cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
SEQUENCE FROM N.A.
TISSUE=Brain;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH44829.1; --
DR HSP; P00974; IUAU.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPRO02223; Prot_Inh_Kunz-m.
DR InterPro; IPRO08197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PSS0279; BPTI_KUNITZ_2; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;

Query Match 72.5%; Score 219; DB 2; Length 143;
Best Local Similarity 68.8%; Pred.No. 3.3e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMFQAGPCLASIPHWYNKKTKICSEFYGGCGGNNNNFOTEICLVTC 51
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
DB 87 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGCGGNNNNFQSKANCLNLC 137

RESULT 5
Q8HZ45 PRELIMINARY; PRT; 133 AA.
ID Q8HZ45
AC Q8HZ45
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Epitidymal protease inhibitor 1.
GN Name=Eppin;
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sivashanmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY141973; ANO8507.1; --
DR HSP; P00974; IUAU.
DR GO; GO:0008263; F:peptidease activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPRO02223; Prot_Inh_Kunz-m.
DR InterPro; IPRO08197; WAP
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.


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DR ProDom; P000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 133 AA; 15277 MW; B33AE57ECBEBE84 CRC64;

Query Match          71.5%; Score 216; DB 2; Length 133;
Best Local Similarity 68.6%; Pred. No. 7.2e-19;
Matches 35; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 CEMPNETGCLAFFIRWYDKONTCTSTFVHGCGQNNNNFQSEANCLNTC 127

RESULT 6
EPPI_MACMU
ID EPPI_MACMU STANDARD; PRT; 133 AA.
AC Q9BDL1.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=SPINLW1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
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CC -----
CC EMBL; AF346414; AAK31336.1; -.
CC HSSP; P00974; 1BPTI.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 1.
CC PRINTS; P000759; BASICTASE.
CC ProDom; P000222; Prot_Inh_Kunz-m; 1.
CC SMART; SM00131; KU; 1.
CC SMART; SM00217; WAP; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.

ProDom; P000222; Prot_Inh_Kunz-m; 1.
SMART; SM00131; KU; 1.
SMART; SM00217; WAP; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 133 AA; 15277 MW; B33AE57ECBEBE84 CRC64;

Query Match          69.9%; Score 211; DB 1; Length 133;
Best Local Similarity 66.7%; Pred. No. 3e-18;
Matches 34; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 CEMPNETGCLAFFIRWYDKONTCTSTFVHGCGQNNNNFQSEANCLNTC 127

RESULT 7
EPPI_MOUSE
ID EPPI_MOUSE STANDARD; PRT; 134 AA.
AC Q9DA01.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=Spinlwl.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
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CC EMBL; AF346414; AAK31336.1; -.
CC HSSP; P00974; 1BPTI.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 1.
CC PRINTS; P000759; BASICTASE.
CC ProDom; P000222; Prot_Inh_Kunz-m; 1.
CC SMART; SM00131; KU; 1.
CC SMART; SM00217; WAP; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
```


OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RA Claus A., Lilja H., Lundwall A.;
RT "A locus on human chromosome 20 contains several genes expressing
RT protease inhibitor domains with homology to whey acidic protein.";
RL Biochem. J. 368:233-242(2002).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clegg S.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharaglaitho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.M., Ramsay H.,
RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BQY6-1; Sequences=Displayed;
CC Name=2;
CC IsoId=Q9BQY6-2; Sequences=VSP_007550, VSP_007551;
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels
CC are found in epididymis, testis and trachea.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC -----
CC EMBL; AF411861; AAN03684.1; -;
CC EMBL; AL031663; CAC36264.1; -;
CC HSP; P02760; 1B1K.
CC Genew; HGNC:16164; WPC6.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 1.
CC PRINTS; PR00759; BASICTPASE.
CC ProDom; PD000222; Prot_Inh_Kunz-m; 1.
CC SMART; SM00131; KU; 1.
CC SMART; SM00217; WAP; 1.
CC PROSITE; PS00317; 4 DISULFIDE CORE; FALSE NEG.
CC PROSITE; PS00280; BPTI_KUNITZ_1; FALSE NEG.
CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.

KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 131 WAP four-disulfide core domain protein 6.
FT DOMAIN 31 69 WAP.
FT DOMAIN 70 128 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT VARSPIC 75 86 IYAVCHRRRLAPA -> VSLTYHKKELE (in isoform 2).
FT /FTid=VSP_007550.
FT Missing (in isoform 2).
FT /FTid=VSP_007551.
SQ SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;
Query Match 54.6%; Score 165; DB 1; Length 131;
Best Local Similarity 96.8%; Pred. No. 1.5e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 KKTICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 97 KKTICSEFIYGGCGGNNNNFQTEAICLVTC 127
RESULT 13
Q6DJB6 PRELIMINARY; PRT; 750 AA.
AC Q6DJB6;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE App-prov protein.
GN Name=app-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RC Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; BC075266; AAH75266.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.


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DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 750 AA; 84927 MW; 4222350843147CAF CRC64;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db CSEQAGTGPCRAMIPRWYIDVTERKCAQFIYGGCGGNNRNFDSQYCNVAVC 339

RESULT 14
ID IBFC_BOVIN STANDARD; PRT; 67 AA.
AC P00976;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Colostrum trypsin inhibitor (Colostrum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Cechova D., Jonakova V., Sorm F.;
RT "Primary structure of trypsin inhibitor from cow colostrum (component B2)".
RL Collect. Czech. Chem. Commun. 36:3342-3357 (1971).
RN [2]
RP DISULFIDE BONDS.
RA Cechova D., Muszynska G.;
RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
RL Collect. Czech. Chem. Commun. 39:680-688 (1974).
RN [3]
RP CHARACTERIZATION.
RX PubMed=11947537;
RA Cechova D., Muszynska G.;
RT "Role of lysine 18 in active center of cow colostrum trypsin inhibitor.";
RL FEBS Lett. 8:84-86 (1970).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01207; TIBOC.
DR HSSP; P02760; 1BIK.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 18 19 Reactive bond for trypsin.
FT DISULFID 8 58
FT DISULFID 17 41
```

```
FT DISULFID 33 54
FT CARBOHYD 27 27 N-linked (GlcNAc...).
SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;

Query Match 54.0%; Score 163; DB 1; Length 67;
Best Local Similarity 49.0%; Pred. No. 1.3e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db CQLPQARGPCAKALLRYFYNSTSNACBPFYGGCGGNNBNFETTEMCLRIC 58

RESULT 15
ID Q6ITB9 PRELIMINARY; PRT; 83 AA.
AC Q6ITB9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mulgin-3.
OS Pseudochis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophilineae; Pseudechis.
OX NCBI_TaxID=8670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filipovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626926; AAT45402.1; -.
DR HSSP; Q16019; IAAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9103 MW; 315C361D8EC89221 CRC64;

Query Match 53.0%; Score 160; DB 2; Length 83;
Best Local Similarity 52.9%; Pred. No. 3.8e-12;
Matches 27; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db CELPADTGPCRVGFPFYPNPDEKKCLEFIYGGCGGNNNFITKECESIC 81

RESULT 16
ID SPT2_MOUSE STANDARD; PRT; 252 AA.
AC Q9WU03; Q9WU04; Q9WU05;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor activator inhibitor type 2) (HAI-2).
DE Name=Spint2; Synonyms=HAI2;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=BALB/c;
RX MEDLINE=99160423; PubMed=10049781; DOI=10.1006/hbrc.1999.0268;
RA Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
RT "Hepatocyte growth factor activator inhibitor type 2 lacking the first
```


RT Kunitz-type serine proteinase inhibitor domain is a predominant
RT product in mouse but not in human.;
RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
CC -!- FUNCTION: Inhibitor of HGF activator.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q9WU03-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9WU03-2; Sequence=VSP_003034;
CC Name=3;
CC IsoId=Q9WU03-3; Sequence=VSP_003035, VSP_003036;
CC -!- TISSUE SPECIFICITY: Isoform 2 is more predominantly expressed than
CC isoform 1.
CC -!- DOMAIN: This inhibitor contains two inhibitory domains.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
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CC -----
DR EMBL; AF099016; AAD22172.1; -;
DR EMBL; AF099019; AAD22173.1; -;
DR EMBL; AF099020; AAD22174.1; -;
DR HSSP; P00974; 1K09.
DR MGD; MGI:1338031; Spint2.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
KW Alternative splicing; Glycoprotein; Repeat; Serine protease inhibitor;
KW Signal; Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 252 Kunitz-type protease inhibitor 2.
FT DOMAIN 28 197 Extracellular (Potential).
FT TRANSMEM 198 218 Potential.
FT DOMAIN 219 252 Cytoplasmic (Potential).
FT DOMAIN 38 88 BPTI/Kunitz inhibitor 1.
FT DOMAIN 133 183 BPTI/Kunitz inhibitor 2.
FT SITE 48 49 Reactive bond (By similarity).
FT SITE 143 144 Reactive bond (By similarity).
FT DISULFID 38 88 By similarity.
FT DISULFID 47 71 By similarity.
FT DISULFID 63 84 By similarity.
FT DISULFID 133 183 By similarity.
FT DISULFID 142 166 By similarity.
FT DISULFID 158 179 By similarity.
FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).
FT VARSPIC 37 93 Missing (in isoform 2 and isoform 3).
FT VARSPIC 114 128 PRKQSAEDLSAIFN -> CFVELSVAALFLFYA (in
FT isoform 3).
FT VARSPIC 129 252 /FTId=VSP_003035.
FT VARSPIC 252 252 Missing (in isoform 3).
FT SEQUENCE 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;
Query Match 53.0%; Score 160; DB 1; Length 252;
Best Local Similarity 49.0%; Pred. No. 1.2e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
DB CGVSKVVGKCRASIPRWYNNITDGSQPFYVGGCEGNGNYSKEBCLDKC 88

RESULT 17
Q6ZNI4
ID Q6ZNI4 PRELIMINARY; PRT; 283 AA.
AC Q6ZNI4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16032.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Nimmiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsu K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AK131196; BAD18391.1; -;
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin-C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP like.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 86206E7309866D30 CRC64;
Query Match 53.0%; Score 160; DB 2; Length 283;
Best Local Similarity 49.0%; Pred. No. 1.3e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
DB 93 CSLPALQGPCKAYAPRWAYNSQTGQCQSFYVGGCEGNGNPFESRACBESC 143
RESULT 18
Q8TEU8
ID Q8TEU8 PRELIMINARY; PRT; 576 AA.
AC Q8TEU8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WFIKNRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyai L., Patthy L.;
RT "A human protein containing multiple types of protease-inhibitory
RT modules".
RL Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709(2001).
RN [2]
RP SEQUENCE FROM N.A.


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RA Trexler M., Banyai L., Paddy L.;
RT "Distinct expression pattern of two related human proteins containing
RL multiple types of protease-inhibitory modules.";
CC Biol. Chem. 383:0-0(2002).
DR -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AF468657; AAL77058.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Query Match 53.0%; Score 160; DB 2; Length 576;
Best Local Similarity 49.0%; Pred. No. 2.7e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 386 CSLPALQGPCAYAPRAYNSQTGCQSFYVGCGEGNGNPFESREACBESC 436

RESULT 19
Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Btkunin hlg.
GN ORFNames=UNQ9235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RX Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
```

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CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAQ88509.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match 53.0%; Score 160; DB 2; Length 576;
Best Local Similarity 49.0%; Pred. No. 2.7e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 386 CSLPALQGPCAYAPRAYNSQTGCQSFYVGCGEGNGNPFESREACBESC 436

RESULT 20
Q7PXZ1 PRELIMINARY; PRT; 2419 AA.
AC Q7PXZ1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP12609 (Fragment).
GN Name=agCG49342; ORFNames=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
[1]
SEQUENCE FROM N.A.
RP STRAIN=PEST;
RC Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008987; EAA01339.1; -.
DR HSSP; P10646; 1IRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
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\ddot{O}

RT "Alternative splicing of papilin and the diversity of Drosophila
RL extracellular matrix during embryonic morphogenesis.";
RN Dev. Dyn. 226:634-642(2003).

RP SEQUENCE FROM N.A.
RA Kramerova I., Fessler J.H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.

DR EMBL; AF529179; AAO84907.1; -;
DR HSP; P12111; 1KTH.

DR FlyBase; FBN0003137; Ppn.
DR GO; GO:0005604; C:basement membrane; IDA.

DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.

DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.

DR InterPro; IPR010309; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.

DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.

DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00047; ig; 2.

DR Pfam; PF00014; Kunitz_BPTI; 10.
DR Pfam; PF00090; TSP_1; 5.

DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.

DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 10.

DR SMART; SM00408; ICG2; 3.
DR SMART; SM00131; KU; 10.

DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 9.

DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00900; PLAC; 1.

DR PROSITE; PS00092; TSP1; 5.
KW Matrix protein.

SQ SEQUENCE 2776 AA; 299741 MW; 92D38A17360D2D42 CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2776;
Best Local Similarity 47.1%; Pred. No. 1.8e-10;

Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
QY 1 CSMPQAGCLASIPHWNTKTKICSEFIYGGCGQNNNFQTEALCLVTC 51

DB 1730 CEQPVESGPGAGNFERWYDNETICRPFTYGGCKGNKNYPTEHACNYNC 1780

RESULT 25
Q7KRX2 PRELIMINARY; PRT; 2894 AA.

AC Q7KRX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE C53103-PA.
GN Names:Ppn; ORFNames=C53103;

OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazew R.G., Champagne M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abrell J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Bau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Buseam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.N., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Floer C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.B., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN Science 287:2185-2195(2000).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Friese E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RL [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RL [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mixta S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tuyp J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RL [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL [6]
RP SEQUENCE FROM N.A.


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RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AE003765; AAF56795.3; -.
DR HSSP; P12111; 1KTH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR003599; IG_c2.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR02223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00409; IGC2; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 5.
SQ SEQUENCE 2894 AA; 312663 MW; A1BFE1BAD9B214BC CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2894;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 1730 CEQVESPCCAGNFERWYDNETDICRPFTYGGCKGNKNYPTEHACNYNC 1780

RESULT 26
O86829 PRELIMINARY; PRT; 2898 AA.
AC O86829;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin 3.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2255133; PubMed=12666201; DOI=10.1002/dvdy.10265;
RA Kramerova I.A., Kramerov A.A., Fessler J.H.;
RT "Alternative splicing of papilin and the diversity of Drosophila
RL extracellular matrix during embryonic morphogenesis.";
RL Dev. Dyn. 226:634-642(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Kramerova I., Fessler J.H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF529180; AAO84908.1; -.

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DR FlyBase; FBgn0003137; Ppn.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR02223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 5.
KW Matrix protein.
SQ SEQUENCE 2898 AA; 313250 MW; 2F992742P2D64A00 CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2898;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 1730 CEQVESPCCAGNFERWYDNETDICRPFTYGGCKGNKNYPTEHACNYNC 1780

RESULT 27
IVBT_OYXSC
ID -IVBT_OYXSC STANDARD; PRT; 62 AA.
AC Q7LZE4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Taicotoxin, serine protease inhibitor component (TCX).
OS Oxyuranus scutellatus scutellatus (Australian taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophilineae; Oxyuranus.
OX NCBI_TaxID=8667;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX PubMed=1485334; DOI=10.1016/0041-0101(92)90511-3;
RA Possani L.D., Martin B.M., Yatani A., Mochca-Morales J., Zamudio F.Z.,
RA Gurrola G.B., Brown A.M.;
RT "Isolation and physiological characterization of taicotoxin, a complex
RL toxin with specific effects on calcium channels.";
RL Toxicon 30:1343-1364(1992).
CC -!- FUNCTION: Taicotoxin blocks the high threshold calcium channel
CC current of excitable membranes in heart and does not affect the
CC low threshold calcium channel current. The block is selective for
CC calcium channels, reversible, does not affect single channel
CC conductance but only changes channel gating, and is voltage
CC dependent with higher affinity for inactivated channels. Is very
CC toxic to mice.
CC -!- SUBUNIT: Linked to an alpha-neurotoxin-like peptide of 8000 Da and
CC a neurotoxic phospholipase of 16000 Da by non-covalent bonds. The

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CC ratio is approximately one phospholipase and one neurotoxin for
CC four protease inhibitors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR: A44180; A44180.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Calcium channel inhibitor; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Serine protease inhibitor; Toxin.
FT DISULFID 7 57 By similarity.
FT DISULFID 16 40 By similarity.
FT DISULFID 32 53 By similarity.
SQ SEQUENCE 62 AA; 7045 MW; A5E0BFBFD1990605 CRC64;

Query Match 52.3%; Score 158; DB 1; Length 62;
Best Local Similarity 51.0%; Pred. No. 5.1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQPEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 7 CHLPKPGPCRAAIPRYFYNNPHSKQCEKFIYGGCHGNANKFKTPDECNYTC 57

RESULT 28
CRPT_BOOMI STANDARD; PRT; 69 AA.
AC P81162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protease inhibitor carpapatin.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE.
RA Fuentes-Prior P., Pereira P.J.B., Mentale R., Bode W.;
RL Submitted (JAN-1998) to Swiss-Prot.
CC -1- FUNCTION: Serine protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSP; P00980; IDTX.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 18 19 Reactive bond (By similarity).
FT DISULFID 8 58 By similarity.
FT DISULFID 17 41 By similarity.
FT DISULFID 33 54 By similarity.
SQ SEQUENCE 69 AA; 7842 MW; E0B14312AC1533BB CRC64;

Query Match 52.3%; Score 158; DB 1; Length 69;
Best Local Similarity 51.0%; Pred. No. 5.6e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQPEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 CVPTADPGCKGPMWYNNIFTSQCEEFYGGCGQNDNRNRYRKEEDKTC 58

RESULT 29
Q6B8G1 PRELIMINARY; PRT; 142 AA.
ID Q6B8G1
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AC Q6B8G1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE KUN-5 (Fragment).
OS Ixodes pacificus (western blacklegged tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Ixodes.
OX NCBI_TaxID=29930;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Ribeiro J.M.C.;
RT "An insight into the transcriptome of the salivary glands of the adult
   female tick, Ixodes pacificus."
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Francischetti I.M., Lane R.S., Pham V.M., Ribeiro J.M.C.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: AV674183; AAT92116.1; -.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 16458 MW; A618BB45CB812C4B CRC64;

Query Match 52.3%; Score 158; DB 2; Length 142;
Best Local Similarity 52.9%; Pred. No. 1.2e-11;
Matches 27; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQPEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 29 CTEVVDEGPCRALIPRYFYNNMETCEEFYGGYGNNNFNESSCTSTC 79

RESULT 30
Q6ITB4 PRELIMINARY; PRT; 83 AA.
AC Q6ITB4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-2.
OS Oxyuranus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: AV626931; AAT45407.1; -.
DR HSP; P10646; 1ADZ.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145B51757014221 CRC64;
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Query Match 52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTAEICLVTC 51
| : | | | | : | | | | | : | | |
Dd 31 CELPADTGPCRVGFPFSFYNDPEKKCLEFIYGCEGANNFITKEECSTC 81

RESULT 31	Q6ITB5	PRELIMINARY;	PRT;	83 AA.
ID	Q6ITB5;			
AC	05-JUL-2004 (TREMBLrel. 27, Created)			
DC	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Microlepudin-1.			
OE	Oxyuranus microlepidotus (Inland taipan).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Eliapidae; Acanthophiinae; Oxyuranus.			
OX	NCBI_TaxId=111177;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Fillipovich I.V., Sorokina N.I.;			
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.			
CC	EMBL; AY626930; AAT5406.1; -.			
DR	HSP; P10646; 1ADZ.			
DR	GO; GO:0004867; E:serine-type endopeptidase inhibitor activity; IEA.			
DR	InterPro; IPR002223; Prot_inh_kunzm.			
DR	Pfam; PF00014; Kunitz_BPTI; 1.			
DR	PRINTS; PR00759; BAG3CPTASE.			
DR	ProDom; PD0000222; Prot_inh_kunzm; 1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS00379; BPTI_KUNITZ_2; 1.			
DR	SEQUENCE 83 AA; 9040 MW; CB4FE517570CF94C CRC64;			

Query Match 52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQZAGPCLASIPHWYNNKTKICSEFIYGGCQGNNNFQTEAICLVTC 51
| : | | | | : | | | | | : | | | | : | | |
pb 31 CELPADTGPCRVGFSPFYNDPKKCLEFIYGGCEGNANFITEESTC 81

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RESULT 32
Q6ITB6 PRELIMINARY; PRT; 83 AA.
ID Q6ITB6
AC Q6ITB6;
OS 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scurellin-2.
OS Oxyuranus scutellatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=8668;
[1] RN
RN SEQUENCE FROM N.A.
RC TISSUE=venom gland;
RP Filippovich I.V., Sorokina N.I.;
RA Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; AY626929; AAT45405.1; -.
HSSP; P10646; 1ADZ.
DR DR
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; I:
DR InterPro; IPRO02223; Prot Inh Kunz-m.

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DR      Dfam: PF00014; Kunitz_BPTI; 1.
DR      PRINTS; PRO0759; BASICPTASE.
DR      ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS00379; BPTI_KUNITZ_2; 1.
DR      PROSITE; PS00379; BPTI_KUNITZ_2; 1.
DR      PROSEQUENCE 83 AA; 9074 MW; 3145851757014221 CRC64;
DR      SO

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Query Match 52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26: Conservative 6: Mismatches 19: Indels 0: Gaps 0:

QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : | | | | : | | | | | | | | | : | |
Db 31 CELPDTGPCRVGFSFYNPDEKCLEFIYGGCGGNANNFITKECESTC 81

RESULT 33	BTIA BOOMI	STANDARD;	PRT;	122 AA.
ID	BTIA BOOMI			
AC	P83609			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Kunitz-type serine protease inhibitor Bmi1-A (Fragments).			
OS	Boophilus microplus (Cattle tick).			
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;			
OC	Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.			
NCBI	_TaxID=6941;			
PN	11			
ON				

SEQUENCE, AND FUNCTION.
 TISSUE=Larva;
 PubMed=10615008; DOI=10.1016/S0162-3109(99)00074-0;
 Tanaka A.S., Andreotti R., Gomes A., Torquato R.J.S., Sampaio M.U.,
 Sampaio C.A.M.;
 "A double headed serine proteinase inhibitor-human plasma kallikrein
 and elastase inhibitor-from *Boophilus microplus* larvae.";
 Immunopharmacology 45:171-177(1999).
 -|- FUNCTION: Inhibits bovine trypsin, bovine chymotrypsin, human
 plasmin, human plasma kallikrein and human neutrophil elastase,
 but not bovine thrombin, human factor Xa or porcine pancreatic
 kallikrein. May play a role in blocking blood coagulation during
 the larvae fixation on cattle.
 -|- SUBCELLULAR LOCATION: Secreted.
 -|- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.

[illegible]

Query Match 52.0%; Score 157; DB 1; Length 122;
Best Local Similarity 52.9%; Pred. No. 1.3e-11;
Matches 27; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCQGNNNNFQTEAICLVTC 51
 Db 71 CLARPESGPCLAYMPMWGYDSKLGQCVEFYGGCDGNDNKYTTTEEECLKSC 121


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RESULT 34
Q7YRQ8 PRELIMINARY; PRT; 234 AA.
ID Q7YRQ8
AC Q7YRQ8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;
RA Du X., Deng F.M., Chand H.S., Kiesel W.;
RT "Molecular cloning, expression, and characterization of bovine tissue
RT factor pathway inhibitor-2."
RL Arch. Biochem. Biophys. 417:96-104(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Deng F.-M., Kiesel W., Sun T.-T.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AY234861; AAO84035.1; -.
DR HSSP; P00981; 1DTK.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26675 MW; 4018EC84D589B422 CRC64;

Query Match 52.0%; Score 157; DB 2; Length 234;
Best Local Similarity 49.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 36 CLLPDDGFCRIPISYYDYRTQSCREPMYGCENANNFETLEACNEAC 86

RESULT 35
Q8IT91 PRELIMINARY; PRT; 759 AA.
ID Q8IT91
AC Q8IT91;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kunitz-like protease inhibitor precursor.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostominae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Baltimore;
RX MEDLINE=22645137; PubMed=12760667;
RA Hawdon J.M., Datu B., Crowell M.;
RT "Molecular cloning of a novel multidomain Kunitz-type proteinase
RT inhibitor from the hookworm Ancylostoma caninum."
RL J. Parasitol. 89:402-407(2003).
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF533590; AAN10061.1; -.
DR HSSP; P31713; ISHP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 12.
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DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 12.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 12.
KW Protease; Signal.
FT SIGNAL 1 16 Potential.
SQ SEQUENCE 759 AA; 84886 MW; C431A3C3F418F40A CRC64;

Query Match 52.0%; Score 157; DB 2; Length 759;
Best Local Similarity 51.0%; Pred. No. 8.5e-11;
Matches 26; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 205 CSQPIKAGPCNMLKRYADNKKRCVQFIYGGCKGNKNFESMEECTRTC 255

RESULT 36
Q90WAL PRELIMINARY; PRT; 83 AA.
ID Q90WAL
AC Q90WAL;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textilin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF402324; AAK95519.1; -.
DR HSSP; P25660; 1JCG.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;

Query Match 51.7%; Score 156; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 1.2e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 31 CELPADTGPCRVFRFFSYFNDEKKCLEFIYGGCGGNANNFITKECESTC 81

RESULT 37
Q6AX20 PRELIMINARY; PRT; 587 AA.
ID Q6AX20
AC Q6AX20;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Apll2 A protein.
DE Name=apll2 A;
GN Xenopus laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR GO: GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR Pfam: PF02177; A4 EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETANMYLOID.
DR PRODOM: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 51.0%; Score 154; DB 2; Length 747;
Best Local Similarity 47.1%; Pred. No. 2e-10;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFOTEALCLVTC 51
DB 287 CSEQATGFCRAMISRWDVTESKCAQFIYGGCGNNNFESDDYCMVAC 337

RESULT 40
Q6NRR1 PRELIMINARY; PRT; 749 AA.
AC Q6NRR1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE App protein.
GN Name=app;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinska M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/gdv.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
```

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[3]
SEQUENCE FROM N.A.
TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: BC070668; AAH70668.1; -.
DR HSSP: Q16019; IEA4.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR GO: GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_EXTRA.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETANMYLOID.
DR PRODOM: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 749 AA; 84766 MW; 33478C6B6A8C295D CRC64;

Query Match 51.0%; Score 154; DB 2; Length 749;
Best Local Similarity 47.1%; Pred. No. 2e-10;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFOTEALCLVTC 51
DB 289 CSEQATGFCRAMISRWDVTESKCAQFIYGGCGNNNFESDDYCMVAC 339

RESULT 41
Q6GQN1 PRELIMINARY; PRT; 984 AA.
AC Q6GQN1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name=PAM;
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Hormathiidae; Calliactis.
OX NCBI_TaxID=6114;
[1]
SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: AF221986; AAG44251.1; -.
DR HSSP: P12111; 1KNT.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0005507; F: copper ion binding; IEA.
DR GO: GO:0004504; F: peptidylglycine monooxygenase activity; IEA.
DR GO: GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0006518; P: peptide metabolism; IEA.
DR InterPro: IPR011044; Amine_DH_B_like.
DR InterPro: IPR001258; NHL.
DR InterPro: IPR000720; Pamonoxigenase.
DR InterPro: IPR008977; PHM_PNGase_F.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF01082; Cu2_monooxygen; 1.
DR Pfam: PF03712; Cu2_monoox_C; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
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DR Pfam; PF01436; NHL; 5.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00790; PAMONOXGNASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110265 MW; 424E4BCEB3B480D CRC64;

Query Match 51.0%; Score 154; DB 2; Length 984;
Best Local Similarity 43.1%; Pred. No. 2.6e-10;
Matches 22; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 730 CMLEHDTGPCRAAMPRWYFDKARSCRTRFIYGGCGGNNNNFASKRECAK 780

RESULT 42
Q9GQN2 PRELIMINARY; PRT; 984 AA.
AC Q9GQN2;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name=PAM;
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyanthaeae; Hormathiidae; Calliactis.
OX NCBI_TaxID=6114;
RN [1]
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimelikhuijzen C.J.P.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF221985; AAG44250.1; -.
DR HSSP; P12111; 1KNT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:004504; F:peptidylglycine monooxygenase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006518; P:peptide metabolism; IEA.
DR InterPro; IPR011044; Amine_DH_B-like.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR008977; PHM_PNGase_F.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF03712; Cu2_monoox_C; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NHL; 5.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PR00790; PAMONOXGNASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110266 MW; 7AFE2D1B74B78EBC CRC64;

Query Match 51.0%; Score 154; DB 2; Length 984;
Best Local Similarity 43.1%; Pred. No. 2.6e-10;
Matches 22; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 730 CMLEHDTGPCRAAMPRWYFDKARSCRTRFIYGGCGGNNNNFASKRECAK 780

Thu Sep 22 07:16:46 2005 us-10-807-204-1_copy_77_127.std.rup Page 20
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KW Proteases.
SQ SEQUENCE 90 AA; 10006 MW; 2BEDCJD2D0852AF CRC64;

Query Match 50.7%; Score 153; DB 2; Length 90;
Best Local Similarity 45.1%; Pred.No.3.le-1l;
Matches 23; Conservative 10; Mismatches 18; Indels 0; Gaps

QY 1 CSMPEAGPCLASIPHWYNKKTICSEFIYGGCGNNNFQTAEIACLVTC 51
DB 31 CYLPADTGPCWANPFRFYDSASKCKKFYGGCHGNANFRETRECRKC 81

RESULT 46
Q770ZS PRELIMINARY; PRT; 224 AA.

ID QT025
AC Q7025;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)

DE MGCEB8843 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OX Xenopodinae; Xenopus.
NX NCBI_TaxID=8355;
RN [1]
RP RESEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold F.S., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins S.E., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.J., Jordan H., Moore T.I., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J.J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnierich A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RW "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
RN RESEQUENCE FROM N.A.
RP TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative."
RL Dev. Dyn. 225:384-391(2002).

RN [3]
RP RESEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S., Strausberg R.;
RA Submitted (AUG-2003) to the ENMBL/genBank/DBJ databases.
CC -!- SIMILARITY: Contains 3 BPIT/Kunitz inhibitor domains.
DR ENML; BC055972; AAAH55972.1; -.
DR DRSP; PQ0974; IBP1.
DR GO; GO:0004867; Friserine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPRO02223; Prot_Inh_Kunzm.
DR Pfam; PF00014; Kunitz_BPTI_3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 14:52:13 ; Search time 31.8938 Seconds
(without alignments)
618.452 Million cell updates/sec

Title: US-10-807-204-2_COPY_52_102
Perfect score: 302
Sequence: 1 CSMPOEAGFCLASIPHWYN.....GCCQGNPNPQTEAICLVTC 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	302	100.0	106	7	ADA19801	Ada19801 Mature fo
2	302	100.0	131	7	ADA19800	Ada19800 Engineer
3	302	100.0	131	7	ADA19811	Ada19811 Engineer
4	292	96.7	131	7	ADA19814	Ada19814 Human DJ1
5	224	74.2	136	7	ADA19815	Ada19815 Mouse DJ1
6	219	72.5	51	2	AAW75257	AAW75257 Fragment
7	219	72.5	51	5	AAE27025	AAE27025 Human gen
8	219	72.5	51	5	AAE27163	AAE27163 Human gen
9	219	72.5	51	8	ADG89845	ADG89845 Human sec
10	219	72.5	58	4	AAE13084	AAE13084 Human ser
11	219	72.5	58	4	AAE60630	AAE60630 Kunitz do
12	219	72.5	58	7	ADF11997	ADF11997 Human CAB
13	219	72.5	58	8	ADL16838	ADL16838 Human Kun
14	219	72.5	58	8	ADR89980	ADR89980 Human CAB
15	219	72.5	64	4	AAE13093	AAE13093 Human ser
16	219	72.5	102	5	AAE27095	AAE27095 Human sec
17	219	72.5	102	5	AAE28009	AAE28009 Human gen
18	219	72.5	102	6	ABU65039	ABU65039 Human sec
19	219	72.5	102	8	ADG89848	ADG89848 Human sec
20	219	72.5	117	5	AAE27094	AAE27094 Human sec
21	219	72.5	117	5	AAE27165	AAE27165 Human gen
22	219	72.5	117	6	ABU65038	ABU65038 Human sec
23	219	72.5	117	8	ADG89847	ADG89847 Human sec
24	219	72.5	133	2	AAW75219	AAW75219 Human sec
25	219	72.5	133	5	AAE26982	AAE26982 Human gen

26	219	72.5	133	5	AAE27120	AAE27120 Human gen
27	219	72.5	133	6	ABU64993	ABU64993 Human sec
28	219	72.5	133	7	ADA19812	ADA19812 Human EPP
29	219	72.5	133	8	ADG89802	ADG89802 Human pro
30	219	72.5	164	3	AAV70010	AAV70010 Human pro
31	219	72.5	179	8	ABM85103	ABM85103 Human dia
32	188	62.3	134	7	ADA19813	ADA19813 Mouse EPP
33	170	56.3	43	4	AAE13096	AAE13096 Human ear
34	169	56.0	571	7	AAE39459	AAE39459 Mouse GDF
35	169	56.0	571	7	ADD93670	ADD93670 Mouse GDF
36	167	55.3	58	2	AAE99146	AAE99146 Aprotinin
37	167	55.3	58	2	AAE13092	AAE13092 Trypsin i
38	166	55.0	54	4	AAE48380	AAE48380 I. ricinu
39	166	55.0	86	4	AAE48380	AAE48380 I. ricinu
40	161	53.3	51	2	AAW25929	AAW25929 Anti-tryp
41	161	53.3	55	2	AAW25931	AAW25931 RPDF-Kuni
42	161	53.3	55	2	AAW27402	AAW27402 Human neu
43	161	53.3	58	2	AAE99160	AAE99160 Genetical
44	161	53.3	58	2	AAE99159	AAE99159 Genetical
45	161	53.3	58	2	AAE99158	AAE99158 Genetical
46	161	53.3	58	8	ADF71964	ADF71964 Kallikrei
47	161	53.3	58	8	ADF71963	ADF71963 Kallikrei
48	161	53.3	58	8	ADF71962	ADF71962 Kallikrei
49	161	53.3	124	2	AAW25933	AAW25933 New prote
50	161	53.3	124	2	AAW25932	AAW25932 New prote

ALIGNMENTS

RESULT 1

ADA19801
ID ADA19801 standard; protein; 106 AA.

AC ADA19801;

DT 20-NOV-2003 (first entry)

DE Mature form of engineered human DJ1 protein SEQ ID NO:2.

DJ1; Kunitz-type protease inhibitor domain; antiinflammatory;
antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
antibacterial; immunosuppressive; antirheumatic; antiarthritic;
nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
acute pancreatitis; pulmonary injury; allergy-induced protease release;
deep vein thrombosis; myocardial infarction; shock; septic shock;
hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
chronic inflammatory bowel disease; psoriasis.

OS Synthetic.

OS Homo sapiens.

Key Location/Qualifiers

Disulfide-bond 8..36 /note = predicted disulfide bond

Disulfide-bond 15..40 /note = predicted disulfide bond

Disulfide-bond 23..35 /note = predicted disulfide bond

Disulfide-bond 29..44 /note = predicted disulfide bond

Domain 52..102 /note = predicted disulfide bond

Disulfide-bond 52..102 /note = Kunitz domain predicted by pfscan

Disulfide-bond 61..85 /note = predicted disulfide bond

Disulfide-bond 77..98 /note = predicted disulfide bond

XX WO2003070770-A2.

PD	28-AUG-2003.	XX	Synthetic.
XX	18-FEB-2003; 2003WO-EP001629.	OS	Homo sapiens.
XX	21-FEB-2002; 2002US-0358683P.	XX	
PR	(GENE-) GENEPROT INC.	Key	Location/Qualifiers
PA	Bougueleret L, Bairoch A, Niknejad A;	FT	Misc-difference 1. .131
PI	WPI; 2003-663849/62.	FT	/note= "eppin-like precursor"
XX		FT	1. .25
XX		FT	/label= signal
XX		FT	26. .131
XX		FT	/note= "mature DJ11 protein"
XX		FT	33. .61
XX		FT	/note = predicted disulfide bond
PT	New engineered human Kunitz-type protease inhibitor for diagnosing,	FT	40. .65
PT	preventing or treating conditions associated with excessive proteinase	FT	/note = predicted disulfide bond
PT	activity, e.g. inflammation, pulmonary injuries, myocardial infarction or	FT	48. .60
PT	hemorrhage.	FT	/note = predicted disulfide bond
XX		FT	54. .69
PS	Claim 5; Page 71; 87pp; English.	FT	/note = predicted disulfide bond
XX		FT	77. .127
CC	The present invention describes an isolated, purified or recombinant DJ11	FT	/note = Kunitz domain predicted by pfscan
CC	polypeptide comprising a Kunitz-type protease inhibitor domain or its	FT	77. .127
CC	biologically active portion. The polypeptide comprises at least 98 %	FT	/note = predicted disulfide bond
CC	identity to residues 77-127 of a 131 amino acid sequence (S1, see	FT	86. .110
CC	ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see	FT	/note = predicted disulfide bond
CC	ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,	FT	102. .123
CC	anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,	FT	/note = predicted disulfide bond
CC	antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary	FT	
CC	activities, and can be used as a protease inhibitor and in gene therapy.	FT	
CC	Composition and methods from the present invention can be used in	PN	
CC	diagnosing, preventing or treating conditions associated with excessive	XX	
CC	proteinase activity, such as acute pancreatitis, pulmonary injury,	XX	
CC	allergy-induced protease release, deep vein thrombosis, myocardial	XX	
CC	infarction, shock (including septic shock), hyperfibrinolytic	XX	
CC	haemorrhage, and especially, inflammatory disorders (e.g. emphysema,	XX	
CC	idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,	XX	
CC	chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may	XX	
CC	be used in preserving platelet function, organ preservation or in wound	XX	
CC	healing. The polynucleotide sequence encoding DJ11 may be used as	XX	
CC	hybridisation probes, in chromosome and gene mapping, in the generation	XX	
CC	of antisense RNA and DNA, and as targets for pharmaceutical intervention.	XX	
CC	The present sequence represents the mature form of an engineered human	XX	
CC	DJ11 protein from the present invention.	XX	
XX		DR	
SQ	Sequence 106 AA;	XX	
	Query Match 100.0%; Score 302; DB 7; Length 106;	PT	
	Best Local Similarity 100.0%; Pred. No. 3.2e-30;	PT	
	Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	
QY	1 CSMPOEAGCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51	PS	
DB	52 CSMPOEAGCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 102	XX	
		XX	
RESULT 2		XX	
ADA19800		CC	
ID	ADA19800 standard; protein; 131 AA.	CC	
XX		CC	
AC	ADA19800;	CC	
XX		CC	
DT	20-NOV-2003 (first entry)	CC	
XX		CC	
DE	Engineered human DJ11 protein SEQ ID NO:1.	CC	
XX		CC	
KW	DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;	CC	
KW	antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;	CC	
KW	antibacterial; immunosuppressive; antirheumatic; antiarthritic;	CC	
KW	nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;	CC	
KW	acute pancreatitis; pulmonary injury; allergy-induced protease release;	CC	
KW	deep vein thrombosis; myocardial infarction; shock; septic shock;	CC	
KW	hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;	CC	
KW	idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;	CC	
KW	chronic inflammatory bowel disease, psoriasis.	CC	

New engineered human Kunitz-type protease inhibitor for diagnosing, preventing or treating conditions associated with excessive proteinase activity, e.g. inflammation, pulmonary injuries, myocardial infarction or hemorrhage.

Claim 5; Page 69-70; 87pp; English.

The present invention describes an isolated, purified or recombinant DJ11 polypeptide comprising a Kunitz-type protease inhibitor domain or its biologically active portion. The polypeptide comprises at least 98 % identity to residues 77-127 of a 131 amino acid sequence (S1, see ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic, anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive, antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary activities, and can be used as a protease inhibitor and in gene therapy. Composition and methods from the present invention can be used in diagnosing, preventing or treating conditions associated with excessive proteinase activity, such as acute pancreatitis, pulmonary injury, allergy-induced protease release, deep vein thrombosis, myocardial infarction, shock (including septic shock), hyperfibrinolytic haemorrhage, and especially, inflammatory disorders (e.g. emphysema, idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis, chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may be used in preserving platelet function, organ preservation or in wound healing. The polynucleotide sequence encoding DJ11 may be used as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and as targets for pharmaceutical intervention. The present sequence represents an engineered human DJ11 protein from the present invention.

XX SQ Sequence 131 AA;
Query Match 100.0%; Score 302; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.1e-30;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
RESULT 3
ADA19811
ID ADA19811 standard; protein; 131 AA.
XX AC ADA19811;
XX DT 20-NOV-2003 (first entry)
XX DE Engineered human DJ11 protein SEQ ID NO:12.
XX AC DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX OS Synthetic.
OS Homo sapiens.
XX WO2003070770-A2.
XX 28-AUG-2003.
XX 18-FEB-2003; 2003WO-EP001629.
XX 21-FEB-2002; 2002US-0358683P.
XX (GENE-) GENEPROT INC.
XX Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX Disclosure; Page 84; 87pp; English.
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may

CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents an engineered human DJ11 protein from the
CC present invention.
XX SQ Sequence 131 AA;

Query Match 100.0%; Score 302; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.1e-30;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127

RESULT 4
ADA19814
ID ADA19814 standard; protein; 131 AA.
XX AC ADA19814;
XX DT 20-NOV-2003 (first entry)
XX DE Human DJ11 protein SEQ ID NO:15.
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

XX OS Homo sapiens.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may

CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a human DJ11 protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.

XX SQ Sequence 131 AA;

Query Match 96.7%; Score 292; DB 7; Length 131;

Best Local Similarity 98.0%; Pred. No. 7.5e-29;

Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51

DB 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 127

RESULT 5

ADA19815

ID ADA19815 standard; protein; 136 AA.

XX AC ADA19815;

XX DT 20-NOV-2003 (first entry)

XX DE Mouse DJ11 protein SEQ ID NO:16.

XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;

XX KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;

XX KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;

XX KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;

XX KW acute pancreatitis; pulmonary injury; allergy-induced protease release;

XX KW deep vein thrombosis; myocardial infarction; shock; septic shock;

XX KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;

XX KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;

XX KW chronic inflammatory bowel disease; psoriasis.

XX OS Mus musculus.

XX XX WO2003070770-A2.

XX XX 28-AUG-2003.

XX XX 18-FEB-2003; 2003WO-EP001629.

XX XX 21-FEB-2002; 2002US-0358683P.

XX XX (GENE-) GENEPROT INC.

XX XX Bouquelaret L, Bairoch A, Niknejad A;

XX XX WPI; 2003-663849/62.

XX XX New engineered human Kunitz-type protease inhibitor for diagnosing,

XX XX preventing or treating conditions associated with excessive proteinase

XX XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or

XX XX hemorrhage.

XX XX Disclosure; Fig 1; 87pp; English.

XX XX The present invention describes an isolated, purified or recombinant DJ11

XX XX polypeptide comprising a Kunitz-type protease inhibitor domain or its

XX XX biologically active portion. The polypeptide comprises at least 98 %

XX XX identity to residues 77-127 of a 131 amino acid sequence (S1, see

XX XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see

XX XX ADA19801). DJ11 has antinflammatory, antiallergic, thrombolytic,

XX XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,

CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a mouse DJ11 protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.

XX SQ Sequence 136 AA;

Query Match 74.2%; Score 224; DB 7; Length 136;

Best Local Similarity 66.7%; Pred. No. 3.2e-20;

Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51

DB 77 CSMPOEAGPCLAYLPRWYNNQETDLCTEFYGGCGQNNNFPSEGITVVC 127

RESULT 6

AAW75257

ID AAW75257 standard; protein; 51 AA.

XX AC AAW75257;

XX DT 29-JAN-1999 (first entry)

XX DE Fragment of human secreted protein encoded by gene 24.

XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;

XX KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

XX KW developmental abnormality; fetal deficiency; blood; allergy; renal;

XX KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

XX KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

XX KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

XX KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

XX KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX OS Homo sapiens.

XX XX WO9840483-A2.

XX XX 17-SEP-1998.

XX XX 12-MAR-1998; 98WO-US004858.

XX XX 14-MAR-1997; 97US-0040710P.

XX XX 14-MAR-1997; 97US-0040762P.

XX XX 30-MAY-1997; 97US-0048100P.

XX XX 30-MAY-1997; 97US-0048189P.

XX XX 30-MAY-1997; 97US-0048357P.

XX XX 30-MAY-1997; 97US-0050934P.

XX XX 06-JUN-1997; 97US-0048970P.

XX XX 05-SEP-1997; 97US-0057765P.

XX XX 19-DEC-1997; 97US-0068368P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

XX XX Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM,

XX XX Ferrie AM;

XX XX WPI; 1998-520811/44.

XX XX N-PSDB; AAV34309.

XX Isolated human poly:nucleotide(s) encoding secretory peptide(s) - used to
 PT develop products for the diagnosis and treatment of e.g. inflammation,
 PT cancers, CNS disorders or immune system disorders.

XX Disclosure; Page 24; 201pp; English.

XX This sequence represents a fragment of a secreted human protein encoded
 CC by the nucleic acid molecule designated Gene 24 (AAV34309). The gene can
 CC be used to generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of
 CC the fused protein as compared to the human protein only. The invention
 CC relates to 28 novel genes and their fragments (nucleic acid sequences:
 CC AAV34286-V34325; amino acid sequences AAV75196-W75235) which are useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. Also, pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 28 polynucleotides, based on
 CC which tissues they are most highly expressed in (see AAV34286 for
 CC described uses)

XX Sequence 51 AA;

Query Match 72.5%; Score 219; DB 2; Length 51;
 Best Local Similarity 68.6%; Pred. No. 4.7e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEALCLVTC 51

DB 1 CEMPKETGFLAYFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 51

RESULT 7

AAE27025

ID AAE27025 standard; protein; 51 AA.

AC AAE27025;

DT 13-DEC-2002 (first entry)

DE Human gene 24 encoded secreted protein variant, SEQ ID NO:118.

XX Human: immunodeficiency; X-linked agammaglobulinemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropic; vulnary; cytostatic; nootropic; cardiant;
 KW anti-HIV; tranquiliser; gout; antiparasitic.

OS Homo sapiens.

XX US2002077287-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00852659.

XX 11-SEP-1998; 98US-00152060.

XX (RUBE/) RUBEN S M.

XX (ROSE/) ROSEN C A.

XX (LIYI/) LI Y.

XX (ZENG/) ZENG Z.

XX (KYAW/) KYAW H.

XX (FISC/) FISCHER C L.

XX (LIHH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEIY/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX WPI; 2002-598780/64.

XX Novel human secreted polypeptides and polynucleotides for diagnosing,

PT preventing, treating immune, hyperproliferative, cardiovascular,

PT neurological, reproductive disorders and identifying modulators of

PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted

CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.

CC AAE27000-AAE27025 represent human secreted protein fragments or their

CC variants. The secreted proteins and genes are useful for preventing,

CC treating or ameliorating medical conditions, e.g., by protein or gene

CC therapy. Specific uses are described for each of the 28 genes, based on

CC the tissues in which they are most highly expressed and include

CC developing products for the diagnosis or treatment of immunodeficiencies,

CC e.g., X-linked agammaglobulinemia, B cell immunodeficiencies, severe

CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus

CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune

CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,

CC Grave's disease, diabetes mellitus, dermatitis, inflammatory bowel

CC including septic shock, sepsis, reperfusion injury, inflammatory disorders

CC disease, Crohn's disease, haematopoietic disorders e.g., inflammatory

CC e.g.; asthma and allergy, gastrointestinal disorders e.g., inflammatory

CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and

CC breast), central nervous system (CNS) disorders e.g., ischaemic brain

CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's

CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,

CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,

CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,

CC sarcoidosis and allogenic transplant rejection, blood-related disorder

CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative

CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,

CC lung cancer, allergic disorders, pneumonitis, renal disorders, endocrine

CC glomerulonephritis, neurological diseases, liver disorders, endocrine

CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,

CC infectious diseases and reproductive system disorders e.g. endometriosis.

CC The present sequence represents a human secreted protein variant of the

CC invention

XX Sequence 51 AA;

XX Query Match 72.5%; Score 219; DB 5; Length 51;

XX Best Local Similarity 68.6%; Pred. No. 4.7e-20;

XX Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEALCLVTC 51

DB 1 CEMPKETGFLAYFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 51

RESULT 8

AAE27163

ID AAE27163 standard; protein; 51 AA.

XX AAE27163;

XX 13-DEC-2002 (first entry)

DE Human gene 24 encoded secreted protein fragment kunitz-type domain.

XX US6180607-B1.
 XX 30-JAN-2001.
 XX 05-AUG-1999; 99US-00369494.
 XX 05-AUG-1999; 99US-00369494.
 XX (DAVI/) DAVIES C.
 XX (CHEN/) CHEN D.
 XX (ROZC/) ROCZNIK S.
 XX Davies C, Chen D, Rocznik S;
 XX WPI; 2001-190860/19.
 XX Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful
 XX for treating emphysema, cystic fibrosis, adult respiratory distress
 XX syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
 XX Disclosure: Col 6; 17pp; English.
 XX
 XX The invention relates to a novel human serine protease inhibitor of the
 XX Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and
 XX AAB60634). The BTL.010 protein is thought to preferentially inhibit
 XX neutral serine proteases such as elastase and proteinase-3, relative to
 XX trypsin-like and chymotrypsin-like proteases. A substantial proportion of
 XX the BTL.010 protein Kunitz domain (AAB60631) was identified via homology
 XX searching in the GenBank high throughput genomic (HTG) DNA sequence
 XX database using the Kunitz domain sequences AAB60630, and was confirmed as
 XX being novel using the Kunitz domain sequences AAB60632, and AAB60633.
 XX This sequence information was extended to provide a larger region of
 XX BTL.010 protein sequence data (AAB60634) by identifying an open reading
 XX frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain
 XX fragment in a 399 bp fragment of human genomic DNA (AAF59750).
 XX corresponding to bases 16016-16414 of GenBank accession number AC004846.
 XX The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from
 XX the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical
 XX compositions comprising it, may be used for inhibiting protease activity,
 XX particularly that of leukocyte elastase, in the prevention, treatment or
 XX amelioration of medical conditions such as emphysema, idiopathic
 XX pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,
 XX rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010
 XX compositions of the invention modulate at least one physiological
 XX condition such as platelet activation, blood coagulation, neutrophil
 XX activation, or monocyte activation. BTL.010 is also useful for the
 XX prophylactic or therapeutic treatment of patients undergoing angioplasty,
 XX and for the treatment of inflammatory diseases and diseases involving
 XX lung and vascular injury. The present sequence represents a Kunitz domain
 XX sequence used to identify the BTL.010 protein
 XX Sequence 58 AA;
 Query Match 72.5%; Score 219; DB 4; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 Db 5 CEMPKEGTGCLAYFLHWYDKKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55
 RESULT 12
 ADF41997
 ID ADF41997 standard; protein; 58 AA.
 XX ADF41997;
 XX
 XX 12-FEB-2004 (first entry)
 XX Human CAB37 Kunitz domain peptide.
 XX

KW albumin fusion; Kunitz domain; cytostatic; haemostatic;
 KW hereditary angioedema; cancer; bleeding; gene therapy; human; CAB37.
 XX Homo sapiens.
 XX WO2003066824-A2.
 XX 14-AUG-2003.
 XX 07-FEB-2003; 2003WO-US003616.
 XX 07-FEB-2002; 2002US-0355547P.
 XX (AVET) AVENTIS BEHRING GMBH.
 XX (AVET) AVENTIS BEHRING LLC.
 XX (DELZ) DELTA BIOTECHNOLOGY LTD.
 XX (DYAX-) DYAX CORP.
 XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
 XX Ley AC;
 XX WPI; 2003-731497/69.
 XX
 XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
 XX useful for preparing a composition for treating a patient with hereditary
 XX angioedema or angioedema-related disease, cancer or bleeding disorder.
 XX Disclosure; Page 20; 110pp; English.
 XX
 XX The invention relates to a novel albumin fusion protein comprising a
 XX Kunitz domain peptide or its fragment or variant and an albumin or its
 XX fragment or variant. The fusion protein of the invention demonstrates
 XX cytostatic and haemostatic activities and may be useful for preparing a
 XX composition for treating a patient with hereditary angioedema, an
 XX angioedema-related disease, cancer, a cancer-related disease or a
 XX bleeding disorder, as well as during gene therapy procedures. The current
 XX sequence is that of the human Kunitz domain peptide of the invention.
 XX Sequence 58 AA;
 Query Match 72.5%; Score 219; DB 7; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 Db 5 CEMPKEGTGCLAYFLHWYDKKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55
 RESULT 13
 ADL16838
 ID ADL16838 standard; peptide; 58 AA.
 XX ADL16838;
 XX
 XX 06-MAY-2004 (first entry)
 XX Human Kunitz domain (KD) peptide.
 XX
 XX BTL.010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;
 XX idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 XX cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 XX inflammatory disease; oxidative burst; platelet activation;
 XX blood coagulation; gene therapy; human; KD.
 XX Homo sapiens.
 XX US6689582-B1.
 XX 10-FEB-2004.
 XX 12-MAY-2000; 2000US-00569670.
 XX

PS 05-AUG-1999; 99US-00369494.
XX (FARB) BAYER PHARM CORP.
PA Davies C, Chen D, Roczniak S;
XX WPI; 2004-141424/14.
XX New isolated polynucleotide encoding BTL010 serine proteinase, useful
PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
PT glomerulonephritis.
XX
XX Disclosure; SEQ ID NO 8; 17pp; English.
PS The invention relates to BTL010, a human serine proteinase inhibitor of
XX the Kunitz family and its corresponding nucleic acid sequences. The
XX sequences of the invention are useful for treating acid diseases, e.g.
XX emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
XX syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
XX glomerulonephritis or inflammatory diseases. The BTL010 protein is also
XX useful for preventing neutrophil and monocyte activation and formation of
XX active oxygen species during the oxidative burst of stimulated
XX granulocytes. It is also useful for reducing platelet activation and
XX blood coagulation. BTL010 DNA is useful in gene therapy. The present
XX sequence is human Kunitz domain (KD) peptide.
XX
XX Sequence 58 AA;
SQ
Query Match 72.5%; Score 219; DB 8; Length 58;
Best Local Similarity 68.6%; Pred. No. 5.4e-20;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGCQGNNNNFQTEAICLVTC 51
DB 5 CEMPKEGTCLAYFLHWWYDKKNTCSMFVYGCQGNNNNFQSKANCLNTC 55
RESULT 14
ADR89980
ID ADR89980 standard; peptide; 58 AA.
XX
XX ADR89980;
AC
DT 18-NOV-2004 (first entry)
XX
XX Human CAB37 protein kunitz domain peptide.
DE
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytostatic; haemostatic; CAB37 protein; human.
XX
XX Homo sapiens.
OS
XX
XX US2004171794-A1.
PN
XX
XX 02-SEP-2004.
PD
XX
XX 07-FEB-2003; 2003US-00361997.
PF
XX
XX 07-FEB-2003; 2003US-00361997.
PR
XX
XX (LADN/) LADNER R C.
PA (LEYA/) LEY A C.
XX
XX Ladner RC, Ley AC;
PI
XX WPI; 2004-625120/60.
DR
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
XX

PS Disclosure; SEQ ID NO 5; 123pp; English.
XX The invention relates to proteins comprising kunitz domain peptide,
CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cytostatic and haemostatic agent. The present sequence is the human CAB37
CC protein (A4) kunitz domain peptide. This sequence is used in the
CC invention.
XX
XX Sequence 58 AA;
SQ
Query Match 72.5%; Score 219; DB 8; Length 58;
Best Local Similarity 68.6%; Pred. No. 5.4e-20;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGCQGNNNNFQTEAICLVTC 51
DB 5 CEMPKEGTCLAYFLHWWYDKKNTCSMFVYGCQGNNNNFQSKANCLNTC 55
RESULT 15
AAE13093
ID AAE13093 standard; peptide; 64 AA.
XX
XX AAE13093;
AC
DT 28-JAN-2002 (first entry)
XX
XX Human serine proteinase inhibitor BTL009 C-terminal peptide.
DE
XX Human; BTL009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
XX Homo sapiens.
OS
XX
XX US6294648-B1.
PN
XX
XX 25-SEP-2001.
PD
XX
XX 20-JUL-1999; 99US-00358569.
PF
XX
XX 20-JUL-1999; 99US-00358569.
PR
XX
XX (FARB) BAYER CORP.
PA
XX
XX Delaria K, Roczniak S, Davies C;
PI
XX WPI; 2001-662224/76.
DR
XX
XX New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
PT
XX
XX Disclosure; Col 6; 16pp; English.
PS The invention relates to human BTL009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL009
CC protein is useful for treating emphysema, cystic fibrosis, rheumatoid
CC adult respiratory distress syndrome, idiopathic pulmonary fibrosis,
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL009 is useful for reducing platelet activation and blood coagulation
CC

XX 02-FEB-2001; 2001US-0265583P.
XX (RUBS/) RUBEN S M.
XX (ROSE/) ROSEN C A.
XX (LIYY/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIHH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2002-574454/61.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
XX Disclosure; Page 17; 209pp; English.
XX
XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment referred to in the disclosure of the invention
XX
XX Sequence 102 AA;
SQ
Query Match 72.5%; Score 219; DB 5; Length 102;
Best Local Similarity 68.6%; Pred. No. 1e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQEAICLVTC 51
DB 46 CEMPKEGTGCLAYFLHWYDKDKNTCSMFYGGCGQNNNNFQSKANCLNTC 96
RESULT 18
ABU65039
ID ABU65039 standard; peptide; 102 AA.
XX
XX AC ABU65039;
XX
XX DT 15-MAY-2003 (first entry)
XX
XX Human secreted protein gene 24, protein #3.
XX
XX Secreted protein; immunodeficiency; multiple sclerosis;

KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
KW body height; hair colour; human.
XX
XX Homo sapiens.
XX
XX US2002172994-A1.
XX
XX 21-NOV-2002.
XX
XX 11-MAY-2001; 2001US-00852797.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057768P.
XX 19-DEC-1997; 97US-0068368P.
XX 12-MAR-1998; 98WO-US004858.
XX 11-SEP-1998; 98US-00152060.
XX 02-FEB-2001; 2001US-0265583P.
XX (RUBS/) RUBEN S M.
XX (ROSE/) ROSEN C A.
XX (LIYY/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIHH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2003-310989/30.
XX
XX New human secreted polypeptides and polynucleotides for diagnosing,
PT prognosing, preventing and treating immune, hyperproliferative, liver,
PT kidney, reproductive disorders and for identifying modulators of
PT therapeutic use.
XX
XX Disclosure; Page 16; 209pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an amino acid
CC sequence at least 95% identical to sequence of 28 human secreted
CC proteins, their fragment, polypeptide domain, epitope, secreted form,
CC variant, allelic variant, or species homologue, or the encoded sequence
CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
CC acids, recombinant vectors, host cells, antibodies, and genes. The
CC proteins and nucleic acids are useful for diagnosing, preventing,
CC treating, prognosing or ameliorating a medical condition e.g.
CC immunodeficiencies (e.g. X-linked agammaglobulinemia, B cell
CC immunodeficiencies, severe combined immunodeficiencies), autoimmune

CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia, multiple
 CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
 CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
 CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
 CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
 CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
 CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
 CC injury and/or stroke, traumatic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
 CC dementia, and prion disease), cardiovascular disorders (e.g.
 CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
 CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
 CC pancreatitis, sarcoidosis, dermatitis, allogeneic transplant rejection),
 CC blood-related disorders (thrombosis, arterial thrombosis),
 CC hyperproliferative disorders, renal disorders (e.g. acute
 CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
 CC hyperthyroidism, hypoparathyroidism, liver diseases and disorders,
 CC reproductive system disorders (e.g. endometriosis), infectious diseases,
 CC and pancreatic disorders. Many other diseases and disorders are listed in
 CC the specification. They also useful as a vaccine adjuvant. Further they
 CC are useful to enhance or inhibit complement mediated cell lysis, for
 CC stimulating wound and tissue repair, angiogenesis, and the repair of
 CC vascular or lymphatic diseases or disorders. They are also useful to
 CC prevent hair loss, to modulate mammalian characteristics such as body
 CC height, weight, hair colour, and to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors or other nutritional components. The proteins are
 CC also useful for identifying binding partners. The present sequence
 CC represents a secreted protein of the invention

XX Sequence 102 AA;

Query Match 72.5%; Score 219; DB 6; Length 102;

Best Local Similarity 68.6%; Pred. No. 1e-19;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPEAGCLASIPHHWNKTKTCTSEFIYGGCGQNNNFQTEALCLVTC 51

DB 46 CEMPKEGTCLAYFLHWYDKDKNTCSMFYGGCGQNNNFQSKANCLNTC 96

RESULT 19

ADG89848

ID ADG89848 standard; protein; 102 AA.

XX AC ADG89848;

DT 11-MAR-2004 (first entry)

XX DE Human secreted protein gene 24 protein #6.

XX Secreted protein; gene therapy; neural disorder; immune system disorders;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; cancer; systemic lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
 KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
 KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
 KW myocardial infarction; AIDS; infection; human.

XX OS Homo sapiens.

XX US2003225009-A1.

XX PD 04-DEC-2003.

XX PF 30-JAN-2002; 2002US-00058993.

XX PR 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0050934P.
 PR 06-JUN-1997; 97US-0048970P.
 PR 05-SEP-1997; 97US-0057765P.
 PR 19-DEC-1997; 97US-0068368P.
 PR 12-MAR-1998; 98WO-US004858.
 PR 11-SEP-1998; 98US-00152060.
 PR 02-FEB-2001; 2001US-0265583P.
 PR 11-MAY-2001; 2001US-0085285P.
 PR 11-MAY-2001; 2001US-00852797.
 PR 11-MAY-2001; 2001US-00853161.

XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (HAST/) HASTINGS G A.

XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM, Hastings GA;

XX WPI; 2004-042167/04.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
 PT treating diseases associated with aberrant expression or activity of the
 PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

XX Disclosure; SEQ ID NO 121; 320pp; English.

CC The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridisable to the nucleotide sequences, a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
 CC or epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the specification, a polynucleotide which
 CC encodes a species homologue of the above amino acid sequences, a
 CC polynucleotide capable of hybridising under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridise
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant vector
 CC comprising the above nucleic acid molecule, making a recombinant host
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC comprising a sequence that is at least 95% identical to the polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosing or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular
 CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,

CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.
XX
SQ Sequence 102 AA;
Query Match 72.5%; Score 219; DB 8; Length 102;
Best Local Similarity 68.6%; Pred. No. 1e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPOBAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 46 CEMPRTGFCFLAYFLHWWYDKDNTCSMFYVGGCGQNNNNFQSKANCLNTC 96
RESULT 20
AAE27094
ID AAE27094 standard; protein; 117 AA.
XX
AC AAE27094;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human secreted protein #1.
XX
KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotrophic; vulnery; cytotatic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.
XX
OS Homo sapiens.
XX
XX
XX US200207287-A1.
XX
XX 20-JUN-2002.
XX
XX 11-MAY-2001; 2001US-00852659.
XX
XX 11-SEP-1998; 98US-00152060.
XX
XX (RUBE/) RUBEN S M.
XX (ROSE/) ROSEN C A.
XX (LIYV/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIHH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
XX Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
XX Ferrie AM;
XX
XX WPI; 2002-598780/64.

XX
PT Novel human secreted polypeptides and polynucleotides for diagnosing,
PT preventing, treating immune, hyperproliferative, cardiovascular, of
PT neurological, reproductive disorders and identifying modulators of
PT therapeutic use.
XX
PS Disclosure; Page 16; 209pp; English.
XX
AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
CC AAE27000-AAE27025 represent human secreted protein fragments or their
CC variants. The secreted proteins and genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Specific uses are described for each of the 28 genes, based on
CC the tissues in which they are most highly expressed and include
CC developing products for the diagnosis or treatment of immunodeficiencies,
CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
CC Grave's disease, diabetes mellitus, dermatitis, inflammatory bowel
CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
CC sarcoidosis and allogenic transplant rejection, blood-related disorder
CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
CC disorders, respiratory disorders e.g., rhinitis, sinusitis, tonsillitis,
CC lung cancer, allergic disorders, pneumonitis, renal disorders, e.g., acute
CC glomerulonephritis, neurological diseases, liver disorders, endocrine
CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
CC infectious diseases and reproductive system disorders e.g., endometriosis.
XX The present sequence represents a human secreted protein of the invention
SQ Sequence 117 AA;
Query Match 72.5%; Score 219; DB 5; Length 117;
Best Local Similarity 68.6%; Pred. No. 1.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPOBAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 61 CEMPRTGFCFLAYFLHWWYDKDNTCSMFYVGGCGQNNNNFQSKANCLNTC 111
RESULT 21
AAE27165
ID AAE27165 standard; protein; 117 AA.
XX
AC AAE27165;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human gene 24 encoded secreted protein fragment #1.
XX
KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotrophic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnery.
XX
XX Homo sapiens.
XX
XX OS
XX US2002076756-A1.
XX
XX PN


```
XX PD 20-JUN-2002.
XX PF 11-MAY-2001; 2001US-00853161.
XX PR 02-FEB-2001; 2001US-0265583P.
XX PA (RUBE//) RUBEN S M.
XX PA (ROSE//) ROSEN C A.
XX PA (LIY//) LI Y.
XX PA (ZENG//) ZENG Z.
XX PA (KYAW//) KYAW H.
XX PA (FISC//) FISCHER C L.
XX PA (LIHH//) LI H.
XX PA (SOPP//) SOPPET D R.
XX PA (GENT//) GENTZ R L.
XX PA (WEI//) WEI Y.
XX PA (MOOR//) MOORE P A.
XX PA (YOUN//) YOUNG P E.
XX PA (GREE//) GREENE J M.
XX PA (FERR//) FERRIE A M.
XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX WPI; 2002-574454/61.
XX DR New nucleic acid molecules encoding 28 human secreted proteins, useful
XX PT for diagnosing, preventing, treating or ameliorating medical conditions
XX PT and as food additives or preservatives.
XX PS Disclosure; Page 17; 209pp; English.
XX CC AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
XX CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
XX CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
XX CC and their corresponding secreted proteins are useful for preventing,
XX CC treating or ameliorating medical conditions, e.g., by protein or gene
XX CC therapy. Secreted protein sequences of the invention are useful for the
XX CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
XX CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
XX CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
XX CC angiotensin), cardiovascular disorders (e.g. cardiac arrest), nervous
XX CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
XX CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
XX CC polypeptides can also be used to aid wound healing and epithelial cell
XX CC proliferation, to prevent skin aging due to sunburn, to maintain organs
XX CC before transplantation, for supporting cell culture of primary tissues,
XX CC to regenerate tissues and in chemotaxis. They can also be used as food
XX CC additives or preservative to increase or decrease storage capabilities,
XX CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
XX CC and other nutritional components. The present sequence represents a human
XX CC secreted protein fragment referred to in the disclosure of the invention
XX SQ Sequence 117 AA;
Query Match 72.5%; Score 219; DB 5; Length 117;
Best Local Similarity 68.6%; Pred. No. 1.2e-19;
Matches 35; Conservative Indels 0; Gaps 0;
QY 1 CSMPEAGPCLASIPHWYNTKTKTCSFTYGGCGNNNNFOTEAICLVTC 51
DB 61 CEMPKEGTGFLAYFLHWYDKDNTCSMFVYGGCGNNNNFQSKANCLNTC 111
RESULT 22
ABU65038
ID ABU65038 standard; protein; 117 AA.
XX AC ABU65038;
XX DT 15-MAY-2003 (first entry)
XX XX Human secreted protein gene 24, protein #4.
XX DE Secreted protein; immunodeficiency; multiple sclerosis;
XX KW severe combined immunodeficiency; autoimmune disorder; cancer;
XX KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
XX KW inflammatory condition; septic shock; inflammatory bowel disease;
XX KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
XX KW gastrointestinal disorder; central nervous system disorder;
XX KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
XX KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
XX KW blood-related disorder; thrombosis; acute glomerulonephritis; renal disorder;
XX KW hyperproliferative disorder; liver disease; reproductive system disorder;
XX KW endocrine disorder; infectious disease; pancreatic disorder; vaccine;
XX KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
XX KW body height; hair colour; human.
XX OS Homo sapiens.
XX XX US2002172994-A1.
XX PN 21-NOV-2002.
XX PD 11-MAY-2001; 2001US-00852797.
XX PF 14-MAR-1997; 97US-0040710P.
XX PR 14-MAR-1997; 97US-0040762P.
XX PR 30-MAY-1997; 97US-0048100P.
XX PR 30-MAY-1997; 97US-0048189P.
XX PR 30-MAY-1997; 97US-0048357P.
XX PR 30-MAY-1997; 97US-0050934P.
XX PR 06-JUN-1997; 97US-0048970P.
XX PR 05-SEP-1997; 97US-0057765P.
XX PR 19-DEC-1997; 97US-0068368P.
XX PR 12-MAR-1998; 98MO-US004858.
XX PR 11-SEP-1998; 98US-00152060.
XX PR 02-FEB-2001; 2001US-0265583P.
XX PA (RUBE//) RUBEN S M.
XX PA (ROSE//) ROSEN C A.
XX PA (LIY//) LI Y.
XX PA (ZENG//) ZENG Z.
XX PA (KYAW//) KYAW H.
XX PA (FISC//) FISCHER C L.
XX PA (LIHH//) LI H.
XX PA (SOPP//) SOPPET D R.
XX PA (GENT//) GENTZ R L.
XX PA (WEI//) WEI Y.
XX PA (MOOR//) MOORE P A.
XX PA (YOUN//) YOUNG P E.
XX PA (GREE//) GREENE J M.
XX PA (FERR//) FERRIE A M.
XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX WPI; 2003-310989/30.
XX DR New human secreted polypeptides and polynucleotides for diagnosing,
XX PT prognosing, preventing and treating immune, hyperproliferative, liver,
XX PT kidney, reproductive disorders and for identifying modulators of
XX PT therapeutic use.
XX PS Disclosure; Page 16; 209pp; English.
XX CC The invention relates to an isolated polypeptide comprising an amino acid
XX CC sequence at least 95% identical to sequence of 28 human secreted
XX CC proteins, their fragment, polypeptide domain, epitope, secreted form,
XX CC variant, allelic variant, or species homologue, or the encoded sequence
XX CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
XX CC acids, recombinant vectors, host cells, antibodies, and genes. The
```


CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.

XX
SQ Sequence 117 AA;

Query Match 72.5%; Score 219; DB 8; Length 117;
Best Local Similarity 68.6%; Pred. No. 1.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
61 CEMPKEGTGCLAYFLHWYDKDNTCSMFYVGGCGGNNNFQSKANCLNTC 111

DB
1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
77 CEMPKEGTGCLAYFLHWYDKDNTCSMFYVGGCGGNNNFQSKANCLNTC 127

RESULT 24
AAW75219

ID AAW75219 standard; protein; 133 AA.

XX
AC AAW75219;

XX
DT 29-JAN-1999 (first entry)

XX
DE Human secreted protein encoded by gene 24 clone HTEBY11.

XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX
OS Homo sapiens.

XX
PN WO98040483-A2.

XX
PD 17-SEP-1998.

XX
PF 12-MAR-1998; 98WO-US004858.

XX
PR 14-MAR-1997; 97US-0040710P.

XX
PR 14-MAR-1997; 97US-0040762P.

XX
PR 30-MAY-1997; 97US-0048100P.

XX
PR 30-MAY-1997; 97US-0048189P.

XX
PR 30-MAY-1997; 97US-0048357P.

XX
PR 30-MAY-1997; 97US-0050934P.

XX
PR 06-JUN-1997; 97US-0048970P.

XX
PR 05-SEP-1997; 97US-0057765P.

XX
PR 19-DEC-1997; 97US-0068368P.

XX
(HUMA-) HUMAN GENOME SCI INC.

XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;
PI Ferrie AM;

XX
WPI: 1998-520811/44.

XX
DR N-PSDB; AAV34309.

XX
PT Isolated human polynucleotide(s) encoding secretory peptide(s) - used to
PT develop products for the diagnosis and treatment of e.g. inflammation,
PT cancers, CNS disorders or immune system disorders.

XX
PS Claim 1; Page 167-168; 201pp; English.

XX
CC This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAV34277) for increasing the stability of the fused protein
CC as compared to the human protein only. The invention relates to 28 novel
CC genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino
CC acid sequences AAW75196-W75235) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 28 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAV34286 for described uses)

XX
SQ Sequence 133 AA;

Query Match 72.5%; Score 219; DB 2; Length 133;
Best Local Similarity 68.6%; Pred. No. 1.3e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
77 CEMPKEGTGCLAYFLHWYDKDNTCSMFYVGGCGGNNNFQSKANCLNTC 127

DB
1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
77 CEMPKEGTGCLAYFLHWYDKDNTCSMFYVGGCGGNNNFQSKANCLNTC 127

RESULT 25
AAE26982

ID AAE26982 standard; protein; 133 AA.

XX
AC AAE26982;

XX
DT 13-DEC-2002 (first entry)

XX
DE Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:34.

XX
KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotropic; vulnery; cytostatic; nootropic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT Peptide 1..21

FT Protein 22..133

FT /label= Signal_peptide

FT /note= "Human mature secreted protein"

XX
PN US2002077287-A1.

XX
PD 20-JUN-2002.

XX
PF 11-MAY-2001; 2001US-00852659.

XX
PR 11-SEP-1998; 98US-00152060.

XX
(RUBE/) RUBEN S M.

XX
(ROSE/) ROSEN C A.

XX
(LIYY/) LI Y.

XX
(ZENG/) ZENG Z.

XX
(KYAW/) KYAW H.

XX
(FISC/) FISCHER C L.

XX (INCY-) INCYTE CORP.
 XX Schmidt JP, Wright RJ, Bruns CM, Marianovic MM, Shen F;
 PI Harchorne TA, Suchorski WT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patry S, Shi X, Suarez CJ;
 XX WPI; 2004-329368/30.
 DR N-PSDB; ACN43755.
 XX
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 XX Sequence 179 AA;
 Query Match 72.5%; Score 219; DB 8; Length 179;
 Best Local Similarity 68.6%; Pred. No. 1.8e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMPOAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
 DB 77 CEMPKETGPCLAYFLHWYDKDNTCSMFYGGCGGNNNNFQSKANCLNTC 127
 RESULT 32
 ADAL19813
 ID ADAL19813 standard; protein; 134 AA.
 XX ADAL19813;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Mouse EPPIN protein SEQ ID NO:14.
 DE
 XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis; EPPIN.
 XX
 OS Mus musculus.
 XX
 PN WO2003070770-A2.

XX 28-AUG-2003.
 PD
 XX 18-FEB-2003; 2003WO-EP001629.
 PF
 XX 21-FEB-2002; 2002US-0358683P.
 PR
 XX (GENE-) GENEPROT INC.
 PA
 XX Bougueleret L, Bairoch A, Niknejad A;
 PI WPI; 2003-663849/62.
 DR
 XX
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 PT
 XX Disclosure; Fig 1; 87pp; English.
 PS
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a mouse EPPIN protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.
 XX
 XX Sequence 134 AA;
 Query Match 62.3%; Score 188; DB 7; Length 134;
 Best Local Similarity 54.9%; Pred. No. 1.1e-15;
 Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 QY 1 CSMPOAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
 DB 77 CSLPKDSGYCMAYFRWFWENKSTQVFYGGCGGNNNNFQSQICQAC 127
 RESULT 33
 AAEL13096
 ID AAEL13096 standard; peptide; 43 AA.
 XX
 XX AAEL13096;
 AC
 XX 28-JAN-2002 (first entry)
 DT
 XX Human serine proteinase inhibitor BTL.009 peptide fragment #2.
 XX
 DE Human; BTL.009 protein; serine proteinase inhibitor; cyclostatic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.
 XX
 XX

RESULT 37	
AAR991146	standard; protein; 58 AA.
XX	
XX	AAR991146;
XX	
XX	12-FEB-1997 (first entry)
XX	
XX	Aprotinin-like Kunitz domain.
XX	
XX	Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW	connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW	alpha antitrypsin; respiratory disorder; cystic fibrosis;
KW	smokers emphysema.
XX	
XX	Synthetic.
OS	
XX	WO9620278-A2.
PN	
XX	04-JUL-1996.
PD	
XX	
XX	15-DEC-1995; 95WO-US016349.
PF	
XX	
XX	16-DEC-1994; 94US-00358160.
PR	
XX	
XX	(PROT-) PROTEIN ENG CORP.
PA	
XX	
PI	Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX	
XX	WPI; 1996-321851/32.
DR	
XX	
XX	New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT	-like Kunitz domain for treating, e.g. cystic fibrosis or other
PT	respiratory disorders.
PT	
XX	
XX	Example 23; Page 47; 105pp; English.
PS	
XX	
XX	Genetically engineered human derived Kunitz domains can be used to
CC	inhibit human neutrophil elastase, an enzyme involved in the elimination
CC	of pathogens and the restructuring of connective tissue. In cases of
CC	reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC	antitrypsin), or the inactivation of API by oxidation (smokers
CC	emphysema), extensive destruction of the lung tissue may result from
CC	uncontrolled elastolytic activity of human neutrophil elastase. Other
CC	respiratory disorders such as cystic fibrosis are thought to be caused by
CC	human neutrophil elastase release by neutrophils. The genetically
CC	engineered human derived Kunitz domains can be used to treat such
CC	respiratory disorders. See AAR991146-R99211
XX	
XX	
SQ	Sequence 58 AA;
Query Match	55.3%; Score 167; DB 2; Length 58;
Best Local Similarity	56.9%; Pred. No. 2.1e-13;
Matches 29; Conservative	5; Mismatches 17; Indels 0; Gaps 0;
Qy	1 CSMQEGAGPCCLASPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
	: : : : : : : : : : : : : : :
	: : : : : : : : : : : : : : :
Db	5 CLLPAETGPCRAMIPRFYFNKSGKCEPFIYGGCGGNANNNFKTEBECRRTC 55
RESULT 38	
AAE13092	
ID	AAE13092 standard; peptide; 54 AA.
XX	
XX	AAE13092;
XX	
XX	28-JAN-2002 (first entry)
DT	
XX	
XX	Trypsin inhibitor peptide.
DE	
XX	
XX	BTI.009 protein; serine proteinase inhibitor; cytostatic; therapeutic;
KW	nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW	


```
DR N-PSDB; AAT79079.
XX
PT New protease inhibitor - useful for treating diseases involving elastase.
XX
XX Claim 2; Page 2; 37pp; Japanese.
XX
CC This is the amino acid sequence of a construct comprising the anti-
CC trypsin inhibitor UTI Kunitz domain 1 (AAT79077) linked at the N-terminus
CC to the peptide Arg-Pro-Asp-Phe. The recombinant sequence is used in the
CC construction of a novel protease inhibitor where the active site residues
CC of the Kunitz domain 1 (see AAT79080, AAT79081 and AAT79083) are
CC substituted. The modified protease inhibitors are targeted to the
CC protease elastase, especially from neutrophils and can be used to treat
CC diseases associated with elastase. Modifications of the active site were
CC done by site directed mutagenesis
XX
SQ Sequence 55 AA;
  Query Match      53.3%; Score 161; DB 2; Length 55;
  Best Local Similarity 51.0%; Pred. No. 1.1e-12;
  Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 COLGYSAGPCIAFFRYFYNGTSMACQTFVYGGCMGNGNMFVTEKCLQTC 55

RESULT 42
AAR27402
ID AAR27402 standard; peptide; 58 AA.
XX
AC AAR27402;
XX
DT 07-OCT-2004 (revised)
DT 25-MAR-2003 (revised)
DT 20-MAY-1998 (first entry)
XX
DE Human neutrophil elastase inhibitor MUTQE.
XX
KW Kunitz Domain serine protease inhibitor; mutant;
KW Bovine pancreatic trypsin inhibitor.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..4
FT /note= "mutated from ITI-D1 (KEDS) -> (RPDF)"
FT Region 15..19
FT /note= "mutated from ITI-D1 (MGMTS) -> (VAMFP)"
FT Region 34
FT /note= "mutated from ITI-D1 (Q) -> (V)"
XX
XX WO215605-A2.
XX
XX 17-SEP-1992.
XX
XX 28-FEB-1992; 92WO-US001501.
XX
XX 01-MAR-1991; 91US-00664989.
XX 17-JUN-1991; 91US-00715834.
XX
XX (PROT-) PROTEIN ENG CORP.
XX
XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX WPI; 1992-331666/40.
XX
XX New peptide inhibitors of elastase or cathepsin G - are e.g. mutants of
XX Kunitz Domain serine protease inhibitors, useful for treating and
XX preventing conditions caused by excessive neutrophil elastase or
XX cathepsin G.
XX
XX Example; Page 103; 126pp; English.
XX
XX
XX The sequence is that of a mutant of inter-alpha trypsin inhibitor-D1 (ITI
XX -D1) MUTQE which is an inhibitor with very strong (Kd<10-11) specific
XX binding activity for human neutrophil elastase (hNE). It can be used for
XX the treatment or prophylaxis of a condition caused by excessive hNE
XX activity, e.g. inflammation, emphysema, cystic fibrosis, adult
XX respiratory distress syndrome or rheumatoid arthritis. It may also be
XX used to purify hNE. See also AAR27373-R27403 and AAR27443. (Updated on 25
XX -MAR-2003 to correct FN field.)
XX
XX Revised record issued on 07-OCT-2004 : Correction to FT field
XX
SQ Sequence 58 AA;
  Query Match      53.3%; Score 161; DB 2; Length 58;
  Best Local Similarity 51.0%; Pred. No. 1.2e-12;
  Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 COLGYSAGPCVAMPFRFYNGTSMACQTFVYGGCMGNGNMFVTEKDLQTC 55

RESULT 43
AAR99160
ID AAR99160 standard; protein; 58 AA.
XX
AC AAR99160;
XX
DT 12-FEB-1997 (first entry)
XX
DE Genetically engineered aprotinin-like Kunitz domain (MUTQE) .
XX
KW Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alaphal antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX
OS Synthetic.
XX
XX WO9620278-A2.
XX
XX 04-JUL-1996.
XX
XX 15-DEC-1995; 95WO-US016349.
XX
XX 16-DEC-1994; 94US-00358160.
XX
XX (PROT-) PROTEIN ENG CORP.
XX
XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX WPI; 1996-321851/32.
XX
XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
XX -like Kunitz domain for treating, e.g. cystic fibrosis or other
XX respiratory disorders.
XX
XX Claim 1; Page 48; 105pp; English.
XX
XX Genetically engineered human derived Kunitz domains can be used to
XX inhibit human neutrophil elastase, an enzyme involved in the elimination
XX of pathogens and the restructuring of connective tissue. In cases of
XX reduction of the circulating alpha-1-protease inhibitor (API or alpha
XX antitrypsin), or the inactivation of API by oxidation (smokers
XX emphysema), extensive destruction of the lung tissue may result from
XX uncontrolled elastolytic activity of human neutrophil elastase. Other
XX respiratory disorders such as cystic fibrosis are thought to be caused by
XX human neutrophil elastase release by neutrophils. The genetically
XX engineered human derived Kunitz domains can be used to treat such
XX respiratory disorders. See AAR99146-R99211
XX
XX Sequence 58 AA;
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XX	AAR99158;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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XX PD 18-DEC-2003.

XX PF 06-JUN-2003; 2003WO-US017665.

XX PR 07-JUN-2002; 2002US-0387239P.

XX PR 28-AUG-2002; 2002US-0407003P.

XX PA (DYAX-) DYAX CORP.

XX PI Ladner RC, Ley AC, Hirani S, Williams A;

XX DR WPI; 2004-062190/06.

XX PT Preventing or reducing ischemia in patient involves administering to

XX PT patient composition comprising a kallikrein inhibitory polypeptide.

XX PS Disclosure; SEQ ID NO 44; 46pp; English.

XX CC The present invention describes a method (M1) for preventing or reducing

XX CC ischaemia in a patient. M1 involves administering to the patient a

XX CC composition comprising a polypeptide (I) having an amino acid sequence of

XX CC ADF71962 and inhibiting kallikrein. (I) has vasotrophic activity, and can

XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or

XX CC reducing ischaemia in a patient such as perioperative blood loss due to a

XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary

XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)

XX CC is also useful for preventing or reducing the onset of systemic

XX CC inflammatory response associated with a surgical procedure in a patient

XX CC which involves administering (I) to a patient. The present sequence is

XX CC used in the exemplification of the present invention.

XX CC Sequence 58 AA;

XX CC Query Match 53.3%; Score 161; DB 8; Length 58;

XX CC Best Local Similarity 51.0%; Pred. No. 1.2e-12;

XX CC Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFTYGGCGGNNNNFOTEALCLVTC 51

DB 5 COLGYSAGPCVAMFPRFYNGTSMACETFYGGCGMGNFNFTKDCQLQTC 55

RESULT 47

ADF71963

ID ADF71963 standard; protein; 58 AA.

XX AC ADF71963;

XX DT 11-MAR-2004 (first entry)

XX DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:43.

XX KW ischaemia; vasotrophic; kallikrein inhibitor; blood loss;

XX KW systemic inflammatory response.

XX OS Homo sapiens.

XX PN WO2003103475-A2.

XX PD 18-DEC-2003.

XX PF 06-JUN-2003; 2003WO-US017665.

XX PR 07-JUN-2002; 2002US-0387239P.

XX PR 28-AUG-2002; 2002US-0407003P.

XX PA (DYAX-) DYAX CORP.

XX PI Ladner RC, Ley AC, Hirani S, Williams A;

XX DR WPI; 2004-062190/06.

XX CC The present invention describes a method (M1) for preventing or reducing

XX CC ischaemia in a patient. M1 involves administering to the patient a

XX CC composition comprising a polypeptide (I) having an amino acid sequence of

XX CC ADF71962 and inhibiting kallikrein. (I) has vasotrophic activity, and can

XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or

XX CC reducing ischaemia in a patient such as perioperative blood loss due to a

XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary

XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)

XX CC is also useful for preventing or reducing the onset of systemic

XX CC inflammatory response associated with a surgical procedure in a patient

XX CC which involves administering (I) to a patient. The present sequence is

XX CC used in the exemplification of the present invention.

XX CC Sequence 58 AA;

XX CC Query Match 53.3%; Score 161; DB 8; Length 58;

XX CC Best Local Similarity 51.0%; Pred. No. 1.2e-12;

XX CC Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFTYGGCGGNNNNFOTEALCLVTC 51

DB 5 COLGYSAGPCVAMFPRFYNGTSMACETFYGGCGMGNFNFTKDCQLQTC 55

PT Preventing or reducing ischemia in patient involves administering to

PT patient composition comprising a kallikrein inhibitory polypeptide.

XX PS Disclosure; SEQ ID NO 43; 46pp; English.

XX CC The present invention describes a method (M1) for preventing or reducing

XX CC ischaemia in a patient. M1 involves administering to the patient a

XX CC composition comprising a polypeptide (I) having an amino acid sequence of

XX CC ADF71926 and inhibiting kallikrein. (I) has vasotrophic activity, and can

XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or

XX CC reducing ischaemia in a patient such as perioperative blood loss due to a

XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary

XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)

XX CC is also useful for preventing or reducing the onset of systemic

XX CC inflammatory response associated with a surgical procedure in a patient

XX CC which involves administering (I) to a patient. The present sequence is

XX CC used in the exemplification of the present invention.

XX CC Sequence 58 AA;

XX CC Query Match 53.3%; Score 161; DB 8; Length 58;

XX CC Best Local Similarity 51.0%; Pred. No. 1.2e-12;

XX CC Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFTYGGCGGNNNNFOTEALCLVTC 51

DB 5 COLGYSAGPCVAMFPRFYNGTSMACOTFYGGCGMGNFNFTKDCQLQTC 55

RESULT 48

ADF71962

ID ADF71962 standard; protein; 58 AA.

XX AC ADF71962;

XX DT 11-MAR-2004 (first entry)

XX DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:42.

XX KW ischaemia; vasotrophic; kallikrein inhibitor; blood loss;

XX KW systemic inflammatory response.

XX OS Homo sapiens.

XX PN WO2003103475-A2.

XX PD 18-DEC-2003.

XX PF 06-JUN-2003; 2003WO-US017665.

XX PR 07-JUN-2002; 2002US-0387239P.

XX PR 28-AUG-2002; 2002US-0407003P.

XX PA (DYAX-) DYAX CORP.

XX PI Ladner RC, Ley AC, Hirani S, Williams A;

XX DR WPI; 2004-062190/06.

XX PT Preventing or reducing ischemia in patient involves administering to

XX PT patient composition comprising a kallikrein inhibitory polypeptide.

XX PS Disclosure; SEQ ID NO 42; 46pp; English.

XX CC The present invention describes a method (M1) for preventing or reducing

XX CC ischaemia in a patient. M1 involves administering to the patient a

XX CC composition comprising a polypeptide (I) having an amino acid sequence of

XX CC ADF71926 and inhibiting kallikrein. (I) has vasotrophic activity, and can

XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or

XX CC reducing ischaemia in a patient such as perioperative blood loss due to a

XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary

XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)

XX CC is also useful for preventing or reducing the onset of systemic

CC inflammatory response associated with a surgical procedure in a patient
CC which involves administering (i) to a patient. The present sequence is
CC used in the exemplification of the present invention.

XX
SQ Sequence 58 AA;

Query Match 53.3%; Score 161; DB 8; Length 58;

Best Local Similarity 51.0%; Pred. No. 1.2e-12;

Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFOTEICLVTC 51

DB 5 COLGYSAGPCVAMFPFRFYNGTSMACQTFYGGCGMGNFNVTXKDLQTC 55

RESULT 49

AAW25933

ID AAW25933 standard; protein; 124 AA.

AC AAW25933;

XX 11-NOV-1997 (first entry)

DE New protease inhibitor Ep7-d21-RPDF-52-55.

XX Trypsin inhibitor; Kunitz domain; protease; active site; elastase;

KW neutrophil; disease; modification; site directed mutagenesis.

XX Synthetic.

OS

XX Key

FT Domain

FT Disulfide-bond

FT Disulfide-bond

FT Misc-difference

FT Disulfide-bond

FT Misc-difference

FT Misc-difference

FT Misc-difference

FT Misc-difference

FT Misc-difference

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DR  N-PSDB; AAT79080.
XX
XX
XX  New protease inhibitor - useful for treating diseases involving elastase.
XX
XX  PS
XX  Claim 5; Page 3; 37pp; Japanese.
XX
XX  This is the amino acid sequence of a novel protease inhibitor based on
CC  the sequence of the anti-trypsin inhibitor UTI. The protein comprises
CC  Kunitz domains 1 and 2 of UTI, but lacks amino acids 1-21. Of the
CC  remaining amino acids, residues 1-4 (22-26 of the native sequence) are
CC  replaced by the peptide Arg-Pro-Asp-Phe. The construct also has the
CC  sequence encoding the active site residue and the adjacent amino acids
CC  (amino acids 36-40 of the wild type sequence) and amino acids 52 and 55
CC  substituted. The modified protease inhibitors are targeted to the
CC  protease elastase, especially from neutrophils and can be used to treat
CC  diseases associated with elastase. Modifications of the active site were
CC  done by site directed mutagenesis
XX
XX  Sequence 124 AA;
XX
XX  Query Match      53.3%; Score 161; DB 2; Length 124;
XX  Best Local Similarity 51.0%; Pred.No. 2.7e-12;
XX  Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
XX
QY  1  CSMFQEQAGCLASIPHHWKKIKICSEFYIGGCGGNHNNFOTSAICLVTC 51
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB  5  CQLGYSAGPIAIFPRFYNGTSMACQTFYVGGCGNGNFFVTEKCLQTC 55
   |||:||||:||||:||||:||||:||||:||||:||||:||||:

Search completed: September 21, 2005, 16:36:51
Job time : 32.8938 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:27:13 ; Search time 9.32743 Seconds
(without alignments)
408.162 Million cell updates/sec

Title: US-10-807-204-2_COPY_52_102
Perfect score: 302
Sequence: 1 CSMPOEAGCLASIPHHWYN.....GCGCGNNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A-COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B-COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCITUS-COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	72.5	54	US-09-358-569D-8	Sequence 8, Appli
2	219	72.5	55	US-09-358-569D-1	Sequence 1, Appli
3	219	72.5	58	US-09-369-494-8	Sequence 8, Appli
4	219	72.5	58	US-09-569-670-8	Sequence 10, Appli
5	219	72.5	64	US-09-358-569D-10	Sequence 75, Appl
6	219	72.5	133	US-09-152-060-75	Sequence 13, Appl
7	170	56.3	43	US-09-358-569D-13	Sequence 113, App
8	170	56.3	66	US-08-358-160-113	Patent No. 5466783
9	170	56.3	79	5466783-7	Patent No. 5466783
10	170	56.3	79	5466783-7	Sequence 71, Appl
11	167	55.3	58	US-08-358-160-71	Sequence 9, Appli
12	166	55.0	54	US-09-358-569D-9	Sequence 123, App
13	166	55.0	67	US-08-358-160-123	Sequence 8, Appli
14	166	55.0	86	US-09-910-430-8	Sequence 17, Appl
15	161	53.3	58	US-08-358-160-17	Sequence 18, Appl
16	161	53.3	58	US-08-358-160-18	Patent No. 5466783
17	160	53.0	77	5466783-4	Patent No. 5466783
18	160	53.0	77	5466783-4	Sequence 211, App
19	157	52.0	61	US-08-829-876-211	Sequence 214, App
20	157	52.0	61	US-08-829-876-214	Sequence 211, App
21	157	52.0	61	US-09-234-874A-211	Sequence 214, App
22	157	52.0	61	US-09-234-874A-214	Sequence 211, App
23	157	52.0	61	US-09-234-873A-211	Sequence 214, App
24	157	52.0	61	US-09-234-873A-214	Sequence 48, Appl
25	156	51.7	58	US-07-664-989B-48	Sequence 51, Appl
26	156	51.7	58	US-07-664-989B-51	Sequence 1, Appli
27	156	51.7	58	US-08-358-160-1	

28	156	51.7	58	1	US-08-358-160-26	Sequence 26, Appl
29	156	51.7	58	1	US-08-463-155A-56	Sequence 56, Appl
30	156	51.7	58	1	US-08-463-432B-56	Sequence 56, Appl
31	156	51.7	61	2	US-08-829-876-180	Sequence 180, App
32	156	51.7	61	2	US-08-829-876-218	Sequence 218, App
33	156	51.7	61	3	US-09-234-874A-180	Sequence 180, App
34	156	51.7	61	3	US-09-234-874A-218	Sequence 218, App
35	156	51.7	61	4	US-09-234-873A-180	Sequence 180, App
36	156	51.7	61	4	US-09-234-873A-218	Sequence 218, App
37	156	51.7	62	1	US-08-358-160-27	Sequence 27, Appl
38	155	51.3	58	1	US-07-664-989B-49	Sequence 49, Appl
39	155	51.3	58	1	US-08-358-160-9	Sequence 9, Appli
40	155	51.3	58	1	US-08-358-160-10	Sequence 10, Appl
41	155	51.3	58	1	US-08-358-160-11	Sequence 11, Appl
42	155	51.3	58	1	US-08-358-160-13	Sequence 15, Appl
43	155	51.3	58	1	US-08-358-160-16	Sequence 16, Appl
44	155	51.3	58	1	US-08-358-160-24	Sequence 24, Appl
45	155	51.3	61	2	US-08-829-876-129	Sequence 129, App
46	155	51.3	61	2	US-08-829-876-139	Sequence 139, App
47	155	51.3	61	2	US-08-829-876-208	Sequence 208, App
48	155	51.3	61	2	US-08-829-876-217	Sequence 217, App
49	155	51.3	61	2	US-08-829-876-222	Sequence 222, App
50	155	51.3	61	3	US-09-234-874A-129	Sequence 129, App

ALIGNMENTS

RESULT 1
US-09-358-569D-8
; Sequence 8, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database

Query Match 72.5%; Score 219; DB 3; Length 54;
Best Local Similarity 68.6%; Pred. No. 3.1e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGCLASIPHHWYNKTKTCSEFIYCGCGNNNNFQTEAICLVTC 51
DB 3 CEMPKEGTCLAYFLHWYDKDNTCSMEFYCGCGNNNNFQSKANCLNTC 53

RESULT 2
US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match      72.5%; Score 219; DB 3; Length 55;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| |||:||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 5 CEMPKEGTGCLAYFLHWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 55

RESULT 3
US-09-369-494-8
; Sequence 8, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Chen, Dadong
; APPLICANT: Davies, Christopher
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-8

Query Match      72.5%; Score 219; DB 3; Length 58;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| |||:||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 5 CEMPKEGTGCLAYFLHWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 55

RESULT 4
US-09-569-670-8
; Sequence 8, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 58;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| |||:||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 5 CEMPKEGTGCLAYFLHWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 55

Query Match      72.5%; Score 219; DB 4; Length 58;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| |||:||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 5 CEMPKEGTGCLAYFLHWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 55

RESULT 5
US-09-358-569D-10
; Sequence 10, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Extension of
; OTHER INFORMATION: Seq Id 1
US-09-358-569D-10

Query Match      72.5%; Score 219; DB 3; Length 64;
Best Local Similarity 68.6%; Pred. No. 3.7e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| |||:||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 7 CEMPKEGTGCLAYFLHWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 57

RESULT 6
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match      72.5%; Score 219; DB 4; Length 133;
Best Local Similarity 68.6%; Pred. No. 8.2e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
Db 77 CEMPKEGTCLAYFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTC 127

RESULT 7
US-09-358-569D-13
; Sequence 13, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: sequence derived from EST database
US-09-358-569D-13

Query Match      56.3%; Score 170; DB 3; Length 43;
Best Local Similarity 68.3%; Pred. No. 5.3e-15;
Matches 28; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 11 LASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
Db 1 LAYFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTC 41

RESULT 8
US-08-358-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-113

Query Match      56.3%; Score 170; DB 1; Length 66;
Best Local Similarity 51.0%; Pred. No. 8.4e-15;
Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
Db 8 CRLPPEQGPKGRIPRYFYNPASRMCSFIYGGCKGNKNNFKTKAECVRAC 58

RESULT 9
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chen, Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 7
; LENGTH: 79
5466783-7

Query Match      56.3%; Score 170; DB 6; Length 79;
Best Local Similarity 51.0%; Pred. No. 1e-14;
Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
Db 1 LAYFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTC 41
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Db 8 CRLPPEQGCKGRIPRYFYNPASRMCSFIYGGCKGNKNFKTKAECVRAC 58

RESULT 10
5466783-7

Patent No. 5466783
; APPLICANT: Wun, Tze-Chien, Kretzmer, Kuniko K., Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 7:
; LENGTH: 79
5466783-7

Query Match 56.3%; Score 170; DB 6; Length 79;
Best Local Similarity 51.0%; Pred. No. 1e-14; Length 79;
Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51

Db 8 CRLPPEQGCKGRIPRYFYNPASRMCSFIYGGCKGNKNFKTKAECVRAC 58

RESULT 11
US-08-358-160-71

Sequence 71, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-71

Query Match 55.3%; Score 167; DB 1; Length 58;
Best Local Similarity 56.9%; Pred. No. 1.8e-14;
Matches 29; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51

Db 5 CLLPAETGPCRAMIPRYFYNNKSKCEPFYGGCGNNNNFKTEECRRTC 55

RESULT 12

US-09-358-569D-9
Sequence 9, Application US/09358569D
Patent No. 6294648
GENERAL INFORMATION:
APPLICANT: Delaria, Kathy
APPLICANT: Rocznia, Steve
APPLICANT: Davies, Christopher
TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
FILE REFERENCE: MSB-7259
CURRENT APPLICATION NUMBER: US/09/358,569D
CURRENT FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 54
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence derived from
OTHER INFORMATION: EST sequence database
US-09-358-569D-9

Query Match 55.0%; Score 166; DB 3; Length 54;
Best Local Similarity 51.0%; Pred. No. 2.2e-14;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51

Db 3 COLPQARGFCKAALLRYFYNSTSNACBPFTYGGCGNNNNFETTEMCLIRIC 53

RESULT 13

US-08-358-160-123
Sequence 123, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William

APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSES: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-123
Query Match 55.0%; Score 166; DB 1; Length 67;
Best Local Similarity 51.0%; Pred. No. 2.8e-14;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
DB 8 COLPQARGPKAALLRYFNSTSNACEPPFYGGCGGNNNFETEMCLRIC 58
RESULT 14
US-09-910-430-8
Sequence 8, Application US/09910430
Patent No. 6794166
GENERAL INFORMATION:
APPLICANT: Godfroi, Edmond
APPLICANT: Bollen, Alex
APPLICANT: Lebouille, Gerard
TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
TITLE OF INVENTION: GLANDS
FILE REFERENCE: VANM229.001CPI

CURRENT APPLICATION NUMBER: US/09/910,430
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: PCT/BB00/00061
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: GB 913425.6
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 86
TYPE: PRT
ORGANISM: Ixodes ricinus
US-09-910-430-8
Query Match 55.0%; Score 166; DB 4; Length 86;
Best Local Similarity 49.0%; Pred. No. 3.7e-14;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
DB 31 CKLPDPDGPFCRARIPIPSYFDRKTKCFEYMGCGEGNNFENITTCQEEC 81
RESULT 15
US-08-358-160-17
Sequence 17, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEV, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:


```
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-17

Query Match 53.3%; Score 161; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQEGAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMFPFYNGTSMACETFYVGGCGNGNMFVTEKDCLOTC 55

RESULT 16
US-08-358-160-18
; Sequence 18, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
```

```
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-18

Query Match 53.3%; Score 161; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQEGAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMFPFYNGTSMACQTFYVGGCGNGNMFVTEKDCLOTC 55

RESULT 17
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain.;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
; 5466783-4

Query Match 53.0%; Score 160; DB 6; Length 77;
Best Local Similarity 47.1%; Pred. No. 1.9e-13;
Matches 24; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQEGAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 8 COLPQARGPCAKALLRYFBSTSNACEPFTYGGCGGNNBNFETTEMCLRIC 58

RESULT 18
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain.;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
; 5466783-4

Query Match 53.0%; Score 160; DB 6; Length 77;
Best Local Similarity 47.1%; Pred. No. 1.9e-13;
Matches 24; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
```



```

; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; STREET: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-664-989B-48

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0;

Qy 1 CSMPEAGPCLASIPHWYTKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
Db 5 CLEPPTYGFCVAMFFRYFNAXAGLCQTFVYGGCGNGNFKSABDCMRTC 55

RESULT 26
US-07-664-989B-51
; Sequence 51, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Barbault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; STREET: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004

```


COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 4.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/664,989B
FILING DATE: 19910301
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-664-989B-51

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPEAGPCIASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
| | | | | : | | | | : | | | | | | | | | | : | |
DB 5 CLEPPYTGPCIAFFPRFYFNKAGLCQTFVYGGCGNGNFKSAEDCMRTC 55

RESULT 27
US-08-358-160-1
Sequence 1, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993

APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-1

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPEAGPCIASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
| | | | | : | | | | : | | | | | | | | | | : | |
DB 5 CLEPPYTGPCVAMPFRFYFNKAGLCQTFVYGGCGNGNFKSAEDCMRTC 55

RESULT 28
US-08-358-160-26
Sequence 26, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEV=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-26

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGPCIAFPFRFYNAKAGLCQTFYGGCMGNGNNFKSAEDCMRTC 55

RESULT 29
US-08-463-155A-56
Sequence 56, Application US/08463155A
Patent No. 5780265
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,155A
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-155A-56

LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-155A-56

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 4.7e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CSEQAEDGPCRAAIPRWYFDVTEGKCAPFIYGGCGGNNRNFDFTEYCAAVC 55

RESULT 30
US-08-463-432B-56
Sequence 56, Application US/08463432B
Patent No. 5786328
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,432B
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-432B-56

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 4.7e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CSEQAEDGPCRAAIPRWYFDVTEGKCAPFIYGGCGGNNRNFDFTEYCAAVC 55

RESULT 31
US-08-829-876-180
Sequence 180, Application US/08829876
Patent No. 5962266
GENERAL INFORMATION:
APPLICANT: White, Tyler R.
APPLICANT: Damm, Deborah
APPLICANT: Lesikar, David D.
APPLICANT: McFadden, Kathleen
APPLICANT: Garrick, Brett L.


```
;
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-180

Query Match 51.7%; Score 156; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCIASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
Db 7 CSEQAETGFCRAGIPRWYFDVTEGKCAPFFYGGCGNNRNNFDTEYCMAVC 57

RESULT 32
US-08-829-876-218
; Sequence 218, Application US/08829876
; Patent No. 5962286
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; APPLICANT: Lardner, David L.
; APPLICANT: Lardner, David L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; US-08-829-876-218
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;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-218

Query Match 51.7%; Score 156; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCIASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
Db 7 CSEQAESGPCRAIYHWYFDVTEGKCAPFFYGGCGNNRNNFDTEYCMAVC 57

RESULT 33
US-09-234-874A-180
; Sequence 180, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; APPLICANT: Lardner, David L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; US-09-234-874A-180
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-874A-180
Query Match 51.7%; Score 156; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
DB 7 CSEQAETGCRAGIPRWYFDVTGKCAPFFYGGCGNNRNNFDTTEYCMAVC 57

RESULT 34
US-09-234-874A-218
; Sequence 218, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-874A-218
Query Match 51.7%; Score 156; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
DB 7 CSEQAESGPCRAAIYHWYFDVTGKCAPFFYGGCGNNRNNFDTTEYCMAVC 57

RESULT 35
```

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US-09-234-873A-180
; Sequence 180, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-873A-180
Query Match 51.7%; Score 156; DB 4; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
DB 7 CSEQAETGCRAGIPRWYFDVTGKCAPFFYGGCGNNRNNFDTTEYCMAVC 57

RESULT 36
US-09-234-873A-218
; Sequence 218, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
```



```

, CITY: Washington
, STATE: D.C.
, COUNTRY: USA
, ZIP: 20007-5109
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, OPERATING SYSTEM: IBM PC compatible
, SOFTWARE: Patentin Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/234,873A
, FILING DATE: 21-Jan-1999
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 08/829,876
, FILING DATE: 02-APR-1997
, APPLICATION NUMBER: 08/436,555
, FILING DATE: 08-MAY-1995
, ATTORNEY/AGENT INFORMATION:
, NAME: Bent, Stephen
, REGISTRATION NUMBER: 29,768
, REFERENCE/DOCKET NUMBER: 056324/0116
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (202)672-5300
, TELEFAX: (202)672-5399
, TELEX: 904136
, INFORMATION FOR SEQ ID NO: 218:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 61 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: protein
, SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-873A-218

Query Match          51.7%;   Score 156;   DB 4;   Length
Best Local Similarity 49.0%;   Pred: No.5e-13;
Matches 25;   Conservative 7;   Mismatches 19;   Indel

QY      1  CSNPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTRAI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      7  CSEQASGSCRAAIYHWYEDVTGKCAFFPYGGCGGNNNNFDTBEY

```

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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-27

Query Match 51.7%; Score 156; DB 1; Length 62;
Best Local Similarity 47.1%; Pred.No.5.1e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0;

Qy 1 CSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCCGNNNNFQTEAICLVTC 51
Db 9 CLEPPYTGCIAPFPFYFNARAGLCQTIVYGGCHGNGNNFKSAEDCMRTC 59

RESULT 38
US-07-664-989B-49
; Sequence 49, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; STREET: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530

```


PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-664-989B-49

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 6.4e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQAGAGCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGPCVAIFPRFYNAKAGLCQTFYGGCGMGNNGNFKSABDCMRTC 55

RESULT 39
US-08-358-160-9
Sequence 9, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-9

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMQAGAGCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CQLGYSAGPCVAMPFRFYNGTSMACETFOYGGCMGNNGNFVTEKDLQTC 55

RESULT 40
US-08-358-160-10
Sequence 10, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/240,160
;; FILING DATE: 02-SEP-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cooper, Iver P.
;; REGISTRATION NUMBER: 28,005
;; REFERENCE/DOCKET NUMBER: LEY=1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 58 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-358-160-10

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMQEGAPCLASIPHHWYKTKICSEFYGGCGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRFYNGTSMACETFYGGCGMGNNGNFFVTEKDCIQTC 55

RESULT 41
US-08-358-160-11
; Sequence 11, Application US/08358160
; Patent No. 5663143

;; GENERAL INFORMATION:
;; APPLICANT: LEY, Arthur C.
;; APPLICANT: LADNER, Robert C.
;; APPLICANT: GUTERMAN, Sonia K.
;; APPLICANT: ROBERTS, Bruce L.
;; APPLICANT: MARKLAND, William
;; APPLICANT: KENT, Rachel B.
;; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
;; NUMBER OF SEQUENCES: 234
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W. Suite 300
;; CITY: Washington
;; STATE: District of Columbia
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/358,160
;; FILING DATE: 16-DEC-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,031
;; FILING DATE: 13-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/009,319
;; FILING DATE: 26-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/664,989
;; FILING DATE: 01-MAR-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/487,063
;; FILING DATE: 02-MAR-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/240,160

;; FILING DATE: 02-SEP-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cooper, Iver P.
;; REGISTRATION NUMBER: 28,005
;; REFERENCE/DOCKET NUMBER: LEY=1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 58 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-358-160-11

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMQEGAPCLASIPHHWYKTKICSEFYGGCGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRFYNGTSMACETFYGGCGMGNNGNFFVTEKDCIQTC 55

RESULT 42
US-08-358-160-15
; Sequence 15, Application US/08358160
; Patent No. 5663143
;; GENERAL INFORMATION:
;; APPLICANT: LEY, Arthur C.
;; APPLICANT: LADNER, Robert C.
;; APPLICANT: GUTERMAN, Sonia K.
;; APPLICANT: ROBERTS, Bruce L.
;; APPLICANT: MARKLAND, William
;; APPLICANT: KENT, Rachel B.
;; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
;; NUMBER OF SEQUENCES: 234
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W. Suite 300
;; CITY: Washington
;; STATE: District of Columbia
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/358,160
;; FILING DATE: 16-DEC-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,031
;; FILING DATE: 13-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/009,319
;; FILING DATE: 26-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/664,989
;; FILING DATE: 01-MAR-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/487,063
;; FILING DATE: 02-MAR-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/240,160
;; FILING DATE: 02-SEP-1988
;; ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-628-5197
TELEX: 248633
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-15

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
Db 5 CQLGYSAGFCVAMFFRYFYNGTSMACETFYGGCGMGNGNFFVTEKDCIQC 55

RESULT 43

US-08-358-160-16
Sequence 16, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

NUMBER OF SEQUENCES: 234

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W. Suite 300

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160

FILING DATE: 16-DEC-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,031

FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,319

FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/664,989

FILING DATE: 01-MAR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,063

FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-16

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
Db 5 CQLGYSAGFCVAMFFRYFYNGTSMACETFYGGCGMGNGNFFVTEKDCIQC 55

RESULT 44

US-08-358-160-24
Sequence 24, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

NUMBER OF SEQUENCES: 234

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W. Suite 300

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160

FILING DATE: 16-DEC-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,031

FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,319

FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/664,989

FILING DATE: 01-MAR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,063

FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: LEY=1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-24

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 6.4e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGCVAIIPRYFYNAKAGLCQTFVYGGCGGNNNNFKSADCKRTC 55

RESULT 45
US-08-829-876-129
; Sequence 129, Application US/08829876
; Patent No. 5962266

GENERAL INFORMATION:
APPLICANT: White, Tyler R.
APPLICANT: Damm, Deborah
APPLICANT: Lesikar, David D.
APPLICANT: McFadden, Kathleen
APPLICANT: Garrick, Brett L.
TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,876
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/436,555
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Pelto, Don J.
REGISTRATION NUMBER: 33,754
REFERENCE/DOCKET NUMBER: 56324/106/SCNO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-829-876-129

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGCVAIIPRYFYNAKAGLCQTFVYGGCGGNNNNFKSADCKRTC 55

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 7 CSEQAETGCPGRAMIPRWYFDVTEGKCAPFFYGGCGGNNNNFDTBEYCNVAVC 57

RESULT 46

US-08-829-876-139
; Sequence 139, Application US/08829876
; Patent No. 5962266
GENERAL INFORMATION:
APPLICANT: White, Tyler R.
APPLICANT: Damm, Deborah
APPLICANT: Lesikar, David D.
APPLICANT: McFadden, Kathleen
APPLICANT: Garrick, Brett L.
TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,876
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/436,555
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Pelto, Don J.
REGISTRATION NUMBER: 33,754
REFERENCE/DOCKET NUMBER: 56324/106/SCNO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-829-876-139

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 7 CSEQAETGCPGRAMISHWYFDVTEGKCAPFFYGGCGGNNNNFDTBEYCNVAVC 57

RESULT 47

US-08-829-876-208
; Sequence 208, Application US/08829876
; Patent No. 5962266
GENERAL INFORMATION:
APPLICANT: White, Tyler R.
APPLICANT: Damm, Deborah
APPLICANT: Lesikar, David D.
APPLICANT: McFadden, Kathleen
APPLICANT: Garrick, Brett L.
TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES


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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-217

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. NO. 6.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0;

Qy 1 CSMQAGCLASIPHWTKTKTCSERIYGGCGNNNNFOTEICLVTC 51
Db 7 CSQAEVGPRAIYHWFDVTGKCAPFGGCGNRRNNFDTBYCMAVC 57

RESULT 49
US-08-829-876-222
; Sequence 222, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 222:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-222

Query Match      51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFOTEAICLVTC 51
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 CSEQAETGRCGRSIRHWYFDVTEGKCAPFFYGGCGGNRRNFDTEYCMAVC 57
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RESULT 50
US-09-234-874A-129
; Sequence 129, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
;
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-09-234-874A-129
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Query Match      51.3%; Score 155; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFOTEAICLVTC 51
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Db 7 CSEQAETGRCRAMIPRWTFDVTGKCAPFFYGGCGGNRRNFDTEYCMAVC 57
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:33:14 ; Search time 31.8938 Seconds
(without alignments)
650.835 Million cell updates/sec

Title: US-10-807-204-2_COPY_52_102

Perfect score: 302
Sequence: 1 CSMPOEAGPCLASIPHWYN.....GCCQGNNNFQTEAICLVTC 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302	100.0	106	16	US-10-807-204-2
2	302	100.0	131	16	Sequence 2, Appli
3	302	100.0	131	16	Sequence 1, Appli
4	292	96.7	131	16	Sequence 12, Appl
5	224	74.2	136	16	Sequence 15, Appl
6	219	72.5	51	15	US-10-807-204-15
7	219	72.5	58	16	Sequence 16, Appl
8	219	72.5	58	17	US-10-058-993-118
9	219	72.5	102	9	Sequence 5, Appli
10	219	72.5	102	9	Sequence 21, Appl
11	219	72.5	117	9	Sequence 120, App
					Sequence 121, App
					Sequence 119, App

12	219	72.5	117	15	US-10-058-993-120
13	219	72.5	133	9	US-09-853-161-75
14	219	72.5	133	9	Sequence 75, Appl
15	219	72.5	133	9	Sequence 75, Appl
16	219	72.5	133	15	US-09-852-797-75
17	219	72.5	133	15	Sequence 75, Appl
18	188	62.3	134	16	US-10-058-993-75
19	169	58.0	571	14	US-10-807-204-13
20	169	58.0	571	14	Sequence 13, Appl
21	169	58.0	571	14	Sequence 14, Appl
22	169	58.0	571	14	Sequence 3, Appli
23	169	58.0	571	14	Sequence 49, Appl
24	169	58.0	571	14	Sequence 3, Appli
25	168	55.6	64	10	US-10-369-736-49
26	168	55.6	64	10	Sequence 49, Appl
27	168	55.6	64	15	US-10-369-738-3
28	167	55.3	58	14	US-10-038-722-5
29	166	55.0	67	10	US-09-896-095-147
30	166	55.0	67	14	Sequence 147, App
31	166	55.0	67	15	US-10-038-722-90
32	166	55.0	86	9	Sequence 90, Appli
33	166	55.0	86	14	Sequence 4, Appli
34	161	53.3	58	14	Sequence 8, Appli
35	161	53.3	58	14	Sequence 17, Appl
36	161	53.3	58	14	Sequence 18, Appl
37	161	53.3	58	14	Sequence 89, Appl
38	161	53.3	58	15	Sequence 89, Appl
39	161	53.3	58	15	Sequence 90, Appl
40	161	53.3	58	15	Sequence 42, Appl
41	161	53.3	58	15	Sequence 43, Appl
42	161	53.3	58	15	Sequence 44, Appl
43	161	53.3	58	18	Sequence 233, App
44	161	53.3	58	18	Sequence 2, Appli
45	161	53.3	58	18	Sequence 2, Appli
46	160	53.0	503	14	Sequence 7, Appli
47	160	53.0	576	9	Sequence 7, Appli
48	160	53.0	576	14	Sequence 7, Appli
49	160	53.0	576	14	Sequence 7, Appli
50	160	53.0	576	14	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN


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; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (23)...(35)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-2
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Query Match 100.0%; Score 302; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.1e-29;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 52 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 102
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RESULT 2
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(25)
; OTHER INFORMATION: predicted by SignalP 2.0
; FEATURE:
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; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (48)...(60)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (54)...(69)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(127)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (86)...(110)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (102)...(123)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-1
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Query Match 100.0%; Score 302; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 77 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 127
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RESULT 3
US-10-807-204-12
; Sequence 12, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-12
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Query Match 100.0%; Score 302; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;
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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
Db 77 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127

RESULT 4
US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015-US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-807-204-15
Query Match 96.7%; Score 292; DB 16; Length 131;
Best Local Similarity 98.0%; Pred. No. 6.5e-28;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
Db 77 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127

RESULT 5
US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015-US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus

US-10-807-204-16
Query Match 74.2%; Score 224; DB 16; Length 136;
Best Local Similarity 66.7%; Pred. No. 1.5e-19;
Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
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Db 77 CSLPQDPGCLAVLPRWYNNQETDLCTEFTYGGCGQNNFPSEGICTVVC 127

RESULT 6
US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-058-993-118
Query Match 72.5%; Score 219; DB 15; Length 51;
Best Local Similarity 68.6%; Pred. No. 2.5e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
Db 1 CEMPKEGPGCLAYFLHWYDKDKONTCSMEFYGGCGQNNNNFQSKANCLNTC 51

RESULT 7
US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84


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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5

Query Match          72.5%; Score 219; DB 16; Length 58;
Best Local Similarity 68.6%; Pred. No. 2.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 CEMPKEGTGCLAYFLHWWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 8
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sadner, Robert C.
; APPLICANT: Stadler, Mark
; TITLE OF INVENTION: POLY-REGULATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match          72.5%; Score 219; DB 17; Length 58;
Best Local Similarity 68.6%; Pred. No. 2.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 CEMPKEGTGCLAYFLHWWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 9
US-09-852-659A-120
; Sequence 120, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; FILING DATE: 1997-05-30
; LENGTH: 102
; TYPE: PRT
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; FILING DATE: 1997-05-30
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120

Query Match          72.5%; Score 219; DB 9; Length 102;
Best Local Similarity 68.6%; Pred. No. 4.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 46 CEMPKEGTGCLAYFLHWWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 96

RESULT 10
US-10-058-993-121
; Sequence 121, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; FILING DATE: 1997-05-30
; LENGTH: 102
; TYPE: PRT
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THE


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; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-75

Query Match      72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQSKANCLNTC 51
Db 77 CEMPKEGTCPLAYFLHWWYDKKDNKTCSEFVYGGCGGNNNNFQSKANCLNTC 127

RESULT 14
US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-75

Query Match      72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 77 CEMPKEGTCPLAYFLHWWYDKKDNKTCSEFVYGGCGGNNNNFQSKANCLNTC 127

RESULT 14
US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-75

Query Match      72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 77 CEMPKEGTCPLAYFLHWWYDKKDNKTCSEFVYGGCGGNNNNFQSKANCLNTC 127
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Db 77 CEMPKEGTCPLAYFLHWWYDKKDNKTCSEFVYGGCGGNNNNFQSKANCLNTC 127

RESULT 15
US-09-852-797-75
; Sequence 75, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-75

Query Match      72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 77 CEMPKEGTCPLAYFLHWWYDKKDNKTCSEFVYGGCGGNNNNFQSKANCLNTC 127

RESULT 16
US-10-058-993-75
; Sequence 75, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
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;; PRIOR FILING DATE: 1998-09-11
;; PRIOR APPLICATION NUMBER: PCT/US98/04858
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/068,368
;; PRIOR FILING DATE: 1997-12-19
;; PRIOR APPLICATION NUMBER: 60/057,765
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/048,970
;; PRIOR FILING DATE: 1997-06-05
;; PRIOR APPLICATION NUMBER: 60/050,934
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/048,100
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/048,189
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/048,357
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/040,710
;; PRIOR FILING DATE: 1997-03-14
;; PRIOR APPLICATION NUMBER: 60/040,762
;; PRIOR FILING DATE: 1997-03-14
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 75
;; LENGTH: 133
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-058-993-75

Query Match 72.5%; Score 219; DB 15; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 77 CEMPETGPCLAYFLHWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 127

RESULT 17
US-10-807-204-13
;; Sequence 13, Application US/10807204
;; Publication No. US20040229312A1
;; GENERAL INFORMATION:
;; APPLICANT: Bougueleret, Lydie
;; APPLICANT: Bairoch, Amos
;; APPLICANT: Niknejad, Anne
;; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
;; TITLE OF INVENTION: Inhibitor
;; FILE REFERENCE: 54720-8015.US00
;; CURRENT APPLICATION NUMBER: US/10/807,204
;; PRIOR FILING DATE: 2004-03-22
;; PRIOR APPLICATION NUMBER: PCT/EP03/01629
;; PRIOR FILING DATE: 2003-02-18
;; PRIOR APPLICATION NUMBER: US 60/358,683
;; PRIOR FILING DATE: 2002-02-21
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13
;; LENGTH: 133
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-807-204-13

Query Match 72.5%; Score 219; DB 16; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 77 CEMPETGPCLAYFLHWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 127

RESULT 18

US-10-807-204-14
;; Sequence 14, Application US/10807204
;; Publication No. US20040229312A1
;; GENERAL INFORMATION:
;; APPLICANT: Bougueleret, Lydie
;; APPLICANT: Bairoch, Amos
;; APPLICANT: Niknejad, Anne
;; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
;; TITLE OF INVENTION: Inhibitor
;; FILE REFERENCE: 54720-8015.US00
;; CURRENT APPLICATION NUMBER: US/10/807,204
;; PRIOR FILING DATE: 2004-03-22
;; PRIOR APPLICATION NUMBER: PCT/EP03/01629
;; PRIOR FILING DATE: 2003-02-18
;; PRIOR APPLICATION NUMBER: US 60/358,683
;; PRIOR FILING DATE: 2002-02-21
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 14
;; LENGTH: 134
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-807-204-14

Query Match 62.3%; Score 188; DB 16; Length 134;
Best Local Similarity 54.9%; Pred. No. 4e-15;
Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 77 CSLPKDSGYCWAYFRWFWNKENSTCQVFIYGGCGGNNNNFQSQICQNAC 127

RESULT 19
US-10-369-736-3
;; Sequence 3, Application US/10369736
;; Publication No. US20030162714A1
;; GENERAL INFORMATION:
;; APPLICANT: HILL, JENNIFER J.
;; APPLICANT: WOLFMAN, NEIL M.
;; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
;; FILE REFERENCE: 08702.0015-00
;; CURRENT APPLICATION NUMBER: US/10/369,736
;; PRIOR FILING DATE: 2003-02-21
;; PRIOR APPLICATION NUMBER: 60/357,846
;; PRIOR FILING DATE: 2002-02-21
;; PRIOR APPLICATION NUMBER: 60/434,645
;; PRIOR FILING DATE: 2002-12-20
;; NUMBER OF SEQ ID NOS: 53
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 571
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-10-369-736-3

Query Match 56.0%; Score 169; DB 14; Length 571;
Best Local Similarity 49.0%; Pred. No. 3.6e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFYVGGCGGNNNNFESRACESC 431

RESULT 20
US-10-369-736-49
;; Sequence 49, Application US/10369736
;; Publication No. US20030162714A1
;; GENERAL INFORMATION:
;; APPLICANT: HILL, JENNIFER J.
;; APPLICANT: WOLFMAN, NEIL M.
;; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS

[illegible]


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; SOFTWARE: PatentIn version

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; SOFTWARE: Patent in version 3.1
CSC ID NO 5; SOFTWARE: Patent in version 3.1
CSC ID NO 5


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; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5

Query Match      55.3%; Score 167; DB 14; Length 58;
Best Local Similarity 56.9%; Pred. No. 6.9e-13;
Matches 29; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 5 CULPAETGFCRAMIPRFYNAKSGKCEPFIYGGCGGNNNNFTEECRTTC 55

RESULT 29
US-09-896-095-147
; Sequence 147, Application US/09896095
; Publication No. US20030219866A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 147
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-896-095-147

Query Match      55.0%; Score 166; DB 10; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 8 CQLPQARGPCKAALLRYFYNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 30
US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS DHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
```

```
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Query Match      55.0%; Score 166; DB 14; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 8 CQLPQARGPCKAALLRYFYNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 31
US-10-115-134-4
; Sequence 4, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kobow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-115-134-4

Query Match      55.0%; Score 166; DB 15; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 8 CQLPQARGPCKAALLRYFYNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 32
US-09-910-430-8
; Sequence 8, Application US/09910430
; Patent No. US20020127235A1
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Leboulle, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM29.001CP1
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
```



```
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
US-09-910-430-8

Query Match      55.0%; Score 166; DB 9; Length 86;
Best Local Similarity 49.0%; Pred. No. 1.3e-12;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 31 CKLPDDGPCRAIPSYFDRKTKCKEPMYGCCEGNNNFENITTCQEEC 81

RESULT 33
US-10-165-605A-8
; Sequence 8, Application US/10165605A
; Publication No. US20030086937A1
; GENERAL INFORMATION:
; APPLICANT: Godfroid, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CP2
; CURRENT APPLICATION NUMBER: US/10/165,605A
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/910,430
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
US-10-165-605A-8

Query Match      55.0%; Score 166; DB 14; Length 86;
Best Local Similarity 49.0%; Pred. No. 1.3e-12;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 31 CKLPDDGPCRAIPSYFDRKTKCKEPMYGCCEGNNNFENITTCQEEC 81

RESULT 34
US-10-038-722-17
; Sequence 17, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSBFIYGGCGQNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 CQLGYSAGFCVAMFPFYNGTSMACQTFYGGCMGNGNNFVTEKDCLOTC 55

RESULT 35
US-10-038-722-18
; Sequence 18, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSBFIYGGCGQNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 CQLGYSAGFCVAMFPFYNGTSMACQTFYGGCMGNGNNFVTEKDCLOTC 55
```

```
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-038-722-17

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSBFIYGGCGQNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 CQLGYSAGFCVAMFPFYNGTSMACQTFYGGCMGNGNNFVTEKDCLOTC 55

RESULT 36
US-10-038-722-19
; Sequence 19, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSBFIYGGCGQNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 CQLGYSAGFCVAMFPFYNGTSMACQTFYGGCMGNGNNFVTEKDCLOTC 55

RESULT 36
US-10-038-722-19
; Sequence 19, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSBFIYGGCGQNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 CQLGYSAGFCVAMFPFYNGTSMACQTFYGGCMGNGNNFVTEKDCLOTC 55
```



```
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-038-722-19
```

```
Query Match 53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
```

```
QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 5 CQLGYSAGPCVAMFPFRYFNGTSMACQTFVYGGCGGNGNMFVTEKDCIQT 55
```

```
RESULT 37
US-10-115-134-88
; Sequence 88, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-115-134-88
```

```
Query Match 53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
```

```
QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 5 CQLGYSAGPCVAMFPFRYFNGTSMACQTFVYGGCGGNGNMFVTEKDCIQT 55
```

```
RESULT 38
US-10-115-134-89
; Sequence 89, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
```

```
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-115-134-89
```

```
Query Match 53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
```

```
QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 5 CQLGYSAGPCVAMFPFRYFNGTSMACQTFVYGGCGGNGNMFVTEKDCIQT 55
```

```
RESULT 39
US-10-115-134-90
; Sequence 90, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-115-134-90
```

```
Query Match 53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
```

```
QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 5 CQLGYSAGPCVAMFPFRYFNGTSMACQTFVYGGCGGNGNMFVTEKDCIQT 55
```

```
RESULT 40
US-10-456-986A-42
; Sequence 42, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
```



```

; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITI-E7-141 Sequence
US-10-456-986A-42

Query Match 53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : |||||
Db 5 COLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCGGNGNMFVTEKDCLOTC 55

RESULT 41
US-10-456-986A-43
; Sequence 43, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUT26A Sequence
US-10-456-986A-43

Query Match 53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : |||||
Db 5 COLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCGGNGNMFVTEKDCLOTC 55

RESULT 42
US-10-456-986A-44
; Sequence 44, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE Sequence
US-10-456-986A-44

Query Match 53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : |||||
Db 5 COLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCGGNGNMFVTEKDCLOTC 55

RESULT 43
US-10-953-902A-42
; Sequence 42, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-42

Query Match 53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : |||||
Db 5 COLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCGGNGNMFVTEKDCLOTC 55

RESULT 44
US-10-953-902A-43
; Sequence 43, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish

```



```
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-43

Query Match          53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : : : : :
Db 5 CQLGYSAGPCVAMPFRPYFYNGASMACQT FVYGGCMGNGNFTVTKDCLQTC 55
```

```
RESULT 45
US-10-953-902A-44
; Sequence 44, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-44

Query Match          53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 5 CQLGYSAGPCVAMPFRPYFYNGTSMACET FVYGGCMGNGNFTVTKDCLQTC 55
```

RESULT 46

```
US-10-007-280A-233
; Sequence 233, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Regipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,640
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 233
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-007-280A-233

Query Match          53.0%; Score 160; DB 14; Length 503;
Best Local Similarity 49.0%; Pred. No. 4e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : : : : :
Db 317 CSLPALQGPCKAYAPRAYNSQTGCQS FVYGGCGNGNPFESREACEBSC 367
```

```
RESULT 47
US-09-794-589-2
; Sequence 2, Application US/09794589
; Patent No. US2002004224A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/09/794,589
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-589-2

Query Match          53.0%; Score 160; DB 9; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : : : : :
Db 386 CSLPALQGPCKAYAPRAYNSQTGCQS FVYGGCGNGNPFESREACEBSC 436
```

```
RESULT 48
US-10-315-380-2
; Sequence 2, Application US/10315380
; Publication No. US20030129577A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/10/315,380
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/794,589
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
```


;; PRIOR FILING DATE: 2000-02-29
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 576
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-315-380-2

Query Match 53.0%; Score 160; DB 14; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 386 CSLPALQGPCKAYAPRWAYNSQTGCQSFYGGCEGNGNFFSREACEESC 436

RESULT 49
US-10-369-736-7
; Sequence 7, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-736-7

Query Match 53.0%; Score 160; DB 14; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 386 CSLPALQGPCKAYAPRWAYNSQTGCQSFYGGCEGNGNFFSREACEESC 436

RESULT 50
US-10-369-738-7
; Sequence 7, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-738-7

Query Match 53.0%; Score 160; DB 14; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 386 CSLPALQGPCKAYAPRWAYNSQTGCQSFYGGCEGNGNFFSREACEESC 436

Search completed: September 21, 2005, 16:45:54
Job time : 32.8938 secs

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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:21:48 ; Search time 7.37168 Seconds
(without alignments)
665.663 Million cell updates/sec

Title: US-10-807-204-2_COPY_52_102
Perfect score: 302
Sequence: 1 CSMPOEAGCLASIPHWYN.....GCCQGNNNFQEAICLVTC 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	170	56.3	110	1 TITRGC	basic proteinase i
2	163	54.0	67	1 TIBOC	trypsin inhibitor,
3	160	53.0	252	2 JG0185	hepatocyte growth
4	158	52.3	62	2 A44180	taicetoxin serine
5	154	51.0	747	2 JH0773	Alzheimer's disease
6	153	50.7	58	1 TIHABK	isoalbinin K (BP
7	153	50.7	62	2 S19327	venom basic protei
8	152	50.3	62	2 S07451	proteinase inhibit
9	152	50.3	922	2 T23573	hypothetical prote
10	149	49.3	57	2 A59204	basic proteinase i
11	148	49.0	65	1 TIVTVC	venom basic protei
12	147	48.7	76	2 S06678	Alzheimer's disease
13	147	48.7	76	2 S03607	Alzheimer's disease
14	147	48.7	484	4 A32761	hypothetical Alzhe
15	147	48.7	770	1 QRHUA4	Alzheimer's disease
16	146	48.3	111	2 S41082	amyloid precursor
17	146	48.3	751	2 A49374	beta-amyloid precu
18	146	48.3	763	2 A49321	amyloid beta (A4)
19	146	48.3	765	2 S42880	amyloid precursor-
20	145	48.0	57	1 TIFHBP	proteinase inhibit
21	145	48.0	122	1 A55115	uterine plasmin/tr
22	145	48.0	1599	2 T16210	hypothetical prote
23	144	47.7	62	2 S01802	chymotrypsin inhib
24	144	47.7	76	2 S04855	Alzheimer's disease
25	144	47.7	100	2 A32282	Alzheimer's disease
26	143	47.4	57	2 B59399	short epsilon-dendr
27	143	47.4	59	1 TIEPED	venom basic protei
28	143	47.4	59	2 A59399	long epsilon-dendr
29	143	47.4	62	2 S01803	chymotrypsin inhib

30	143	47.4	302	1 TITRGC	tissue factor path
31	143	47.4	352	1 HCHU	alpha-1-microglobu
32	143	47.4	372	2 JC2556	alpha-1-microglobu
33	142	47.0	61	1 TIVITI	venom basic protei
34	142	47.0	337	1 TIPGBI	alpha-1-microglobu
35	142	47.0	352	1 TIBOBI	alpha-1-microglobu
36	141	46.7	1522	2 H88380	protein T22P7.3 (i
37	140	46.4	123	2 A29652	inter-alpha-trypsi
38	140	46.4	1558	2 C89114	protein C37C3.6a (
39	140	46.4	2167	2 T34395	hypothetical prote
40	138	45.7	61	1 TIHCBP	proteinase inhibit
41	138	45.7	125	1 TIHOBI	alpha-1-microglobu
42	138	45.7	265	2 A53390	Kunitz-type protei
43	137	45.4	235	2 A54951	tissue factor path
44	136	45.0	100	1 TIBO	basic proteinase i
45	136	45.0	805	2 T34212	hypothetical prote
46	135	44.7	1743	2 T26859	hypothetical prote
47	134	44.4	59	2 S00371	isoeprotinin G1 -
48	134	44.4	60	1 TIBOR	serum basic protei
49	134	44.4	1474	2 D88550	protein ZC84.6 (im
50	134	44.4	2844	2 S28291	hypothetical prote

ALIGNMENTS

RESULT 1

TITRGC
basic proteinase inhibitor - loggerhead
C:Species: Caretta caretta (loggerhead)
C>Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C:Accession: A01224
R:Kato, I.; Tominaga, N.
Fed. Proc. 38, 832, 1979
A:Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tan
A:Reference number: A01224
A:Accession: A01224
A:Molecule type: protein
A:Residues: 1-110 <KAT>
A:Cross-references: UNIPROT:P00993
C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain
C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inh
C:Keywords: pyroglutamic acid; serine proteinase inhibitor
F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:63-105/Domain: antileukoproteinase repeat homology <ALP>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8-58,17-41,33-54,67-93,76-97,80-92,86-101/Disulfide bonds: #status predicted
F:18/inhibitory site: Lys (trypsin) #status predicted

Query Match 56.3%; Score 170; DB 1; Length 110;
Best Local Similarity 51.0%; Pred. No. 28-13;
Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOEAGCLASIPHWYNKTKICSBEFYGGCGGNNNFQEAICLVTC 51
DB 8 CRLPPEQSGCKGRIPRYFYNPASRMCESEFYGGCKGNKNFNKAECEVRAC 58

RESULT 2

TIBOC
trypsin inhibitor, colostrum (BPI type) - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A01207
R:Cechova, D.; Jonakova, V.; Sorm, F.
Collect. Czech. Chem. Commun 36, 3342-3357, 1971
A:Title: Primary structure of trypsin inhibitor from cow colostrum (component B2).
A:Reference number: A09028
A:Accession: A01207
A:Molecule type: protein
A:Residues: 1-26,'B',28-67 <CEC>
A:Cross-references: UNIPROT:P00976
A>Note: the residue identified as Asx is bound to carbohydrate; therefore, we have show

Query Match 52.3%; Score 158; DB 2; Length 62;
Best Local Similarity 51.0%; Pred. No. 3.2e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNKTKICSEFTYGGCGGNNNNFQEAICLVTC 51
DB :
7 CHLPFGPCRAIRPFYFNPHSKCEKTYIGGCHGNANKFKTPDECNVTC 57

RESULT 5

JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmentally regulated expression in the developing brain.
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OK>
A:Cross-references: GB:S52417; NID:G263150; PIDN:AAB24853.1; PID:G263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 51.0%; Score 154; DB 2; Length 747;
Best Local Similarity 47.1%; Pred. No. 1e-10;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNKTKICSEFTYGGCGGNNNNFQEAICLVTC 51
DB CSQAETGPCRAMISRWYDVTEKCAQFIYGGCGNRNFFSDDYCMVC 337

RESULT 6

TIHABK
isoInhibitor K (BPI type) - Roman snail
C:Species: Helix pomatia (Roman snail)
C>Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C:Accession: A91232; A01225
R:Tschesche, H.; Dietl, T.
Eur. J. Biochem. 58, 439-451, 1975
A:Title: The amino acid sequence of isoInhibitor K from snails (Helix pomatia).
A:Reference number: A91232; MUID:76043680; PMID:1183446
A:Accession: A91232
A:Molecule type: protein
A:Residues: 1-58 <TCS>
A:Cross-references: UNIPROT:P00994
R:Dietl, T.; Tschesche, H.
Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976
A:Title: Die Disulfidbruecken des Trypsin-Kallikrein-Inhibitors K aus Weinbergschnecke.
A:Contents: annotation; disulfide bonds
C:Comment: This is one of several isoInhibitors of broad specificity that are members of the Kunitz-type proteinase inhibitor family.
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor
C:Keywords: pyroglutamic acid; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:1/57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 50.7%; Score 153; DB 1; Length 58;
Best Local Similarity 49.0%; Pred. No. 1.2e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;


```
RESULT 7
S19327
venom basic proteinase inhibitor - leaf-nosed viper
N/Alternate names: trypsin inhibitor (Kunitz-type)
C/Species: Eristocophis macmahoni (leaf-nosed viper)
C/Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S19327
R/Siddiqui, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A/Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf-
A/Reference number: S19327; MUID:92077130; PMID:1743283
A/Accession: S19327
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-62 <SID>
A/Cross-references: UNIPROT:P24541
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C/Keywords: serine proteinase inhibitor; venom
F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 50.7%; Score 153; DB 2; Length 62;
Best Local Similarity 51.0%; Pred. No. 1.3e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51
| : | | | | | : | | : | | | | | | | | | | | | | |
Db 2 CYLPDPGVCKAHPFYNNPASNCKNFIYGGCGNANNFETRAECRHTC 52
| : | | | | | : | | : | | | | | | | | | | | | | |

RESULT 8
S07451
proteinase inhibitor 5.II - snake-locks sea anemone
C/Species: Anemonia sulcata (snake-locks sea anemone)
C/Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C/Accession: S07451; B27222
R/Wunderer, G.; Machleidt, W.; Fritz, H.
Meth. Enzymol. 80, 816-820, 1981
A/Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia
A/Reference number: S07451
A/Accession: S07451
A/Molecule type: protein
A/Residues: 1-59 <WRN>
A/Cross-references: UNIPROT:P10280
A/Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R/Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A/Title: Isolierung und strukturaufklaerung eines haemolytisch aktiven peptids aus der
A/Reference number: A94700
A/Accession: B27222
A/Molecule type: protein
A/Residues: 1-38, 'R', 40, 'B', 42, 'BB', 45-48, 'ZZ', 51, 'Z', 53-62 <KRB>
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C/Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 50.3%; Score 152; DB 2; Length 62;
Best Local Similarity 49.0%; Pred. No. 1.7e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51
| : | | | | | : | | : | | | | | | | | | | | | | |
Db 5 CELPKVVGPCRRPFYYNNSSKRCBKFIYGGCGNANNFHTLECEKVC 55
| : | | | | | : | | : | | | | | | | | | | | | | |

RESULT 9
T23573
hypothetical protein K10D3.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23573
R/McMurray, A.
submitted to the EMBL Data Library, June 1996
A/Reference number: Z19762
```

```
A/Accession: T23573
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-922 <WIL>
A/Cross-references: UNIPROT:Q21418; EMBL:Z75545; PIDN:CAA99886.1; GSPDB:GN00019; CESP:K1
A/Experimental source: clone K10D3
C/Genetics:
A/Gene: CESP:K10D3.4
A/Map position: 1
A/Introns: 60/1, 228/1, 278/1, 355/1, 743/1, 802/1; 885/2

Query Match 50.3%; Score 152; DB 2; Length 922;
Best Local Similarity 51.0%; Pred. No. 2.2e-10;
Matches 26; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51
| : | | | | | : | | : | | | | | | | | | | | | | |
Db 411 CKLPREQNGCGYSNRWFNFKTNCERFIYGGCGNANNFETKECDYC 461
| : | | | | | : | | : | | | | | | | | | | | | | |

RESULT 10
A59204
basic proteinase inhibitor - great pond snail
N/Alternate names: trypsin inhibitor
C/Species: Lymnaea stagnalis (great pond snail)
C/Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C/Accession: A59204
R/Nagle, G.
submitted to the Protein Sequence Database, March 2000
A/Description: Lymnaea trypsin inhibitor.
A/Reference number: A59204
A/Accession: A59204
A/Molecule type: protein
A/Residues: 1-57 <NAG>
A/Cross-references: UNIPROT:Q7M411
A/Experimental source: albumen gland
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor
C/Keywords: glycoprotein; serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;5-55, 14-38, 30-51/Diulfide bonds: #status predicted
F;15/inhibitory site: Lys (trypsin) #status predicted
F;24/binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 49.3%; Score 149; DB 2; Length 57;
Best Local Similarity 47.1%; Pred. No. 3.6e-11;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51
| : | | | | | : | | : | | | | | | | | | | | | | |
Db 5 CSLPSETGPKGNFLRYHYNSTNACDSFVGGCKGNANNFQIDIDCKAAC 55
| : | | | | | : | | : | | | | | | | | | | | | | |

RESULT 11
T1VIVC
venom basic proteinase inhibitor III - sand viper
N/Alternate names: venom chymotrypsin inhibitor
C/Species: Vipera ammodytes (sand viper)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C/Accession: A01223
R/Ritonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 746, 138-145, 1983
A/Title: The primary structure Of Vipera ammodytes venom chymotrypsin inhibitor.
A/Reference number: A01223
A/Accession: A01223
A/Molecule type: protein
A/Residues: 1-65 <RII>
A/Cross-references: UNIPROT:P00992
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C/Keywords: serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;7-57, 16-40, 32-53/bisulfide bonds: #status predicted
F;17/inhibitory site: Leu (chymotrypsin) #status predicted
```


A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:gl78613; PIDN:AAB59502.1; PID:gl78616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-530, 'QWLMVPVPAFWKVKGR' <YOS2>
A;Cross-references: GB:M34875; NID:gl78608; PIDN:AAB59501.1; PID:gl78615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:gl78618; PIDN:AAA51727.1; PID:gl78620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 689-716, 'F', 718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Ort, H.T.; Payami, H.; Wijisman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arkis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692, 'G', 694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288, 'V', 365-770 <KAN>
A;Cross-references: GB:Y00364; NID:g28525; PIDN:CRA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A;Cross-references: GB:M16765; NID:gl78539; PIDN:AAA51722.1; PID:gl78540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584

A;Molecule type: mRNA
A;Residues: 674-756, 'S', 758-770 <GOL>
A;Cross-references: GB:M15533; NID:gl78706; PIDN:AAA35540.1; PID:gl78707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near ti
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:gl77957; PIDN:AAA51564.1; PID:gl77958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Nev
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associa
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Heu, D.; Greenberg, B.; D
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Asht
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288, 'V', 365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:gl78572; PIDN:AAA51726.1; PID:gl78573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 60

Query Match 48.3%; Score 146; DB 2; Length 765;
Best Local Similarity 45.1%; Pred. No. 9.8e-10;
Matches 23; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
DB 312 CSQEAQTGCRVMPRWFDLSKGKVRFIYGGCGNNNFQTEAICLVTC 362

RESULT 20
TirHPB
protease inhibitor - flesh fly (Sarcophaga bullata)
C:Species: Sarcophaga bullata
C:Date: 07-Feb-1992 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C:Accession: A37294
R:Papayanopoulos, I.A.; Biemann, K.
Protein Sci. 1, 278-288, 1992
A:Title: Amino acid sequence of a protease inhibitor isolated from Sarcophaga bullata de
A:Reference number: A37294; MUID:93284121; PMID:1304909
A:Accession: A37294
A:Molecule type: protein
A:Residues: 1-57 <PAP>
A:Cross-references: UNIPROT:P26228
A:Experimental source: hemolymph
C:Superfamily: basic proteinase inhibitor
C:Keywords: serine proteinase inhibitor
F:6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:6-56,15-39,31-52/Disulfide bonds: #status predicted
F:16/inhibitory site: Arg (chymotrypsin) #status predicted

Query Match 48.0%; Score 145; DB 1; Length 57;
Best Local Similarity 49.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
DB 6 CLQPEVGPCKRSDFVFFYNADTKACEEFLYGGCGNNNFQTEAICLVTC 56

RESULT 21
A5515
uterine plasmin/trypsin inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A55115
R:Stallings-Wann, M.L.; Burke, M.G.; Trout, W.E.; Roberts, R.M.
J. Biol. Chem. 269, 24090-24094, 1994
A:Title: Purification, characterization, and cDNA cloning of a Kunitz-type proteinase in
A:Reference number: A55115; MUID:95014140; PMID:7929061
A:Accession: A55115
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <STA>
A:Cross-references: UNIPROT:Q29100; GB:L14282; NID:G682652; PIDN:AAAG2425.1; PID:G682653
A:Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Ar
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:38-88/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.0%; Score 145; DB 1; Length 122;
Best Local Similarity 47.1%; Pred. No. 2.2e-10;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
DB 38 CREPPYTGPCSAHFVRYFNATTGLCQSFYGGCGKQNNFMDEKECLHTC 88

RESULT 22
T16210
hypothetical protein F30H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16210
R:Pauley, A.; Stellies, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmids F30H5.
A:Reference number: Z18478
A:Accession: T16210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1599 <PAU>
A:Cross-references: UNIPROT:Q09983; EMBL:U29096; NID:G861393; PID:G861393; PIDN:AAA68408
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F30H5.3
A:Introns: 12/1; 59/2; 85/3; 124/3; 217/2; 534/3; 560/1; 1549/1

Query Match 48.0%; Score 145; DB 2; Length 1599;
Best Local Similarity 49.0%; Pred. No. 2.6e-09;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
DB 563 CSQPLRLGDKQSVRYVYNAVTRACIEFDYTGCGNDNNPETLLEQCQNTC 613

RESULT 23
S01802
chymotrypsin inhibitor I - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01802
R:Sasaaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3075972
A:Accession: S01802
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:Cross-references: UNIPROT:P10831
C:Superfamily: basic proteinase inhibitor
C:Keywords: serine proteinase inhibitor
F:9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.7%; Score 144; DB 2; Length 62;
Best Local Similarity 60.0%; Pred. No. 1.5e-10;
Matches 27; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 7 AGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
DB 16 SGPCFAYIKLYSNOKTKCEFIYGGCGNDNNRFTILAEQKQC 60

RESULT 24
S04855
Alzheimer's disease amyloid A4 protein - mouse (fragment)
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S04855
R:Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.
Nucleic Acids Res. 17, 5396, 1989
A:Title: Sequence of the protease inhibitor domain of the A4 amyloid protein precursor
A:Reference number: S04855; MUID:89345111; PMID:2569710
A:Accession: S04855
A:Molecule type: mRNA
A:Residues: 1-76 <FUK>
A:Cross-references: UNIPROT:P12023; EMBL:X15210; NID:G49965; PIDN:CAA33280.1; PID:G9301
A:Note: the authors translated the codon GAR for residue 74 as Val
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.7%; Score 144; DB 2; Length 76;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;

Qy 7 AGPCLASIPHWYNNKTKICSEFIYGGCQGNNNFQTEAICLVTC 51
:
Db 16 SGPCFAYIKLYSYNOKTKKEEFYGGCKGNDNRFDTLAECEQKC 60

RESULT 30
TIR1GK
tissue factor pathway inhibitor precursor - rat
N:Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibitor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JX0213
R:Enjujoi, K.; Emi, M.; Mukai, T.; Kato, H.
J. Biochem. 111, 681-687, 1992
A:Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).
A:Reference number: JX0213. MUID:923448361. PMID:1639767

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Query Match      47.4%; Score 143; DB 1; Length 302;
Best Local Similarity 49.0%; Pred.No.9.2e-10;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMQEAQPCILASIPHWYNNKTKICISBFYFGCGGNNNNFQTBAILCLVTC 51
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 53 CAMKAEQGPCAMIKRSYVFNNNSHOCSEFYFGCGRGNKNRFDTLLECRKTC 103

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RESULT 31

HCHU

alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human

N:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) protein

N:Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor rich protein

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1992 #sequence revision 30-Jun-1987 #text change 09-Jul-2004

C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; P0450; B39079; A61580; B253217

R:Vetr, H.; Gebhard, W.

Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990

A:Title: Structure of the human alpha(1)-microglobulin-bikunin gene.

A:Reference number: S13433; UID:91214554; PMID:1708673

R;Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
Nucleic Acids Res. 14, 7839-7850, 1986
A:Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-
A:Reference number: A93642; MUID:87040757; PMID:2430261
A:Accession: A93642
A:Molecule type: mRNA
A:Residues: 1-352 <KNU>
A:Cross-references: GB:X04494; NID:g24478; PIDN:CAA28182.1; PID:g24479
R;Lopez Otin, C.; Grubb, A.O.; Mendez, E.
Arch. Biochem. Biophys. 228, 544-554, 1984
A:Title: The complete amino acid sequence of human complex-forming glycoprotein heterogly-
A:Reference number: A90074; MUID:84126849; PMID:6198962
A:Accession: A90074
A:Molecule type: protein
A:Residues: 20-56, 58-202 <LOP>
A:Experimental source: individual with tubular proteinuria
A:Note: no evidence of sequence heterogeneity could be found, in spite of persistent het
R;Takagi, T.; Takagi, K.; Kawai, T.
Biochem. Biophys. Res. Commun. 98, 997-1001, 1981
A:Title: Complete amino acid sequence of human alpha-1-microglobulin.
A:Reference number: A90225; MUID:91184038; PMID:6164372
A:Accession: A90225
A:Molecule type: protein
A:Residues: 20-47; 58-136, 138-141, 'T', 143-144, 146-198 <TAK>
A:Experimental source: pooled urine of patients with tubular proteinuria
R;Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempart, K.; Salier, J.P.
Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
A:Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains i
A:Reference number: A90686; MUID:85225968; PMID:2408638
A:Accession: A90686
A:Molecule type: protein
A:Residues: 206-290, 'VI', 293-342, 'E', 344-350 <REI>
R;Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Druceke, T.; Daudon, M.
Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
A:Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of cr
A:Reference number: P90450; MUID:93221481; PMID:8466493
A:Accession: P90450
A:Molecule type: protein
A:Residues: 206-214, 'X' <ATM1>
R;Engild, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V
J. Biol. Chem. 265, 747-751, 1991
A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood pro
A:Reference number: A39079; MUID:91093267; PMID:1898736
A:Accession: A39079
A:Molecule type: protein
A:Residues: 206-225 <ENGL>
R;Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
Int. J. Biochem. 23, 1201-1203, 1991
A:Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inh
A:Reference number: A61580; MUID:92175157; PMID:1794445
A:Accession: A61580
A:Molecule type: protein
A:Residues: 214, 'X', 216-222, 'X' <CHI>
R;McKeehan, W.B.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.
J. Biol. Chem. 261, 5378-5383, 1986
A:Title: Two apparent human endothelial cell growth factors from human hepatoma cells a
A:Reference number: A92583; MUID:86168278; PMID:3007499
A:Accession: A92583
A:Molecule type: protein
A:Residues: 206-214, 'X', 216-230, 'X', 232-239, 'X', 241-248, 'XX', 251-252, 'X', 254 <MCK>
R;Engild, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-a
A:Reference number: A92736; MUID:89380192; PMID:2476436
A:Accession: A92736
A:Molecule type: protein
A:Residues: 206-225 <ENG2>
R;Traboni, C.; Cortese, R.
Nucleic Acids Res. 14, 6340, 1986
A:Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobu
A:Reference number: A25303; MUID:86312901; PMID:2428011
A:Accession: A25303
A:Molecule type: mRNA


```
QY 1 CSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 CNAEPDAGFCGVQRHFYNNSSSMACOLFYGCGMGNNFVTERECLQSC 285

RESULT 33
TIT0BI
venom basic proteinase inhibitor I - western sand viper
N;Alternate names: venom trypsin inhibitor I
C;Species: Vipera ammodytes ammodytes (western sand viper)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C;Accession: A01222
Biochim. Biophys. Acta 748, 429-435, 1983
A;Title: The primary structure of Vipera ammodytes venom trypsin inhibitor I.
A;Reference number: A01222; MUID:84053385; PMID:6639951
A;Accession: A01222
A;Molecule type: protein
A;Residues: 1-61 <RIT>
A;Cross-references: UNIPROT:P00991
C;Comment: This protein inhibits trypsin and kallikrein.
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: pyroglutamic acid; serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;7-57,16-40,32-53/Diulfide bonds: #status predicted
F;17/Inhibitory site: Lys (trypsin) #status predicted

Query Match 47.0%; Score 142; DB 1; Length 61;
Best Local Similarity 47.1%; Pred. No. 2.6e-10;
Matches 24; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 CYLPADPGRCCKAHPFYDYSASNKCNKFIYGGCGPGNANNFKTWDECRQTC 57

RESULT 34
TIT0BI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
N;Alternate names: bikunin; ITI; PI-14 (inhibitory fragment of ITI)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: S11066; S13493; A01208
R;Gebhard, W.; Schreitmuller, T.; Vetr, H.; Wachter, E.; Hochstrasser, K.
FEBS Lett. 269, 32-36, 1990
A;Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microglobulin
A;Reference number: S11066; MUID:90353595; PMID:1696914
A;Accession: S11066
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-337 <GBB>
A;Cross-references: UNIPROT:P04366; EMBL:X53685; NID:g1877; PIDN:CAA37725.1; PID:g1878
R;Tavakkol, A.
Biochim. Biophys. Acta 1088, 47-56, 1991
A;Title: Molecular cloning of porcine alpha (1)-microglobulin/HI-30 reveals developmental
A;Reference number: S13493; MUID:9113729; PMID:1703444
A;Accession: S13493
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'M', 3-48, 'M', 50-337 <TAV>
A;Cross-references: GB:X52087; NID:g1881; PIDN:CAA36306.1; PID:g1882
A;Note: the authors translated the codon GTG for residue 2 as a Met initiation codon
R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-
A;Reference number: A90685; MUID:85225967; PMID:2408637
A;Accession: A01208
A;Molecule type: protein
A;Residues: 212-258, 'Q', 260-269, 'S', 271-277, 'Q', 279-282, 'A', 284, 'IR', 287-292, 'A', 294-310
C;Comment: This inhibitory fragment, released from native ITI after limited proteolysis
first domain interacts weakly with PMN-granulocytic elastase and not at all with pancreas
```

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C;Comment: The amino acid at position P2' (228-Met) appears to determine the specificity
nd elastase; those with leucine interact strongly.
C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain prec
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;20-173/Domain: lipocalin homology <LIP>
F;216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;216-266,225-249,241-262,272-322,281-305,297-318/Diulfide bonds: #status predicted
F;226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F;235/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;282/Inhibitory site: Arg (trypsin) #status predicted

Query Match 47.0%; Score 142; DB 1; Length 337;
Best Local Similarity 47.1%; Pred. No. 1.4e-09;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 216 CQLGYSGQFCGLMKRYFYNGSSMACETFYGGCGGNGNFFVSEKELQTC 266

RESULT 35
TIT0BI
alpha-1-microglobulin / inter-alpha-trypsin inhibitor precursor [validated] - bovine
N;Alternate names: BI-14 (inhibitory fragment of ITI); Bikunin; ITI
C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Feb-1985 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: S68149; A91717; A90685; S31219; A01209
R;Lindqvist, A.; Akerstrom, B.
Biochim. Biophys. Acta 1306, 98-106, 1996
A;Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver
A;Reference number: S68149; MUID:96201710; PMID:8611630
A;Accession: S68149
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352 <LIN>
A;Cross-references: UNIPROT:P00978; EMBL:U35642; NID:g1016297; PIDN:AAB07599.1; PID:g1016297
R;Hochstrasser, K.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-
A;Reference number: A91717; MUID:84133807; PMID:6199275
A;Accession: A91717
A;Molecule type: protein
A;Residues: 227-267, 'L', 269-273, 'Q', 275-297, 'AP', 300-329, 'Q', 331-345, 'R', 347-348 <HOC>
R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-
A;Reference number: A90685; MUID:85225967; PMID:2408637
A;Accession: A90685
A;Molecule type: protein
A;Residues: 347-349 <HOC2>
R;Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-
A;Reference number: A91718; MUID:84133808; PMID:6199276
A;Contents: annotation; reactive sites
R;Castillo, G.M.; Templeton, D.M.
FEBS Lett. 318, 292-296, 1993
A;Title: Subunit structure of bovine ESF (extracellular-matrix stabilizing factor(s)) .
A;Reference number: S31219; MUID:93178646; PMID:7680011
A;Accession: S31219
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-214, 'X', 216, 'X', 218-220 <CAS>
C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain prec
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;35-188/Domain: lipocalin homology <LIP>
F;231-281/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;241/Inhibitory site: Leu (chymotrypsin, elastase) #status experimental
F;250/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;297/Inhibitory site: Arg (trypsin) #status experimental
```


Query Match 47.0%; Score 142; DB 1; Length 352;
Best Local Similarity 45.1%; Pred. No. 1.4e-09;
Matches 23; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 231 QQLDYGSPCLGLPKFYNGTSMACETFLYGGCMGNFNFLSEKECLQC 281

RESULT 36

H88380
Protein T22F7.3 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: H88380
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999; and
A:Accession: H88380
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1522 <STO>
A:Cross-references: GB:chr III; PIDN:AAA20672.1; PID:G529714; GSPDB:GN00021; CESP:T22F7.3
A>Note: highly similar to ZC84.1
C:Genetics:
A:Gene: T22F7.3
A:Map position: 3

Query Match 46.7%; Score 141; DB 2; Length 1522;
Best Local Similarity 43.1%; Pred. No. 7.5e-09;
Matches 22; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 533 CTQPKRLGDCTSAVRVWYNNAATSCSFMQVTGCGQNDNFNTLMACQQKC 583

RESULT 37

A29652
inter-alpha-trypsin inhibitor (BPI type) - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Dec-1998 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29652
R:Raap, G.; Hochstrasser, K.; Wächter, E.; Reisinger, P.W.M.
Biochim. Chem. Hoppe-Seyler 368, 727-731, 1987
A:Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha-trypsin inhibitor, XI.)
A:Reference number: A29652; MUID:872999012; PMID:2441725
A:Accession: A29652
A:Molecule type: protein
A:Residues: 1-123 <RAS>
A:Cross-references: UNIPROT:P13371
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precursor
C:Keywords: serine proteinase inhibitor
P:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match 46.4%; Score 140; DB 2; Length 123;
Best Local Similarity 45.1%; Pred. No. 9e-10;
Matches 23; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 COLGYSGPCLGMPKRYNGTSMACETFLYGGCMGNFPPESEKECLQC 55

RESULT 38

C89114
protein C37C3.6a [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: C89114
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: C89114
A>Status: preliminary
A:Molecule type: DNA
A/Residues: 1-1558 <STO>
A/Cross-references: UNIPROT:Q8I7I0; GB:chr_V; PIDN:AAC25867.1; PID:g3294501; GSPDB:GN000
C/Genetics:
A:Gene: C37C3.6a
A:Map position: 5

Query Match 46.4%; Score 140; DB 2; Length 1558;
Best Local Similarity 43.1%; Pred. No. 1e-08;
Matches 22; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASPHWYNNKTKICSEFIYGCOCGNNNNFQTEAICLVTC 51
Db 1447 CDEAKDTGCTNFVTKYNNKADGTCNRFHYGCQGTNNRFDNEQOQKAAC 1497

RESULT 39
T34395
hypoetical protein C37C3.6b - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T34395; T34394
R;Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A/Description: The sequence of C. elegans cosmid C37C3.
A/Reference number: Z21518
A/Accession: T34395
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A/Residues: 1-2167 <GEI>
A/Cross-references: UNIPROT:O76840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C
A/Experimental source: strain Bristol N2; clone C37C3
A/Accession: T34394
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A/Residues: 1-1555, 'SKF' <GR2>
A/Cross-references: EMBL:U64857; PIDN:AAC35867.1; GSPDB:GN00023; CESP:C37C3.6a
A/Experimental source: strain Bristol N2; clone C37C3
C/Genetics:
A:Gene: CESP:C37C3.6b; CESP:C37C3.6a
A:Map position: 5
A/Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/

Query Match 46.4%; Score 140; DB 2; Length 2167;
Best Local Similarity 43.1%; Pred. No. 1.4e-08;
Matches 22; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASPHWYNNKTKICSEFIYGCOCGNNNNFQTEAICLVTC 51
Db 1447 CDEAKDTGCTNFVTKYNNKADGTCNRFHYGCQGTNNRFDNEQOQKAAC 1497

RESULT 40
T3HCEP
proteinas inhibitor (BPI-type) - horseshoe crab (Tachypleus tridentatus)
C/Species: Tachypleus tridentatus
C/Date: 08-Mar-1989 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C/Accession: A26923
R;Nakamura, T.; Hirai, T.; Tokunaga, F.; Kawabata, S.; Iwanaga, S.
J. Biochem. 101, 1297-1306, 1987
A>Title: Purification and amino acid sequence of Kunitz-type protease inhibitor found in
A/Reference number: A26923; MUID:88007472; PMID:3308864
A/Accession: A26923

A:Molecule type: protein
A:Residues: 1-61 <NAK>
A:CROSS-references: UNIPROT:P16044
A:Experimental source: hemocytes
C:Comment: The inhibitory activity is similar to bovine basic proteinase inhibitor.
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C:Keywords: serine proteinase inhibitor
F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:8-58,17-41,33-54/Disulfide bonds: #status predicted
F:18/inhibitory site: Arg (chymotrypsin, elastase, trypsin, plasmin, plasma kallikrein)

Query Match 45.7%; Score 138; DB 1; Length 61;
Best Local Similarity 45.1%; Pred. No. 8e-10;
Matches 23; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHHWYKTKCSBFIYGGCGGNNNNFQTEAICLVTC 51
DB 8 CTSPPVTGFCRAFGKRYNTRTKQCEPPKYGCKGNRYKSEQDCLDAC 58

RESULT 41
TIHOBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
N:Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
C:Species: Equus caballus (domestic horse)
C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: A01210; A45653
R:Hochstrasser, K.; Wächter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-1-microglobulin/inter-alpha-trypsin inhibitor
A:Reference number: A90685; MUID:85225967; PMID:2408637
A:Accession: A01210
A:Molecule type: protein
A:Residues: 3-125 <HOC>
A:CROSS-references: UNIPROT:P04355
R:Veeraragavan, K.; Singh, K.; Wächter, E.; Hochstrasser, K.
Biochem. Int. 26, 405-413, 1992
A:Title: Characterization of a trypsin inhibitor from equine urine.
A:Reference number: A45653; MUID:92328813; PMID:1627153
A:Accession: A45653
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12, 'E', 14-33 <VEE>
A:CROSS-references: PIDN:AAB22430.1; PID:9250858
A:Experimental source: urine
A:Note: sequence extracted from NCBI backbone (NCBIP:107966)
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis of first domain interacts weakly with PMN-granulocytic elastase and not at all with pancreatic elastase; The amino acid at position P2' (19-Met) appears to determine the specificity of elastase; those with leucine interact strongly.
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precursor
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
F:17/inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:73/inhibitory site: Arg (trypsin) #status predicted

Query Match 45.7%; Score 138; DB 1; Length 125;
Best Local Similarity 45.1%; Pred. No. 1.6e-09;
Matches 23; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHHWYKTKCSBFIYGGCGGNNNNFQTEAICLVTC 51
DB 7 CQLDHAQGPCLGMSIRFYFNGTSMACETFOYGGCLGNNFASQKSLQTC 57

RESULT 42
A53390
Kunitz-type proteinase inhibitor precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C:Accession: A53390
R:Kramer, K.K.; Duffy, J.Y.; Klemann, S.W.; Bixby, J.A.; Low, B.G.; Pope, W.F.; Roberts, J. Biol. Chem. 269, 7255-7261, 1994
A:Title: Selective cloning of cDNA for secretory proteins of early embryos. Identification of a novel Kunitz-type proteinase inhibitor
A:Reference number: A53390; MUID:94171738; PMID:7510284
A:Accession: A53390
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-265 <KRA>
A:CROSS-references: UNIPROT:Q29428; GB:U00165; NID:9501024; PIDN:AAA19108.1; PID:9392040
C:Keywords: serine proteinase inhibitor
F:208-259/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 45.7%; Score 138; DB 2; Length 265;
Best Local Similarity 41.2%; Pred. No. 3.3e-09;
Matches 21; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHHWYKTKCSBFIYGGCGGNNNNFQTEAICLVTC 51
DB 208 CLPEKVTGDCNATMTRYFNTQTGLCBQFVYTGCGNGNFFENLEDCKMTC 258

RESULT 43
A54951
tissue factor pathway inhibitor-2 precursor - human
N:Alternate names: placental protein 5 (PP5)
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: A54951; I55185; A34029; B34029
R:Spracher, C.A.; Kistler, W.; Mathewes, S.; Foster, D.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3353-3357, 1994
A:Title: Molecular cloning, expression, and partial characterization of a second human tissue factor pathway inhibitor
A:Reference number: A54951; MUID:94211862; PMID:8159751
A:Accession: A54951
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:CROSS-references: UNIPROT:P48307; GB:L27624; NID:9441149; PIDN:AAA20094.1; PID:9441150
A:Experimental source: placenta
R:Miyagi, Y.; Koshikawa, N.; Yasumitsu, H.; Miyagi, E.; Hirahara, F.; Aoki, I.; Mäugli, J. Biochem. 116, 939-942, 1994
A:Title: CDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by human placenta
A:Reference number: I55185; MUID:95204397; PMID:7896752
A:Accession: I55185
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-235 <RE2>
A:CROSS-references: GB:D29992; NID:9484050; PIDN:BAAO6272.1; PID:9484051
A:Note: parts of this sequence, including the amino end of the mature protein, were determined from a cDNA clone of the mature protein.
R:Buetzow, R.; Huhtala, M.L.; Bohn, H.; Virtanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A:Title: Purification and characterization of placental protein 5.
A:Reference number: A34029; MUID:88106628; PMID:3276312
A:Accession: A34029
A:Molecule type: protein
A:Residues: 'A', 24-33, 'X', 35 <BUB>
A:Accession: C34029
A:Molecule type: protein
A:Residues: 47-50, 'X', 52-53 <BU2>
A:Accession: B34029
A:Molecule type: protein
A:Residues: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>
C:Genetics:
A:Gene: GDB:TFPI2
A:CROSS-references: GDB:354485
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C:Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-235/Product: tissue factor pathway inhibitor-2 #status predicted <MAT>
F:36-86/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:96-149/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:158-208/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F:36-86, 45-69, 61-82, 96-149, 106-130, 122-145, 158-208, 167-191, 183-204/Disulfide bonds: #status predicted

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| | | | | : : : | : | : | : | : | : | : | : | : | :
Db 6 CLEPPYTGPCKAMIRYFNAGLCPFYVGGCRACKSNFKSAEDCMRTC 56

RESULT 48
TIBOR
serum basic proteinase inhibitor - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 09-Jul-2004
C/Accession: A01206
R/Wachter, E.; Deppner, K.; Hochstrasser, K.; Lempart, K.; Geiger, R.
FEBS Lett. 119, 58-62, 1980
A/Rittle: A new Kunitz-type inhibitor from bovine serum amino acid sequence determination
A/Reference number: A01206; MUID:81044408; PMID:7428928
A/Accession: A01206
A/Molecule type: protein
A/Residues: 1-60 <MAC>
A/Cross-references: UNIPROT:P00975
C/Comment: This inhibitor has activity very similar to that of the basic proteinase inhibitor
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homo
C/Keywords: serine proteinase inhibitor
F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F/17/Inhibitory site: Lys (trypsin) #status experimental

Query Match 44.4%; Score 134; DB 1; Length 60;
Best Local Similarity 41.2%; Pred. No. 2.4e-09;
Matches 21; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| | | | | : : : | : | : | : | : | : | : | : | : | :
Db 7 CLEPPYTGPCKAMIRYFNAGLCPCTFYVGGCRACKSNFKSAEDCMRTC 57

RESULT 49
D88550
protein ZC84.6 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: D88550
R/anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.el
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A/Accession: D88550
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1474 <STO>
A/Cross-references: UNIPROT:O62504; GB:chr_III; PIDN:CAA79570.1; PID:G3881447; GSPDB:GN
C/Genetics:
A/Gene: ZC84.6
A/Map position: 3

Query Match 44.4%; Score 134; DB 2; Length 1474;
Best Local Similarity 43.1%; Pred. No. 5.1e-08;
Matches 22; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| | | | | : : : | : | : | : | : | : | : | : | : | :
Db 439 CTOLRVGNCDRSVRYYWYSAAATRECQSFEYTCQGNDNNFETLVDCQTFC 489

RESULT 50
S28291
hypothetical protein ZC84.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S28291
R/Thomas, J.
submitted to the EMBL Data Library, December 1992
A/Reference number: S28285


```

ID AC Q6IE19 PRELIMINARY; PRT; 182 AA.
DT Q6IE19;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE WAP four-disulfide core 6-like 1.
GN Name=wfdc611;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15060002; DOI=10.1101/gr.1946304;
RA Puente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -|- SIMILARITY: Contains 1 BPTi/Kunitz inhibitor domain.
CC -|- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; EN000374; CAB51900.1; -.
DR HSSP; P00974; 1KGU.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EB12D7BFF756707E CRC64;

Query Match 73.8%; Score 223; DB 2; Length 182;
Best Local Similarity 66.7%; Pred. No. 1.3e-19;
Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 CSMPEGAGPCLASIPHWYKTKICSEPIYGGCGNNNFOTEICLVTC 51
Db 77 CSLPQDAGCLAYLRWYKTKTNLCTQPIYGGCGNTNNFLSKDICTSIC 127

RESULT 3
EPPI HUMAN
ID EPPI HUMAN STANDARD; PRT; 133 AA.
AC Q95975; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Eppin precursor (Epitidymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
DE domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINLW1; Synonyms=WAP7, WFDC7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epitidymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French F.S., O'Rand M.G.;
RT "Cloning and sequencing of human Eppin: a novel family of protease
RT inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stavrides G.S., Huckie E.J., Deloukas P.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN

[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaesalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.F., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tzomana A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -|- SUBCELLULAR LOCATION: Secreted (Potential).
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=095925-1; Sequence=Displayed;
CC Name=2;
CC IsoId=095925-2; Sequence=VSP_006755;
CC -|- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -|- SIMILARITY: Contains 1 BPTi/Kunitz inhibitor domain.
CC -|- SIMILARITY: Contains 1 WAP-type domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
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DR Probom: P0000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 133 AA; 15277 MW; B33ABE57ECBEBE84 CRC64;

Query Match          71.5%; Score 216; DB 2; Length 133;
Best Local Similarity 68.6%; Pred. No. 7.2e-19;
Matches 35; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
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Db 77 CEMPNETGCLAFFIRWYDKKNNTCTSFVHGCGGNNNFQSEANCLNTC 127

RESULT 6
EPPI_MACMU
ID EPPI_MACMU STANDARD; PRT; 133 AA.
AC Q9BDL1;
DT 28-FEB-2003 (Rel. 41, Created)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
inhibitor-like with Kunitz and WAP domains 1).
GN Name=SPINLW1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
-----
DR EMBL; AF346414; AAK31336.1; -.
DR HSP; P00974; 1BPI
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR Probom; P0000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
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FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 133 AA; 15279 MW; 433ABE946E39A35E9 CRC64;

Query Match          69.9%; Score 211; DB 1; Length 133;
Best Local Similarity 66.7%; Pred. No. 3e-18;
Matches 34; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 CEMPNETGCLAFFIRWYDKKNNTCTSFVHGCGGNNNFQSEANCLNTC 127

RESULT 7
EPPI_MOUSE
ID EPPI_MOUSE STANDARD; PRT; 134 AA.
AC Q9DA01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
inhibitor-like with Kunitz and WAP domains 1).
GN Name=Spinlwl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Daila E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawagawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Borje A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kigawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
```


OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=BALE/c;
RX MEDLINE=22636519; PubMed=12595574; DOI=10.1210/me.2002-0366;
RT Hall J.J., Qiu Y., Hewick R.M., Wolfman N.M.;
RA "Regulation of myostatin in vivo by growth and differentiation factor-
RT associated serum protein-1: a novel protein with protease inhibitor
RT and follistatin domains";
RL Mol. Endocrinol. 17:1144-1154(2003).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR ENBL; AY308804; AAF72503.1; -;
DR HSSP; P00974; 1K09.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007179; P:transforming growth factor beta receptor si. . .; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00189; NTR; 1.
SQ SEQUENCE 571 AA; 63321 MW; B28B676B3DC71256 CRC64;

Query Match 56.0%; Score 169; DB 2; Length 571;
Best Local Similarity 49.0%; Pred.No.2.le-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps

QY 1 CSMPOBAGPCLASIPHWYNNKTKICSEFYIGGCGGNNNFOTEAICLVTC 51
DB 381 CSIPALQGPCKAYPRWAYNSQTGLCSFYVGCGEGNPFSEACESC 431

RESULT 10
Q9GPI5 ID Q9GPI5 PRELIMINARY; PRT; 86 AA.
AC Q9GPI5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Ixodes ricinus (Sheep tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
OX NCBI_TaxID=34613;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary glands;
RX MEDLINE=22134277; PubMed=12139212;
RA Lebouille G., Rochez C., Louahed J., Rutti B., Brossard M., Bollen A.,
RA Godfroid E.;
RT "Isolation of Ixodes ricinus salivary gland mRNA encoding factors
RT induced during the blood feeding process.";
RL Am. J. Trop. Med. Hyg. 66:225-233(2002).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR ENBL; AJ269641; CAB55816.1; -;
DR HSSP; P12111; 1KNT.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.


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NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=22304654; PubMed=12206714; DOI=10.1042/EJ20020869;
Clausen A., Lilja H., Lundwall A.;
"A locus on human chromosome 20 contains several genes expressing
protease inhibitor domains with homology to whey acidic protein.";
Biochem. J. 368:233-242(2002).
[2]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
Elliott A.G., Frankland J.A., Fraser A., French L., Garner P.,
Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaestaho M.H., Leverhna M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,
Milde S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prachalingam S.R., Plumb R.W., Ramsey H.,
Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultston J.E.,
Swann R.N., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Wilming I., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BQY6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9BQY6-2; Sequence=VSP_007550, VSP_007551;
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed but the highest levels
are found in epididymis, testis and trachea.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-gib.ch/announce/
or send an email to license@isb-gib.ch).
CC EMBL; AF411861; AA003684.1; -
CC EMBL; AL031663; CAC36264.1; -
CC HSP; P02760; 1BIK.
CC Genew; HGNC:16164; WFOC6.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP.
CC Pfam; PF00004; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 1.
CC PRINTS; PR00759; BASICPTASE.
CC ProDom; PD00022; Prot_Inh_Kunz-m; 1.
CC SMART; SM00131; KU; 1.
CC SMART; SM00217; WAP; 1.
CC PROSITE; PS00317; 4 DISULFIDE CORE; FALSE_NEG.
CC PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
CC PROSITE; PS50279; BPTI_KUNITZ_2; 1.

```

KW	Alternative splicing; Serine protease inhibitor; Signal potential.
FT	SIGNAL 1 25
FT	CHAIN 26 131 WAP four-disulfide core domain protein 6.
FT	DOMAIN 31 69 WAP.
FT	DOMAIN 70 128 BPTI/Kunitz inhibitor.
FT	DISULFID 33 61 By similarity.
FT	DISULFID 48 60 By similarity.
FT	DISULFID 54 69 By similarity.
FT	VARSPLIC 75 86 IYAVCHRRRLAPA -> VSLTLVHKKELE (in isoform 2).
FT	/FTid=VSP_007550.
FT	Misng (in isoform 2).
FT	/FTid=VSP_007551.
SQ	SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;
	Query Match 54.6%; Score 165; DB 1; Length 131;
	Best Local Similarity 96.8%; Pred. No. 1-5e-12;
	Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy	21 KTKKICSEFYGGCGGNNNNFQTEAICLVTC 51
Dd	97 KTKKICSEFYGGSGNNGNNNFQTEAICLVTC 127
RESULT 13	
ID Q6DJB6 PRELIMINARY; PRT; 750 AA.	
AC Q6DJB6;	
DT 25-OCT-2004 (T-EMBLrel. 28, Created)	
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)	
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)	
DE App-prov protein.	
GS Name-app-prov;	
OS Xenopus tropicalis (Western clawed frog) (<i>Xenopus laevis</i>).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;	
OC Xenopodinae; Xenopus.	
OX NCBI_TaxId=8364;	
RN [1]	
RN SEQUENCE FROM N.A.	
RC TISSUE=Whole body;	
RX MEDLINE=22398257; Pubmed=12477932; DOI=10.1073/pnas.242603899;	
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA Altschul S.F., Zeeberg B., Buetow T.K., Schaefer C.F., Bhat N.K.,	
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heide F.,	
RA Diatchenko L., Marusica K., Farmer A.A., Rubin G.M., Hong L.,	
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA Brownstein M.J., Ustin T.B., Toshnyuki S., Carninci P., Prange C.,	
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerck J.E.,	
RA Jones S.J., Marra M.A.;	
RT "Generation and initial analysis of more than 15,000 full-length human	
RT and mouse cDNA sequences."	
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN [2]	
RN SEQUENCE FROM N.A.	
RP TISSUE=Whole body;	
RC Klein S., Gerhard D.S.;	
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.	
DR EMBL: BC075266; AAH75266.1;	
DR GO: CO:0016021; C:integral to membrane; IEA.	
DR GO: CO:0005488; P:binding; IEA.	
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.	
DR InterPro: IPRO08155; A4 APP.	

[illegible]

RT Kunitz-type serine proteinase inhibitor domain is a predominant
product in mouse but not in human.;
RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
CC -!- FUNCTION: Inhibitor of HGF activator.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q9WU03-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9WU03-2; Sequence=VSP_003034;
CC Name=3;
CC IsoId=Q9WU03-3; Sequence=VSP_003035, VSP_003036;
CC -!- TISSUE SPECIFICITY: Isoform 2 is more predominantly expressed than
isoform 1.
CC -!- DOMAIN: This inhibitor contains two inhibitory domains.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC
CC EMBL; AF099016; AAD22172.1; -;
CC EMBL; AF099019; AAD22173.1; -;
CC EMBL; AF099020; AAD22174.1; -;
CC HSSP; P00974; 1K09.
CC MGD; MGI:1338031; Spint2.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC PRINTS; PR00759; BASICTPASE.
CC ProDom; PD000222; Prot_Inh_Kunz-m; 2.
CC SMART; SM00131; KU; 2.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC PROSITE; PS0279; BPTI_KUNITZ_2; 2.
KW Alternative splicing; Glycoprotein; Repeat; Serine protease inhibitor;
KW Signal; Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 252 Kunitz-type protease inhibitor 2.
FT DOMAIN 28 197 Extracellular (Potential).
FT TRANSMEM 198 218 Potential.
FT DOMAIN 219 252 Cytoplasmic (Potential).
FT DOMAIN 38 88 BPTI/Kunitz inhibitor 1.
FT DOMAIN 133 183 BPTI/Kunitz inhibitor 2.
FT SITE 48 49 Reactive bond (By similarity).
FT SITE 143 144 Reactive bond (By similarity).
FT DISULFID 38 88 By similarity.
FT DISULFID 47 71 By similarity.
FT DISULFID 63 84 By similarity.
FT DISULFID 133 183 By similarity.
FT DISULFID 142 166 By similarity.
FT DISULFID 158 179 By similarity.
FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 37 93 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 114 128 /FTId=VSP_003034.
FT PRKQSAEDLSAEIFN -> CFVLSVAALFLFYA (in
FT isoform 3).
FT VARSPLIC 129 252 /FTId=VSP_003035.
FT VARSPLIC 129 252 Missing (in isoform 3).
FT /FTId=VSP_003036.
FT VARSPLIC 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;
SQ
Query Match 53.0%; Score 160; DB 1; Length 252;
Best Local Similarity 49.0%; Pred. No. 1.2e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

RESULT 17
Q6ZNI4
ID Q6ZNI4 PRELIMINARY; PRT; 283 AA.
AC Q6ZNI4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16032.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Nimomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamiyama K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; AK131196; BAD18391.1; -;
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP-like.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 86206E7309866D30 CRC64;
Query Match 53.0%; Score 160; DB 2; Length 283;
Best Local Similarity 49.0%; Pred. No. 1.3e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMQEAGPCIASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
DB 93 CSLPALQGFCKAYAPRWYNSQTGQSFYGGCEGNGNFFESRACEESC 143
RESULT 18
Q8TEU8
ID Q8TEU8 PRELIMINARY; PRT; 576 AA.
AC Q8TEU8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WFIKNRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyai L., Piaty L.;
RT "A human protein containing multiple types of protease-inhibitory
RT modules";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709(2001).
RN [2]
RP SEQUENCE FROM N.A.


```
RA Trexler M., Banyai L., Patthy L.;
RT "Distinct expression pattern of two related human proteins containing
RL multiple types of protease-inhibitory modules.";
RL Biol. Chem. 383:0-0(2002).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AF468657; AAL77058.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD00222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBF121F81 CRC64;

Query Match 53.0%; Score 160; DB 2; Length 576;
Best Local Similarity 49.0%; Pred. No. 2,7e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCPLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 386 CSLPALQGPCKAYAPRWYNSQTGCQSFVYGGCGGNNNFESRACEESC 436

RESULT 19
Q6UXZ9
AC Q6UXZ9 PRELIMINARY; PRT; 576 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bikunin hlg.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brugh J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
```

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CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAQ88509.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD00222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match 53.0%; Score 160; DB 2; Length 576;
Best Local Similarity 49.0%; Pred. No. 2,7e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCPLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 386 CSLPALQGPCKAYAPRWYNSQTGCQSFVYGGCGGNNNFESRACEESC 436

RESULT 20
Q7PXZ1
AC Q7PXZ1 PRELIMINARY; PRT; 2419 AA.
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP12609 (Fragment).
GN Name=agCG49342; ORFNames=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008987; EAA01339.1; -.
DR HSSP; P10646; 1IRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
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OC Ephydroidea: Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mentrulov G., Milghina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodgett W., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.H., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.F., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirekas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirekas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.
EMBL: AE003765; AAF56794.3; --
HSPB; P12111, 1KTH.
DR FlyBase; FBgn0003137; Ppn.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF00014; Kunitz_BPTI; 10.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PR000222; Prot_Inh_Kunz-m; 10.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 10.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 9.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS0835; IG_Like; 3.
DR PROSITE; PS0900; PLAC; 1.
DR PROSITE; PS0092; TSP1; 5.
SQ SEQUENCE 2772 AA; 299154 MW; 3965DC92D30CCAAA CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2772;
Best Local Similarity 47.1%; Pred. No. 1.8e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMQEQAGPCPLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 1730 CEQPVESGFCAGNFERWYDNETDLCRFTYGGCKGNKNYPTHEACNYNC 1780

RESULT 24
Q869A0 PRELIMINARY; PRT; 2776 AA.
AC Q869A0;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin 2.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22552133; PubMed=12666201; DOI=10.1002/dvdy.10265;
RA Kramerova I.A., Kramerov A.A., Fessler J.H.;

RT "Alternative splicing of papilin and the diversity of Drosophila
RL extracellular matrix during embryonic morphogenesis.";
RN Dev. Dyn. 226:634-642(2003).

RP SEQUENCE FROM N.A.
RA Kramerova I., Fessler J.H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.
DR EMBL; AF529179; AAO84907.1; -;
DR HSSP; P12111; 1KTH.

DR FlyBase; F8gn0003137; Ppn.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.

DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00047; ig; 2.
DR Pfam; PF00014; Kunitz_BPTI; 10.
DR Pfam; PF00090; TSP1; 5.
DR Pfam; PF00095; WAP; 1.

DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 10.
DR SMART; SM00408; ICG2; 3.
DR SMART; SM00131; KU; 10.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 9.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS0835; IG LIKE; 3.
DR PROSITE; PS0900; PLAC; 1.
DR PROSITE; PS05092; TSP1; 5.

KW Matrix protein.
SQ SEQUENCE 2776 AA; 299741 MW; 92D38A17360D2D42 CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2776;
Best Local Similarity 47.1%; Pred. NO. 1.8e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPQAGCLASIPHWYNNKTKICSEFIYGCQGNVNFQTEALCLVTC 51
DB 1730 CEQPVESGFCAGNFERWYDNETDICRPFTYGCCKGNKNYPTEHACNYNC 1780

RESULT 25
Q7KRX2 PRELIMINARY; PRT; 2894 AA.

AC Q7KRX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG33103-PA.

GN Names:Ppn; ORFNames:CG33103;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

RA MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
Abriel J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Bernan P.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).

RL [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426065; PubMed=12537568;
RX Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RL [3]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426070; PubMed=12537573;
RX Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RL [4]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426069; PubMed=12537572;
RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RL [5]
RN SEQUENCE FROM N.A.
RP FlyBase;

RG Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
RL [6]
RN SEQUENCE FROM N.A.


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RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AE003765; AAF56795.3; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; IG; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1_5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD00222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00409; IG; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 5.
SQ SEQUENCE 2894 AA; 312663 MW; A1BFE1BAD9B214BC CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2894;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 1730 CEQPVESGFCAGNFERWYDNETDICRPFTYGGCKGNKNYPTHEACNYNC 1780

RESULT 26
Q86829 PRELIMINARY; PRT; 2898 AA.
AC Q86829;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin 3.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22552133; PubMed=12666201; DOI=10.1002/dvdy.10265;
RA Kramerova I.A., Kramarov A.A., Fessler J.H.;
RT "Alternative splicing of papilin and the diversity of Drosophila
RT extracellular matrix during embryonic morphogenesis.";
RL Dev. Dyn. 226:634-642(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Kramerova I., Fessler J.H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF529180; AAO84908.1; -.

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DR HSSP; P12111; 1KTH.
DR FlyBase; FBgn0003137; Ppn.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; IG; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1_5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD00222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00408; IGC2_3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 5.
KW Matrix protein.
SQ SEQUENCE 2898 AA; 313250 MW; 2F992742F2D64A00 CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2898;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 1730 CEQPVESGFCAGNFERWYDNETDICRPFTYGGCKGNKNYPTHEACNYNC 1780

RESULT 27
IVBT_OXYSC
ID IVBT_OXYSC STANDARD; PRT; 62 AA.
AC Q7LZE4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Taicotoxin, serine protease inhibitor component (TCX).
OS Oxyuranus scutellatus scutellatus (Australian taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Serpentes; Colubroides;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=8667;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RX PubMed=1485334; DOI=10.1016/0041-0101(92)90511-3;
RA Possani L.D., Martin B.M., Yatani A., Mochca-Morales J., Zamudio F.Z.,
RA Gurrola G.B., Brown A.M.;
RT "Isolation and physiological characterization of taicotoxin, a complex
RT toxin with specific effects on calcium channels.";
RL Toxin 30:1343-1364(1992).
CC -!- FUNCTION: Taicotoxin blocks the high threshold calcium channel
CC current of excitable membranes in heart and does not affect the
CC low threshold calcium channel current. The block is selective for
CC calcium channels, reversible, does not affect single channel
CC conductance but only changes channel gating, and is voltage
CC dependent with higher affinity for inactivated channels. Is very
CC toxic to mice.
CC -!- SUBUNIT: Linked to an alpha-neurotoxin-like peptide of 8000 Da and
CC a neurotoxic phospholipase of 16000 Da by non-covalent bonds. The

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CC ratio is approximately one phospholipase and one neurotoxin for
CC four protease inhibitors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC
DR PIR: A44180; A44180.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
DR Calcium channel inhibitor; Direct protein sequencing; Toxin.
KW Ionic channel inhibitor; Neurotoxin; Serine protease inhibitor; Toxin.
FT DISULFID 7 57 By similarity.
FT DISULFID 16 40 By similarity.
FT DISULFID 32 53 By similarity.
SQ SEQUENCE 62 AA; 7045 MW; ABE0BEPD1990605 CRC64;

Query Match 52.3%; Score 158; DB 1; Length 62;
Best Local Similarity 51.0%; Pred. No. 5.1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQPEAGFCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 7 CHLPKPGPCRAAIPRFYNNPHSKQCEKFIYGGCGHGNANKFTPDCEVTC 57

RESULT 28
CRPT-BOOMI
ID CRPT-BOOMI STANDARD; PRT; 69 AA.
AC P81162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protease inhibitor carapatin.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE.
RA Fuentes-Prior P., Pereira P.J.B., Mentale R., Bode W.;
RL Submitted (JAN-1998) to Swiss-Prot.
CC -1- FUNCTION: Serine protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC
DR HSP; P00980; IDTX.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 18 19 Reactive bond (By similarity).
FT DISULFID 8 58 By similarity.
FT DISULFID 17 41 By similarity.
FT DISULFID 33 54 By similarity.
SQ SEQUENCE 69 AA; 7842 MW; E0B14312AC1533BB CRC64;

Query Match 52.3%; Score 158; DB 1; Length 69;
Best Local Similarity 51.0%; Pred. No. 5.6e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQPEAGFCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 8 CVPTADPGCKGFPMWYNNIFTSQCEEFYGGCGQNDNRRTKEECDKTC 58

RESULT 29
Q6B8G1
ID Q6B8G1 PRELIMINARY; PRT; 142 AA.

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AC Q6B8G1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE KUN-5 (Fragment).
OS Ixodes pacificus (western blacklegged tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Ixodes.
OX NCBI_TaxID=29930;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Ribeiro J.M.C.;
RT "An insight into the transcriptome of the salivary glands of the adult female tick, Ixodes pacificus."
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Francischetti I.M., Lane R.S., Pham V.M., Ribeiro J.M.C.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: AV674183; AAT92116.1; -.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 16458 MW; A618BE45CB812C4B CRC64;

Query Match 52.3%; Score 158; DB 2; Length 142;
Best Local Similarity 52.9%; Pred. No. 1.2e-11;
Matches 27; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQPEAGFCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 29 CTEVVDGPGCRALIPRFYNNMETEKCEBFDYGGCYGNNNNFNESSCTSTC 79

RESULT 30
Q6ITB4
ID Q6ITB4 PRELIMINARY; PRT; 83 AA.
AC Q6ITB4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-2.
OS Oxyuranus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: AV626931; AAT45407.1; -.
DR HSP; P10646; IADZ.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

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Query Match          52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 CELPADTGPCRVGFPFSFYNNPDEKKCLEFIYGGCGGNNNNFITKECESTC 81

RESULT 31
Q61TB5 PRELIMINARY; PRT; 83 AA.
AC Q61TB5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Microlepidin-1.
OS Oxururus microlapidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxururus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; AY626930; AAT45406.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 83 AA; 9040 MW; C84F5E17570CF94C CRC64;

Query Match          52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 CELPADTGPCRVGFPFSFYNNPDEKKCLEFIYGGCGGNNNNFITKECESTC 81

RESULT 32
Q61TB6 PRELIMINARY; PRT; 83 AA.
AC Q61TB6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Scutellin-2.
OS Oxururus scutellatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxururus.
OX NCBI_TaxID=8668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; AY626929; AAT45405.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
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DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Query Match          52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 CELPADTGPCRVGFPFSFYNNPDEKKCLEFIYGGCGGNNNNFITKECESTC 81

RESULT 33
BTIA_BOOMI
ID BTIA_BOOMI STANDARD; PRT; 122 AA.
AC P83609;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kunitz-type serine protease inhibitor BmTI-A (Fragments).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE AND FUNCTION.
RC TISSUE=Larva;
RX PubMed=10615008; DOI=10.1016/S0162-3109(99)00074-0;
RA Tanaka A.S., Andreotti R., Gomes A., Torquato R.J.S., Sampaio M.U.,
RA Sampaio C.A.M.;
RT "A double headed serine proteinase inhibitor-human plasma kallikrein
and elastase inhibitor-from Boophilus microplus larvae.";
RL Immunopharmacology 45:171-177(1999).
CC -!- FUNCTION: Inhibits bovine trypsin, bovine chymotrypsin, human
plasmin, human plasma kallikrein and human neutrophil elastase,
but not bovine thrombin, human factor Xa or porcine pancreatic
kallikrein. May play a role in blocking blood coagulation during
the larvae fixation on cattle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR InterPro; IPR002223; Kunitz_BPTI.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW Direct protein sequencing; Repeat; Serine protease inhibitor.
FT DOMAIN 10 60
FT DISULFID 62 112 BPTI/Kunitz inhibitor 1.
FT DISULFID 10 60 BPTI/Kunitz inhibitor 2.
FT DISULFID 35 56 By similarity.
FT NON_CONS 69 70 By similarity.
FT DISULFID 71 121 By similarity.
FT DISULFID 80 104 By similarity.
FT DISULFID 96 117 By similarity.
FT SITE 19 20 Reactive bond (By similarity).
FT SITE 71 72 Reactive bond (By similarity).
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13736 MW; 8F5B1F48E10C566F CRC64;

Query Match          52.0%; Score 157; DB 1; Length 122;
Best Local Similarity 52.9%; Pred. No. 1.3e-11;
Matches 27; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 71 CLARPESGPCLAYMPMGYDCKGQCVEFIYGGCGGNDKNTTBECLKSC 121
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RESULT 34
Q7YR08 PRELIMINARY; PRT; 234 AA.
AC Q7YR08;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;
RA Du X., Deng F.M., Chand H.S., Kisiel W.;
RT "Molecular cloning, expression, and characterization of bovine tissue
factor pathway inhibitor-2."
RL Arch. Biochem. Biophys. 417:96-104(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Deng F.-M., Kisiel W., Sun T.-T.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DE EMBL; AY234861; AA084035.1; -.
DR HSP; P00981; IDTK
GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26675 MW; 401EBC84D589B422 CRC64;

Query Match 52.0%; Score 157; DB 2; Length 234;
Best Local Similarity 49.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMQAGAGCLASIPHHWYKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
DB 36 CLLPDDGCRARIPSYDYRYTQSCREFYGGCGNANNFETLEACNEAC 86

RESULT 35
Q8IT91 PRELIMINARY; PRT; 759 AA.
AC Q8IT91;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kunitz-like protease inhibitor precursor.
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostominae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Baltimore;
RY MEDLINE=22645137; PubMed=12760667;
RA Hawdon J.M., Datu B., Crowell M.;
RT "Molecular cloning of a novel multidomain Kunitz-type proteinase
inhibitor from the hookworm Ancylostoma caninum."
RL J. Parasitol. 89:402-407(2003).
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DE EMBL; AF533590; AA010061.1; -.
DR HSP; P31713; 1GHP
GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 12.
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DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 12.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 12.
KW Protease; Signal.
FT SIGNAL 1 16 Potential.
SQ SEQUENCE 759 AA; 84886 MW; C431A3C3F418F40A CRC64;

Query Match 52.0%; Score 157; DB 2; Length 759;
Best Local Similarity 51.0%; Pred. No. 8.5e-11;
Matches 26; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMQAGAGCLASIPHHWYKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
DB 205 CSQPIAGPCMAWKRYAYDNKKKRCVQFIYGGCKGNKNFESMEECTRTC 255

RESULT 36
Q90WAL PRELIMINARY; PRT; 83 AA.
AC Q90WAL;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textlinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Venom gland;
RC Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.,
RA Flippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DE EMBL; AF40324; AA035519.1; -.
DR HSP; P25660; IJUC6.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;

Query Match 51.7%; Score 156; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 1.2e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQAGAGCLASIPHHWYKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
DB 31 CELPADTGPCRVRFPSFYNPDEKKCLEFIYGGCGNANNFITKECESTC 81

RESULT 37
Q6AX20 PRELIMINARY; PRT; 587 AA.
AC Q6AX20;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Aolp2 A protein.
DR Namesaplp2 A;
GN Xenopus laevis (African clawed frog).
OC Xenopus laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RN Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC079801; AAH79801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR Pfam; PF02177; A4 EXTRA; I.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot Inh_Kunz-m; 1.
DR SMART; SM00006; A4 EXTRA; I.
DR SMART; SM00131; KU_1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW SIGNAL.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 751 amyloid-beta-like protein A.
SQ SEQUENCE 751 AA; 85200 MW; C5E8FE7302C36B58 CRC64;
Query Match 51.7%; Score 156; DB 2; Length 587;
Best Local Similarity 49.0%; Pred. No. 8.7e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 1 CSMQAEAGCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 284 CSQEAITGCRAMPWRWYFNLGQKCFRFYGGCGNNRNFESDYCMAVC 334
RESULT 38
Q70820
ID Q70820 PRELIMINARY; PRT; 751 AA.

Q70820;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amyloid-beta-like protein A precursor.
GN Name=aplp2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Collin R.W.J., van Strien D., Leunissen J.A., Martens G.J.M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ608932; CAE75662.1; -.
DR HSSP; Q16019; 1AAP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR002223; Prot Inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; I.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot Inh_Kunz-m; 1.
DR SMART; SM00006; A4 EXTRA; I.
DR SMART; SM00131; KU_1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW SIGNAL.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 751 amyloid-beta-like protein A.
SQ SEQUENCE 751 AA; 85200 MW; C5E8FE7302C36B58 CRC64;
Query Match 51.7%; Score 156; DB 2; Length 751;
Best Local Similarity 49.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 1 CSMQAEAGCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 292 CSQEAITGCRAMPWRWYFNLGQKCFRFYGGCGNNRNFESDYCMAVC 342
RESULT 39
Q91963
ID Q91963 PRELIMINARY; PRT; 747 AA.
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE APP747.
GN Name=APP747;
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae;
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93129227; PubMed=1282805;
RA Okado H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; S52417; AAB24853.1; -.
DR HSSP; Q16019; 1H23.


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DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 747 AA; 84893 MW; A75B81885681D948 CRC64;

Query Match 51.0%; Score 154; DB 2; Length 747;
Best Local Similarity 47.1%; Pred. No. 2e-10;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 287 CSEQATGPRAMISRWYDVTSKCAQFIYGGCGGNNNNFSDDDYCMVAVC 337

RESULT 40
Q6NRR1 PRELIMINARY; PRT; 749 AA.
ID Q6NRR1
AC Q6NRR1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE App protein.
GN Name: app;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalsek U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
Dev. Dyn. 225:384-391 (2002).
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RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.,
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; RC070668; AAH70668.1; -.
DR HSSP; Q16019; 1BA4.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 749 AA; 84766 MW; 33478C6B6A8C295D CRC64;

Query Match 51.0%; Score 154; DB 2; Length 749;
Best Local Similarity 47.1%; Pred. No. 2e-10;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 289 CSEQATGPRAMISRWYDVTSKCAQFIYGGCGGNNNNFSDDDYCMVAVC 339

RESULT 41
Q9GQN1 PRELIMINARY; PRT; 984 AA.
ID Q9GQN1
AC Q9GQN1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name: PAM;
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynatheae; Hormathiidae; Calliactis.
OX NCBI_TaxID=6114;
RN [1]
RP SEQUENCE FROM N.A.
RL Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RL Submitted (Jan-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF221986; AAG44251.1; -.
DR HSSP; P12111; 1KNT.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005507; F: copper ion binding; IEA.
DR GO; GO:0004504; F: peptidylglycine monooxygenase activity; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006518; P: peptide metabolism; IEA.
DR InterPro; IPR011044; Amine DH B-like.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR000720; Pamonooxygenase.
DR InterPro; IPR008977; PHM_PNGase F.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF03712; Cu2_monoox_C; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
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DR Pfam: PF01436; NHL; 5.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110265 MW; 4C24E4BCEB3B480D CRC64;

Query Match 51.0%; Score 154; DB 2; Length 984;
Best Local Similarity 43.1%; Pred. No. 2.6e-10;
Matches 22; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYTNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 730 CMLEHDTGCRAMPWPYFDKARSCTRFIYGGCGGNNNFASKRECAKC 780

RESULT 42
Q9GQN2 PRELIMINARY; PRT; 984 AA.
AC Q9GQN2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name=PAM;
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Hormathiidae; Calliactis.
OX NCBI_TaxID=6114;
RN [1]
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RC Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF221985; AG44250.1; -.
DR HSP; P12111; IKNT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0004504; F:peptidylglycine monooxygenase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0005518; P:peptide metabolism; IEA.
DR InterPro; IPR011044; A:amine DH_B-like.
DR InterPro; IPR000323; Cu2 monooxygenase.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR000720; P:ammonooxygenase.
DR InterPro; IPR008977; PHM PNGase F.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF01082; Cu2 monooxygen; 1.
DR Pfam; PF03712; Cu2 monoox C; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR Pfam; PF01436; NHL; 5.
DR PRINTS; PR00759; BASICTPASE.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110266 MW; 7AFE2D1B74B78EBC CRC64;

Query Match 51.0%; Score 154; DB 2; Length 984;
Best Local Similarity 43.1%; Pred. No. 2.6e-10;
Matches 22; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYTNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 730 CMLEHDTGCRAMPWPYFDKARSCTRFIYGGCGGNNNFASKRECAKC 780

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RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=92077130; PubMed=1743283; DOI=10.1016/0014-5793(91)81361-B;
RA Siddiqi A.R., Zaidi Z.H., Joernvall H.;
RT Purification and characterization of a Kunitz-type trypsin inhibitor
RT from leaf-nosed viper venom.";
RL FEBS Lett. 294:141-143(1991).
CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR, S19327; S19327.
DR HSP; P25660; 1JC6.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 12 13 Reactive bond (By similarity).
FT DISULFID 2 52 By similarity.
FT DISULFID 11 35 By similarity.
FT DISULFID 27 48 By similarity.
SQ SEQUENCE 62 AA; 6772 MW; 0A2ED0ADB20DF938 CRC64;

Query Match 50.7%; Score 153; DB 1; Length 62;
Best Local Similarity 51.0%; Pred. No. 2.1e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB CYPDPGVCKAHPFYNNPASNCKNFKFYGGCGGNNNNFETRAECRHTC 52

RESULT 45
Q6T6S5 PRELIMINARY; PRT; 90 AA.
AC Q6T6S5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Kunitz protease inhibitor 2.
OS Bitis gabonica (Gaboon adder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OX NCBI_TaxID=8694;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15274202; DOI=10.1016/j.gene.2004.03.024;
RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
RA Ribeiro J.M.;
RT "Bitis gabonica (Gaboon viper) snake venom gland: toward a catalog for
RT the full-length transcripts (cDNA) and proteins.";
RL Gene 337:55-69(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY430413; AAR24535.1; -.
DR HSP; Q16019; 1AAP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.

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KW Protease.
SQ SEQUENCE 90 AA; 10006 MW; 2BEDC1D2020852AF CRC64;

Query Match 50.7%; Score 153; DB 2; Length 90;
Best Local Similarity 45.1%; Pred. No. 3.1e-11;
Matches 23; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB CYPDPGVCKAHPFYNNPASNCKNFKFYGGCGGNNNNFETRAECRHTC 52

RESULT 46
Q7T0Z5 PRELIMINARY; PRT; 224 AA.
AC Q7T0Z5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC68843 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/gvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; BC055972; AAH55972.1; -.
DR HSP; P00974; 1BPI.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 3.

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SQ SEQUENCE 224 AA; 25538 MW; 11C3D1C4C789445B CRC64;
Query Match 50.7%; Score 153; DB 2; Length 224;
Best Local Similarity 49.0%; Pred. No. 7.7e-11;
Matches 25; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 CSMQAEAGCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
D- - - - - : : : : : : : : : : : : : : : : : : : : : :
DB 30 CLLPLDEGCKALIPHYYYDRYTQCEFFYGGCGNANNFVSMEDCEKFC 80

RESULT 47
IP52 ANESU
ID IP52 ANESU STANDARD; PRT; 62 AA.
AC P10280;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protease inhibitor 5 II (SAS II).
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anemonia.
OX NCBI_TaxID=6108;
RN [1]
RP SEQUENCE OF 1-59.
RA Wunderer G., Machleidt W., Fritz H.;
RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
RT Anemonia sulcata.";
RL Meth. Enzymol. 80:816-820(1981).
RN [2]
RP SEQUENCE.
RA Krebs H.C., Habermehl G.G.;
RT "Isolation and structural determination of a hemolytic active peptide
RT from the sea anemone Metridium senile.";
RL Naturwissenschaften 74:395-396(1987).
CC -|- FUNCTION: Inhibitor of kallikreins.
CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S07451; S07451.
DR HSP; F31713; ISHP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 15 16 Reactive bond (By similarity).
FT DISULFID 5 55 By similarity.
FT DISULFID 14 38 By similarity.
FT DISULFID 30 51 By similarity.
FT VARIANT 13 13 P -> R.
FT VARIANT 16 16 A -> G.
FT VARIANT 17 17 R -> G.
FT VARIANT 25 25 S -> L.
FT VARIANT 28 28 K -> R.
FT VARIANT 39 39 G -> R.
SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;
Query Match 50.3%; Score 152; DB 1; Length 62;
Best Local Similarity 49.0%; Pred. No. 2.8e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 1 CSMQAEAGCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
D- - - - - : : : : : : : : : : : : : : : : : : : : : :
DB 5 CELPKVVGPCARFRFRYYNSSKRCCKEKFYGGCGNANNFHTLECEKVC 55

RESULT 48
Q90WAO
ID Q90WAO PRELIMINARY; PRT; 83 AA.
AC Q90WAO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textilinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Flippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF402325; AAK95520.1; -.
DR HSP; P25660; 1UC6.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9179 MW; 67E589AD27175930 CRC64;
Query Match 50.3%; Score 152; DB 2; Length 83;
Best Local Similarity 49.0%; Pred. No. 3.8e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMQAEAGCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
D- - - - - : : : : : : : : : : : : : : : : : : : : : :
DB 31 CELPDTGTCRVFRFPFVYNDEQKCLEFFYGGCGNANNFITKECESTC 81

RESULT 49
Q6ITB7
ID Q6ITB7 PRELIMINARY; PRT; 83 AA.
AC Q6ITB7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scutellin-1.
OS Oxyuranus scutellatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Elapidae; Acanthophinae; Oxyuranus.
OX NCBI_TaxID=8668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Flippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626928; AAT45404.1; -.
DR HSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9047 MW; 249FD51757014221 CRC64;
Query Match 50.3%; Score 152; DB 2; Length 83;
Best Local Similarity 49.0%; Pred. No. 3.8e-11;
```


Matches	25;	Conservative	7;	Mismatches	19;	Indels	0;	Gaps	0;
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Qy 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
| : | | | | | | | | | | | | | | | : | | |
Db 31 CELPADTGP^{CRV}GFPSPFYNNPDEKKCLEFIYGGCEGANNFITKEECSTC 81

RESULT 50

Q9NOX3	PRELIMINARY;	PRT;	154 AA.
ID	Q9NOX3		
AC	Q9NOX3;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Kunitz domain protein 2 (Fragment).		
DE	Name=TKDP2;		
GN	Ovis aries (Sheep).		
OS	Ovis aries; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Peri-implantation whole conceptus;		
RC	Green J.A., Maclean J.A. II, Gan X., Xie S., Roberts R.M.;		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.		
DR	EMBL; AF241828; AAF64495.1; ..		
DR	HSSP; P00974; 2KAI.		
DR	GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.		
DR	InterPro; IPR002233; Prot_Inh_Kunz-m.		
DR	Pfam; PF00014; Kunitz_BPTI; 1.		
DR	PRINTS; PR00759; BASICPTASE.		
DR	ProDom; PD000222; Prot_Inh_Kunz-m; 1.		
DR	SMART; SM00131; KU; 1		
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.		
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 1.		
DR	NON TER		
DR	1		
DR	SEQUENCE		
DR	154 AA; 17069 MW; B81A91E833212F52A CRC64;		

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Query Match      50.3%; Score 152; DB 2; Length 154;
Best Local Similarity 49.0%; Pred. No. 7e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
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QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFOTEICLVTC 51
| - : | | | : : | | | - : | | | : | | | : | | | |
Db 97 CLEPELKGCKDQMTFYFNATAGCEPFYGGCGNNNNFOTLSDCLVTC 147

Search completed: September 21, 2005, 16:40:11
Job time : 29.1327 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2005, 16:47:56 ; Search time 79 Seconds

(without alignments)
3877.395 Million cell updates/sec

Title: US-10-807-204-11

Perfect score: 764

Sequence: 1 atgggactctcaggacttct.....cctgcaaaaaataaccattaa 396

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Command line parameters: -DEV=xlh

-MODE=frame_n2p.model -DEV=xlh
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-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=std.rag -MINMATCH=0.1 -LOOPFCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=50 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741	97.0	131	ADAI19800	Adai19800 Engineere
2	741	97.0	131	ADAI19811	Adai19811 Engineere
3	739	96.7	131	ADAI19814	Adai19814 Human DJ1
4	613	80.2	106	ADAI19801	Adai19801 Mature fo
5	559	73.2	98	ADAI19808	Adai19808 Engineere
6	480	62.8	136	ADAI19815	Adai19815 Mouse DJ1
7	455	59.6	133	AAW75219	AAW75219 Human sec
8	455	59.6	133	AAE26982	AAE26982 Human gen
9	455	59.6	133	AAE27120	AAE27120 Human gen
10	455	59.6	133	ABU64993	ABU64993 Human sec

11	455	59.6	133	7	ADAI19812	ADAI19812 Human EPP
12	455	59.6	133	8	ADG89802	ADG89802 Human PRO
13	455	59.6	164	3	AAI70010	AAI70010 Human PRO
14	455	59.6	179	8	ABM85103	ABM85103 Human dia
15	455	59.6	86	5	ABP69809	ABP69809 Human pol
16	412	53.9	86	6	ABJ26667	ABJ26667 Human pro
17	412	53.9	101	4	ABB12236	ABB12236 Human epp
18	389.5	51.0	117	5	AAE27094	AAE27094 Human sec
19	389.5	51.0	117	5	AAE27165	AAE27165 Human gen
20	389.5	51.0	117	6	ABU65038	ABU65038 Human sec
21	389.5	51.0	117	8	ADG89847	ADG89847 Human sec
22	388	50.8	102	5	AAE27095	AAE27095 Human sec
23	388	50.8	102	5	AAE28009	AAE28009 Human gen
24	388	50.8	102	5	ABU65039	ABU65039 Human gen
25	388	50.8	102	8	ADG89848	ADG89848 Human sec
26	386	50.5	134	7	ADAI19813	ADAI19813 Mouse EPP
27	254	33.2	43	7	ADAI19804	ADAI19804 Engineere
28	242	31.7	64	4	AAE13093	AAE13093 Human epr
29	236.5	31.0	101	8	ADG66734	ADG66734 Novel hum
30	236	30.9	58	4	AAE13084	AAE13084 Human epr
31	236	30.9	58	4	AAE60630	AAE60630 Kunitz do
32	236	30.9	58	7	ADF41997	ADF41997 Human CAB
33	236	30.9	58	8	ADL16838	ADL16838 Human Kun
34	236	30.9	58	8	ADR89980	ADR89980 Human CAB
35	219	28.7	51	2	AAW75257	AAW75257 Fragment
36	219	28.7	51	5	AAE27025	AAE27025 Human gen
37	219	28.7	51	5	AAE27163	AAE27163 Human gen
38	219	28.7	51	8	ADG89845	ADG89845 Human sec
39	182.5	23.9	560	2	AAE62523	AAE62523 Hookworm
40	181	23.7	2858	4	ABB71150	ABB71150 Drosophil
41	181	23.7	3060	4	ABE58064	ABE58064 Drosophil
42	180.5	23.6	571	7	AAE39498	AAE39498 Cloned mo
43	180.5	23.6	571	7	AAE39459	AAE39459 Mouse GDF
44	180.5	23.6	571	7	ADD93670	ADD93670 Mouse GDF
45	180	23.6	33	7	ADAI19806	ADAI19806 Engineere
46	180	23.6	33	7	ADAI19809	ADAI19809 Engineere
47	177	23.2	58	2	AAE99146	AAE99146 Apotinin
48	175	22.9	43	4	AAE13096	AAE13096 Human epr
49	175	22.9	54	4	AAE13092	AAE13092 Trypsin i
50	173	22.6	58	2	AAE27402	AAE27402 Human neu

ALIGNMENTS

RESULT 1
ADAI19800
ID ADAI19800 standard; protein; 131 AA.
XX
AC ADAI19800;
XX
DT 20-NOV-2003 (first entry)
XX
DE Engineered human DJ11 protein SEQ ID NO:1.
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..131 /note= "eppin-like precursor"
FT Peptide 1..25 /label= signal
FT Protein 26..131

FT Disulfide-bond /note= "mature DJ11 protein"
 FT 33. .61
 FT /note = predicted disulfide bond
 FT Disulfide-bond /note = predicted disulfide bond
 FT 40. .65
 FT /note = predicted disulfide bond
 FT Disulfide-bond /note = predicted disulfide bond
 FT 48. .60
 FT /note = predicted disulfide bond
 FT Disulfide-bond /note = predicted disulfide bond
 FT 54. .69
 FT /note = predicted disulfide bond
 FT 77. .127
 FT /note = Kunitz domain predicted by pfscan
 FT Disulfide-bond /note = predicted disulfide bond
 FT 77. .127
 FT Disulfide-bond /note = predicted disulfide bond
 FT 86. .110
 FT /note = predicted disulfide bond
 FT Disulfide-bond /note = predicted disulfide bond
 FT 102. .123
 FT /note = predicted disulfide bond
 XX WO2003070770-A2.
 XX
 XX 28-AUG-2003.
 XX
 XX 18-FEB-2003; 2003WO-EP001629.
 XX
 XX 21-FEB-2002; 2002US-0358683P.
 XX
 XX (GENE-) GENEPROT INC.
 XX
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX N-PSDB; ADA19810.
 XX
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 FT preventing or treating conditions associated with excessive proteinase
 FT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 FT hemorrhage.
 XX
 XX Claim 5; Page 69-70; 87pp; English.
 XX
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.
 XX
 XX Sequence 131 AA;
 SQ

Alignment Scores:
 Pred. No. : 1.64e-68 Length: 131
 Score: 741.00 Matches: 130
 Percent Similarity: 99.24% Conservative: 0
 Best Local Similarity: 99.24% Mismatches: 1
 Query Match: 96.99% Indels: 0
 DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19800 (1-131)
 Qy 1 ATGGGACTCTCAGGACTTCTGCCAAATCCTGGTACCATTATCCTTTGGGGACATCCAG 60
 |||||
 Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
 |||||
 Qy 61 GAACCTGGGCACGCTGAAGGCATCCTTTGGCAAGCCGTGCCAAAATCAAAAGTGAATGC 120
 |||||
 Db 21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysIleValGluCys 40
 |||||
 Qy 121 GAAGTGGAGAAATAGACCAAGTGTACCAAAACCAGAGATTGCCAGAAAACATGAAGTGT 180
 |||||
 Db 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAenMetLysCys 60
 |||||
 Qy 181 TGCCCGTTACGCCGTGGAAAGAAATGTTAGACTTCAGAAAGAGATATATCAGTATGCCA 240
 |||||
 Db 61 CysProPheSerCysGlyLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
 |||||
 Qy 241 CAGGAGGCTGGCCCTGGCTCCATACCACTGGTGGTGTACATAAATAAATAAAGTAAG 300
 |||||
 Db 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisIleTrpTyrAenLysLysThrLys 100
 |||||
 Qy 301 ATCTGCTCGAATTCTATGCGGTTGCCAGGGGAACAATAACAACACTTCCAAACTGAA 360
 |||||
 Db 101 IleCysSerGluPheIleTyrGlyCysGlnGlyAenAenAenAenPheGlnThrGlu 120
 |||||
 Qy 361 GCTATCTGTCTGCTCACCTGCCAAAATAATACCAT 393
 |||||
 Db 121 AlaIleCysLeuValThrCysLysLysTyrHis 131
 |||||
 RESULT 2
 ADA19811
 ID ADA19811 standard; protein; 131 AA.
 XX
 AC ADA19811;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Engineered human DJ11 protein SEQ ID NO:12.
 XX
 KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO2003070770-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 18-FEB-2003; 2003WO-EP001629.
 XX
 PR 21-FEB-2002; 2002US-0358683P.
 XX
 XX (GENE-) GENEPROT INC.
 XX
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX

PS Disclosure; Page 84; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents an engineered human DJ11 protein from the
XX present invention.

SQ Sequence 131 AA;

Alignment Scores:

Pred. No.: 1.64e-68 Length: 131
Score: 741.00 Matches: 130
Percent Similarity: 99.24% Conservatve: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 96.93% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19811 (1-131)

QY 1 ATGGAGCTCTCAGGACTTCTGCAATCTGTGGTACCATTATCTTTTGGGGACATCCAG 60
DB 1 MetGlyLeuSerGlyLeuLeuProlleuValProPheIleLeuLeuGlyAspIleGln 20
QY 61 GAACCTGGCAGCGCTGAAGGACATCTTGGCAAGCGGTGTCCAAATCAAAAGTGAATGC 120
DB 21 GluProGlyHisAlaGlyIleLeuGlyLysProCysProLysIleLysValGluCys 40
QY 121 GAAGTGGAGAAATAGACAGTGTACCAACCCAGAGATGCCAGAAAACATGAAGTGT 180
DB 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
QY 181 TCCCGTTTCAGCGGTGGAAAGAAATGTTTAGACTTCAGAAAGATATATGCAATATGCCA 240
DB 61 CysProPheSerCysGlyLysLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
QY 241 CAGGAGGCTGGCCCTGCTGCCCTCCATACCACACTGGTGTAACAATAAAAACTAAG 300
DB 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTyrTrpTyrAsnLysLysThrLys 100
QY 301 ATCTGCTCGGAATTATCTATCGCGGTTCACGGGGGAACAATAACACTTCCAAACTGAA 360
DB 101 IleCysSerGluPheIleTyrGlyGlyCysGlnGlyAsnAsnAsnAsnPheGlnThrGlu 120
QY 361 GCTATCTGTCTGCTACCTGCAAAAATAACAT 393
DB 121 AlaIleCysLeuValThrCysLysLysIleHis 131

RESULT 3

ADA19814

ID ADA19814 standard; protein; 131 AA.

XX ADA19814;

AC ADA19814;

XX 20-NOV-2003 (first entry)

XX Human DJ11 protein SEQ ID NO:15.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
XX antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX nephrotropic; antiporiatic; vulnary; protease inhibitor; gene therapy;
XX acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX deep vein thrombosis; myocardial infarction; shock; septic shock;
XX hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX chronic inflammatory bowel disease; psoriasis.

XX Homo sapiens.

OS WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents a human DJ11 protein given in comparison
XX with DJ11 proteins in the exemplification of the present invention.

XX Sequence 131 AA;

Alignment Scores:

Pred. No.: 2.65e-68 Length: 131
Score: 739.00 Matches: 130
Percent Similarity: 99.24% Conservatve: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 96.73% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19814 (1-131)

QY 1 ATGGAGCTCTCAGGACTTCTGCAATCTGTGGTACCATTATCTTTTGGGGACATCCAG 60

Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
 Qy 61 GAACCTGGGACGCTGAAGGCATCTTGGCAAGCGGTGTCCCAAAATCAAAAGTGGATGC 120
 Db 21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysIleLeuValGluCys 40
 Qy 121 GAAGTGGAGAAATAGACCGAGTGTACCAAAACCCAGAGNTTCCCGAGAAACATGAAGTGT 180
 Db 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
 Qy 181 TGCCCGCTTCCGCGCTGGAAGAAATGTTTACACTTCAGAAAGGATATATGAGTATGCGCA 240
 Db 61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLysAspLleCysSerMetPro 80
 Qy 241 CAGAGGCTGCCCTGCTGCCTGCCATACCACTGGTGGTGTACATATAAAAACTAAG 300
 Db 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTrpTyrAsnLysLysThrLys 100
 Qy 301 ATCTGCTCCGAATTCATCTATGCGGTGTCCAGGGGACATACCACTTCCAACTGAA 360
 Db 101 IleCysSerGluPheIleTyrGlyGlySerGlnGlyAsnAsnAsnPheGlnThrGlu 120
 Qy 361 GCTATCTGCTGCTGCTGCACTGCAAAAAATACCAT 393
 Db 121 AlaIleCysLeuValThrCysLysLysTyrHis 131

RESULT 4

ID ADA19801 standard; protein; 106 AA.

AC ADA19801;

DT 20-NOV-2003 (first entry)

DE Mature form of engineered human DJ11 protein SEQ ID NO:2.

KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

OS Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 8..36 /note = predicted disulfide bond
 FT Disulfide-bond 15..40 /note = predicted disulfide bond
 FT Disulfide-bond 23..35 /note = predicted disulfide bond
 FT Disulfide-bond 29..44 /note = predicted disulfide bond
 FT Domain 52..102 /note = predicted disulfide bond
 FT Disulfide-bond 52..102 /note = predicted disulfide bond
 FT Disulfide-bond 61..85 /note = predicted disulfide bond
 FT Disulfide-bond 77..98 /note = predicted disulfide bond
 FT Disulfide-bond 77..98 /note = predicted disulfide bond

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENBPROT INC.

XX Bouguesleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX hemorrhage.

XX Claim 5; Page 71; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
 XX biologically active portion. The polypeptide comprises at least 98 %
 XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
 XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 XX antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
 XX activities, and can be used as a protease inhibitor and in gene therapy.
 XX Composition and methods from the present invention can be used in
 XX diagnosing, preventing or treating conditions associated with excessive
 XX proteinase activity, such as acute pancreatitis, pulmonary injury,
 XX allergy-induced protease release, deep vein thrombosis, myocardial
 XX infarction, shock (including septic shock), hyperfibrinolytic
 XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 XX be used in preserving platelet function, organ preservation or in wound
 XX healing. The polynucleotide sequence encoding DJ11 may be used as
 XX hybridisation probes, in chromosome and gene mapping, in the generation
 XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 XX The present sequence represents the mature form of an engineered human
 XX DJ11 protein from the present invention.

XX Sequence 106 AA;

XX Alignment Scores:

Pred. No.: 3-72e-55 Length: 106

Score: 613.00 Matches: 105

Percent Similarity: 99.06% Conservative: 0

Best Local Similarity: 99.06% Mismatches: 1

Query Match: 80.24% Indels: 0

DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19801 (1-106)

Qy 76 GAAGGCATCTTGGCAAGCGGTGTCCCAAAATCAAAAGTGGAAATCGGAAGTGAAGAATA 135
 Db 1 GluGlyIleLeuGlyLysProCysProLysIleLysValGluCysGluValGluGluIle 20

Qy 136 GACCAGTGTACCAACCCAGAGATTGCCCGAAACATGAAGTGTGCCCGTTCAGCCGT 195
 Db 21 AspGlnCysThrLysProArgAspCysProGluAsnMetLysCysCysProPheSerCys 40

Qy 196 GGAAGAAGATGTTTAGACTTCAGAAAGGATATATGCAGTATGCCACAGGAGGTGGCCCC 255
 Db 41 GlyLysLysCysLeuAspPheArgLysAspLleCysSerMetProGlnGluAlaGlyPro 60

Qy 256 TGCTTGCTCCCATACACACTGGTGTACAATAAAAACTAAGATCTCTCCGAATTC 315
 Db 61 CysLeuAlaSerIleProHisTrpTyrAsnLysLysThrLysIleCysSerGluPhe 80

Qy 316 ATCTATGGCGGTGCCAGGGGACAAATACAACTTCCAACTGAAGCTATCTGTCTGGTC 375
 Db 81 IleTyrGlyGlyCysGlnGlyAsnAsnAsnAsnPheGlnThrGluAlaIleCysLeuVal 100

Qy 376 ACCTGCAAAAAAATACCAT 393


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Db      101 ThrCysLysTyHis 106
|||||
RESULT 5
ADAL19808
ID      ADA19808 standard; protein; 98 AA.
XX
AC      ADAL19808;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Engineered human DJ11 partial amino acid sequence SEQ ID NO:9.
XX
KW      DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW      anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW      antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW      nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW      acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW      deep vein thrombosis; myocardial infarction; shock; septic shock;
KW      hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW      idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW      chronic inflammatory bowel disease; psoriasis.
XX
OS      Synthetic.
OS      Homo sapiens.
XX
XX      WO2003070770-A2.
XX      28-AUG-2003.
XX
XX      18-FEB-2003; 2003WO-EP001629.
XX
XX      21-FEB-2002; 2002US-0358683P.
XX
XX      (GENE-) GENEPROT INC.
XX
XX      Bougueleret L, Bairoch A, Niknejad A;
XX
XX      WPI; 2003-663849/62.
XX
XX      New engineered human Kunitz-type protease inhibitor for diagnosing,
XX      preventing or treating conditions associated with excessive proteinase
XX      activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX      hemorrhage.
XX
XX      Disclosure; Page 82; 87pp; English.
XX
XX      The present invention describes an isolated, purified or recombinant DJ11
XX      polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX      biologically active portion. The polypeptide comprises at least 98 %
XX      identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX      ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX      ADA19801). DJ11 has antinflammatory, antibacterial, thrombolytic,
XX      anticoagulant, cardiant, vasotropic, antirheumatic, immunosuppressive,
XX      antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
XX      activities, and can be used as a protease inhibitor and in gene therapy.
XX      Composition and methods from the present invention can be used in
XX      diagnosing, preventing or treating conditions associated with excessive
XX      proteinase activity, such as acute pancreatitis, pulmonary injury,
XX      allergy-induced protease release, deep vein thrombosis, myocardial
XX      infarction, shock (including septic shock), hyperfibrinolytic
XX      haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX      idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX      chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX      be used in preserving platelet function, organ preservation or in wound
XX      healing. The polynucleotide sequence encoding DJ11 may be used as
XX      hybridisation probes, in chromosome and gene mapping, in the generation
XX      of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX      The present sequence represents a partial engineered human DJ11 protein
XX      amino acid sequence from the present invention.
XX
XX      Sequence 98 AA;
SQ

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Alignment Scores:
Pred. No.: 1.6e-49 Length: 98
Score: 559.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.17% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19808 (1-98)
QY      1 ATGGGACTCTCAGGACTTCTGCCAATCTCGGTACCATTCATCTTTTGGGGGACATCCAG 60
DB      1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
QY      61 GAACCTGGGCACGCTGAAGGCATCTTGGCAAGCCGTGTCCCAAAATCAAAAGTGAATGC 120
DB      21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysIleLysValGluCys 40
QY      121 GAAGTGGAGAAATAGACCACTGTACCAAAACCCAGAGATTGCCAGAAACATGAAGTGT 180
DB      41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
QY      181 TGCCCGTTTCAGCCGCTGGGAAGAAATGTTTACACTTCAGAAAGGATATATGTCAGTATGCCA 240
DB      61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
QY      241 CAGGAGGCTGGCCCTCGCTGGCTCCATACCACACTGGTGGTACAAATAAAAAA 294
DB      81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTrpTrpTyrAsnLysLys 98

RESULT 6
ADAL19815
ID      ADA19815 standard; protein; 136 AA.
XX
AC      ADAL19815;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Mouse DJ11 protein SEQ ID NO:16.
XX
KW      DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW      anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW      antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW      nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW      acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW      deep vein thrombosis; myocardial infarction; shock; septic shock;
KW      hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW      idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW      chronic inflammatory bowel disease; psoriasis.
XX
OS      Mus musculus.
XX
XX      WO2003070770-A2.
XX
XX      28-AUG-2003.
XX
XX      18-FEB-2003; 2003WO-EP001629.
XX
XX      21-FEB-2002; 2002US-0358683P.
XX
XX      (GENE-) GENEPROT INC.
XX
XX      Bougueleret L, Bairoch A, Niknejad A;
XX
XX      WPI; 2003-663849/62.
XX
XX      New engineered human Kunitz-type protease inhibitor for diagnosing,
XX      preventing or treating conditions associated with excessive proteinase
XX      activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX      hemorrhage.
XX
XX      Disclosure; Fig 1; 87pp; English.
XX
XX

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QY 61 GAACCTGGCAGCTGAAGCATCTTGGCAAGCGCTGCCAAATCAAAATCAAAATCAAAATGTC 120
 Db ||||| : : : : :
 21 GlyProGlyLeuThrAspGlyLeuPheProArgCysProLeuValLeuValLeuValGln 40
 QY 121 GAAGTGGAGAAATAGCAGTGTACCAACCCAGAGATTGCCAGAAACATCAAGTGT 180
 Db ||||| : : : : :
 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60
 QY 181 TGCCCGTTTCAGCGCGTGAAGAAATGTTTAGACTTCAGAAAGGATATATGTCAGTATGCCA 240
 Db ||||| : : : : :
 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
 QY 241 CAGGAGGTGGCCCTGCTGCTGCCATCCACACACTGCTGCTACATAAATAAATAAAGTAA 300
 Db ||||| : : : : :
 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTyrTyrAspLysLysAspAsn 100
 QY 301 ATCTGCTCGAATTCATCTATGCGCGTTCAGGGGGAACATACAACTTCNAACTGAA 360
 Db ||||| : : : : :
 101 ThrCysSerMetPheValTyrGlyCysGlnGlyAsnAsnAsnAsnAsnAsnAsn 120
 QY 361 GCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
 Db ||||| : : : : :
 121 AlaAsnCysLeuAsnThrCysLys 128

RESULT 8
 AAE26982
 ID AAE26982 standard; protein; 133 AA.
 XX
 AC AAE26982;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:34.
 XX
 KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropic; vulnery; cytostatic; nootropic; cardiac;
 KW anti-HIV; tranquilliser; gout; antiparasitic.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..21
 FT Protein /label= Signal_peptide
 FT 22..133 /note= "Human mature secreted protein"
 XX
 US2002077287-A1.
 XX
 20-JUN-2002.
 XX
 11-MAY-2001; 2001US-00852659.
 XX
 11-SEP-1998; 98US-00152060.
 XX
 (RUBE/) RUBEN S M.
 (ROSE/) ROSEN C A.
 (LIYY/) LI Y.
 (ZENG/) ZENG Z.
 (KYAW/) KYAW H.
 (FISC/) FISCHER C L.
 (LIHH/) LI H.
 (SOPP/) SOPP D R.
 (GENT/) GENTZ R L.
 (WEIV/) WEI Y.

PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX WPI; 2002-598780/64.
 DR N-PSDB; AAD44659.
 XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 XX Claim 11; Page 185-186; 209pp; English.
 PS AAD4636-AAD4676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., Parkinson's
 CC injury and/or stroke, neurodegenerative disorders e.g., Alzheimer's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcolidosis and allogenic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g., rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders, e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g., endometriosis.
 CC The present sequence represents a human secreted protein of the invention
 XX
 SQ Sequence 133 AA;
 Alignment Scores:
 Pred. No.: 1.26e-38 Length: 133
 Score: 455.00 Matches: 77
 Percent Similarity: 74.22% Conservative: 18
 Best Local Similarity: 60.16% Mismatches: 33
 Query Match: 59.55% Indels: 0
 DB: 5 Gaps: 0
 US-10-807-204-11 (1-396) x AAE26982 (1-133)
 QY 1 ATGGGACTCTCAGGACTTCTGCAATCTGTGTGATTCATCTTTTGGGGACATCCAG 60
 Db ||||| : : : : :
 1 MetGlySerSerGlyLeuLeuSerLeuValLeuValLeuValLeuAlaAsnValGln 20
 QY 61 GAACCTGGCAGCTGAAGGATCTTGGCAAGCGCTGCCAAATCAAAATCAAAATGTC 120
 Db ||||| : : : : :
 21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProLeuValLeuValGlnCys 40
 QY 121 GAAGTGGAGAAATAGCAGTGTACCAACCCAGAGATTGCCAGAAACATCAAGTGT 180
 Db ||||| : : : : :
 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60

AC ABU64993;
 DT 15-MAY-2003 (first entry)
 XX Human secreted protein gene 24, protein #1.
 DE
 XX Secreted protein; immunodeficiency; multiple sclerosis;
 KW severe combined immunodeficiency; autoimmune disorder; cancer;
 KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
 KW inflammatory condition; septic shock; inflammatory bowel disease;
 KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
 KW gastrointestinal disorder; central nervous system disorder;
 KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
 KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
 KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
 KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
 KW endocrine disorder; liver disease; reproductive system disorder;
 KW endometriosis; infectious disease; pancreatic disorder; vaccine;
 KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
 KW body height; hair colour; human.
 XX
 OS Homo sapiens.
 XX
 XX US2002172994-A1.
 PN
 XX
 XX 21-NOV-2002.
 XX
 XX 11-MAY-2001; 2001US-00852797.
 XX
 XX 14-MAR-1997; 97US-0040710P.
 PR 14-MAR-1997; 97US-0040762P.
 PR 30-MAY-1997; 97US-0048100P.
 PR 30-MAY-1997; 97US-0048189P.
 PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0050934P.
 PR 06-JUN-1997; 97US-0048970P.
 PR 05-SEP-1997; 97US-0057763P.
 PR 19-DEC-1997; 97US-0068368P.
 PR 12-MAR-1998; 98WO-US004858.
 PR 11-SEP-1998; 98US-0015206P.
 PR 02-FEB-2001; 2001US-0265583P.
 XX
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIVY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUNG/) YOUNG P E.
 PA (GREENE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX
 PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 XX WPI: 2003-310989/30.
 DR N-PSDB; ABX96989.
 DR
 XX New human secreted polypeptides and polynucleotides for diagnosing,
 PT prognosing, preventing and treating immune, hyperproliferative, liver,
 PT kidney, reproductive disorders and for identifying modulators of
 PT therapeutic use.
 XX
 XX Claim 11; Page 185; 209pp; English.
 PS
 XX The invention relates to an isolated polypeptide comprising an amino acid
 CC sequence at least 95% identical to sequence of 28 human secreted
 CC

CC proteins, their fragment, polypeptide domain, epitope, secreted form,
 CC variant, allelic variant, or species homologue, or the encoded sequence
 CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
 CC acids, recombinant vectors, host cells, antibodies, and genes. The
 CC proteins and nucleic acids are useful for diagnosing, preventing,
 CC treating, prognosing or ameliorating a medical condition e.g.
 CC immunodeficiencies (e.g. X-linked agammaglobulinemia, B cell
 CC immunodeficiencies, severe combined immunodeficiencies), autoimmune
 CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,
 CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
 CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
 CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
 CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
 CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
 CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
 CC injury and/or stroke, traumatic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
 CC dementia, and prion disease), cardiovascular disorders (e.g.
 CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
 CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
 CC pancreatitis, sarcoidosis, dermatitis, allogenic transplant rejection),
 CC blood-related disorders (thrombosis, arterial thrombosis),
 CC hyperproliferative disorders, renal disorders (e.g. acute
 CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
 CC hyperthyroidism, hyperpituitarism), liver diseases and disorders,
 CC reproductive system disorders (e.g. endometriosis), infectious diseases,
 CC and pancreatic disorders. Many other diseases and disorders are listed in
 CC the specification. They also useful as a vaccine adjuvant. Further they
 CC are useful to enhance or inhibit complement mediated cell lysis, for
 CC stimulating wound and tissue repair, angiogenesis, and the repair of
 CC vascular or lymphatic diseases or disorders. They are also useful to
 CC prevent hair loss, to modulate mammalian characteristics such as body
 CC height, weight, hair colour, and to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors or other nutritional components. The proteins are
 CC also useful for identifying binding partners. The present sequence
 CC represents a secreted protein of the invention
 XX
 SQ Sequence 133 AA;
 Alignment Scores:
 Pred. No.: 1.26e-38 Length: 133
 Score: 455.00 Matches: 77
 Percent Similarity: 74.22% Conservative: 18
 Best Local Similarity: 60.16% Mismatches: 33
 Query Match: 59.55% Indels: 0
 Ds: 6 Gaps: 0
 US-10-807-204-11 (1-396) x ABU64993 (1-133)
 QY 1 ATGGGACTCTCAGGACTTCTGCAATCCTGGTACCATTCTCTTTGGGGACATCCAG 60
 DB 1 MetGlySerSerGlyLeuLeuSerLeuLeuValLeuPheValLeuLeuAlaAsnValGln 20
 QY 61 GAACCTGGGCACGCTGAAAGGCATCTTGGCAAGCGTGTCCCAAAATCAAAGTGAATGC 120
 DB 21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProLysIleAargGluCys 40
 QY 121 GAAGTGGGAAGAAATAGACAGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
 DB 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAsnLysLysCys 60
 QY 181 TGCCCGTTTCAGCGTGGGAAAGAAATGTTTAGACTTCAGAAAGATATATGCAGTATGCCA 240
 DB 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGlnMetPro 80
 QY 241 CAGGAGGCTGGCCCTCGCTGCTCCATACACACTGGTGTACATAAAAAAACTAAG 300
 DB 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpTyrAspLysLysAspAsn 100
 QY 301 ATCTCTCGGAATTCTATGCGCGTTCGCCGGGGAACATTAACAACCTCCAACTGNA 160
 CC
 CC

US-10-807-204-11 (1-396) x ABM85103 (1-179)

```
QY 1 ATGGGACTCTCAGACTCTCTGCCAATCTCGTACCATTCATCTCTTTGGGGGACATCCAG 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MetGlySerSerGlyLeuLeuSerLeuLeuValLeuPheValLeuLeuAlaAsnValGln 20
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAACCTGGCGACGCTGAAGGATCTCTGGCAAGCGGTGTCCTCCAAATCAAAGTGAATGC 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProLysIleArgGluGluCys 40
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 GAATGGGAAGAAATAGACAGTGTACCAACCCAGAGATTGCCCGAGAAACATGAAGTGT 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TGCCCGTTTCAGCGCGGAAAGAAATGTTTACACTTCAGAAAGATATATGAGTATGCCA 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 CAGGAGGCTGCGCCCTCGCTGCCCTCCATACACACTGGTGATCAATAAACTAAAG 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTyrAspLysLysAspAsn 100
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ATCTCTCCGAAATTCATCTATGCGCGGTGGCCAGGGGAACAATAACAATTCCTCAACTGAA 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 101 ThrCysSerMetPheValTyrGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerLys 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 GCTATCTCTGCTGGTCACTGCAAA 384
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 AlaAsnCysLeuAsnThrCysLys 128
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 15

ABP69809

ID ABP69809 standard; protein; 86 AA.

XX

AC ABP69809;

XX

DT 20-JAN-2003 (first entry)

XX

DE Human polypeptide SEQ ID NO 1856.

XX

KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; neutropenic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.

OS Homo sapiens.

XX

PN WO200270539-A2.

XX

PD 12-SEP-2002.

XX

PF 05-MAR-2002; 2002WO-US005095.

XX

PR 05-MAR-2001; 2001US-00799451.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Zhou P, Goodrich RW, Auandi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

PI Wehrman T, Wang J, Wang D, Drmanac RT;

XX

DR WPI; 2002-759812/82.

DR N-PSDB; AB212026.

XX

PT New polynucleotides comprising sequences assembled from expressed

PT sequence tags (ESTs), useful for treating cell-proliferative,

PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet

PT or coagulation disorders.

XX

PS Claim 9; SEQ ID NO 1856; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (AB211119-
XX AB212066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP69802-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX or Alzheimer's disease), neurodegenerative diseases (Parkinson's
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX platelet or coagulation disorders, wound, burns, incision, ulcers, liver
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX arthritis, etc. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 86 AA;

Alignment Scores:

Pred. No.:	3.58e-34	Length:	86
Score:	412.00	Matches:	74
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	53.93%	Indels:	0
DB:	5	Gaps:	0

US-10-807-204-11 (1-396) x ABP69809 (1-86)

QY 1 ATGGGACTCTCAGACTCTCTGCCAATCTCGTACCATTCATCTCTTTGGGGGACATCCAG 60

Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20

QY 61 GAACCTGGCGACGCTGAAGGATCTCTGGCAAGCGGTGTCCTCCAAATCAAAGTGAATGC 120

Db 21 GluProGlyHisAlaGluGlyIleLeuGlyProCysProLysIleLysValGluCys 40

QY 121 GAATGGGAAGAAATAGACAGTGTACCAACCCAGAGATTGCCCGAGAAACATGAAGTGT 180

Db 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60

QY 181 TGCCCGTTTCAGCGCGGAAAGAAATGTTTACACTTCAGAAAGTGAATGC 222

Db 61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLys 74

RESULT 16

ABU26667

ID ABU26667 standard; protein; 86 AA.

XX

AC ABU26667;

XX

DT 01-MAY-2003 (first entry)

XX

DE Human protein modification + maintenance molecule protein SEQ ID NO 21.

XX

KW Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
KW cerebroprotective; antiparkinsonian; neutropenic; antiinflammatory;
KW antitumor; hepatotropic; gynaecological; antibacterial; virucide;
KW protozoacide; antiparasitic; cell proliferative disease; PMOB;
KW protein modification and maintenance molecule; immunogenic fragment;
KW cancer; autoimmune; inflammatory disease; neurological disorder;
KW gastrointestinal; developmental; vesicle trafficking disorder; infection;
KW protein-protein interaction; drug-target interaction;
KW gene expression profile; human.

OS Homo sapiens.

XX

PN WO2003000844-A2.

XX

PT 03-JAN-2003.

XX

CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 SQ Sequence 101 AA;

Alignment Scores:
 Pred. No.: 3,7e-34 Length: 101
 Score: 412.00 Matches: 74
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.93% Indels: 0
 DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x ABB12236 (1-101)

QY 1 AFGGACTCTCAGGACTTCTGCGCAATCCTGTGACCATTCCTTTGGGGACATCCAG 60
 Db 16 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 35
 QY 61 GAACCTGGGCGACCTGAAGGCATCTCTGCGACGCGTGTCCAAATCAAAGTGAATGC 120
 Db 36 GluProGlyHisAlaGluGlyIleLeuGlyProCysProGlyIleValGluCys 55
 QY 121 CAAGTGGGAAGTAATAGACAGGTGTACCAAAACCAGAGATTGCCAGAAAACATGAAGTGT 180
 Db 56 GluValGluGluLeuAspGlnCysThrIysProArgAspCysProGluAsnMetIysCys 75
 QY 181 TGCCCGTTCAGCCGTGGAAAGAAATGTTTAGACTTCAGAAAG 222
 Db 76 CysProPheSerArgGlyIysIysCysLeuAspPheArgLys 89

RESULT 18

ID AAE27094
 AC AAE27094 standard; protein; 117 AA.

AC AAE27094;

DT 13-DEC-2002 (first entry)

XX Human secreted protein #1.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropic; vulnery; cytostatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.

OS Homo sapiens.
 PN US2002077287-A1.
 XX 20-JUN-2002.
 XX 11-MAY-2001; 2001US-00852659.
 XX 11-SEP-1998; 98US-00152060.

PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYI/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CH, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;

XX WPI; 2002-598780/64.

PT Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

CC AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogenic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders, e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention

SQ Sequence 117 AA;

Alignment Scores: 8.57e-32 Length: 117
 Pred. No.:

PI	Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI	Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI	Ferrie AM;
XX	
XX	WPI; 2002-574454/61.
XX	
PT	New nucleic acid molecules encoding 28 human secreted proteins, useful
PT	for diagnosing, preventing, treating or ameliorating medical conditions
PT	and as food additives or preservatives.
XX	
PS	Disclosure; Page 17; 209pp; English.
XX	
CC	AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC	protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC	AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC	and their corresponding secreted proteins are useful for preventing,
CC	treating or ameliorating medical conditions, e.g., by protein or gene
CC	therapy. Secreted protein sequences of the invention are useful for the
CC	diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC	rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC	the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC	angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC	system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC	bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC	polypeptides can also be used to aid wound healing and epithelial cell
CC	proliferation, to prevent skin aging due to sunburn, to maintain organs
CC	before transplantation, for supporting cell culture of primary tissues,
CC	to regenerate tissues and in chemotaxis. They can also be used as food
CC	additives or preservative to increase or decrease storage capabilities,
CC	fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC	and other nutritional components. The present sequence represents a human
CC	secreted protein fragment referred to in the disclosure of the invention
XX	
SQ	Sequence 117 AA;
Alignment Scores:	
Pred. No.:	8.57e-32 Length: 117
Score:	389.50 Matches: 65
Percent Similarity:	77.00% Conservative: 12
Best Local Similarity:	65.00% Mismatches: 22
Query Match:	50.98% Indels: 1
DB:	5 Gaps: 1
US-10-807-204-11 (1-396) x AAE27165 (1-117)	
Qy	85 CTTGGCAAGCCGTGTCCTCCAAATCAAGTGAATGCGAATGGAAGAAATAGACCACTGT 144
Db	14 LeuGlyArg--CysProLysIleAArgGluGluCysGluPheGlnGluArgAspValCys 32
Qy	145 ACCAAACCCAGAGATTGCCAGAAACATGAAGTGTTCGCCGTTCAGCCGCTGGGAAGAAA 204
Db	33 ThrLysAspArgGlnCysGlnAspAsnLysLysCysValPheSerCysGlyLysLys 52
Qy	205 TGTTTAGACTTCAGAAAGGATATATGCAGTATGCCACAGGAGGCTGCCCTGCTGGCC 264
Db	53 CysLeuAspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAla 72
Qy	265 TCCATACCACTGGTGTACAAATAAAAACTAAGATCTCTCGAATTCATCTATGGC 324
Db	73 TyrPheLeuHisTrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGly 92
Qy	325 GGTTCGCCAGGGGAACAATAACAACTCCAAACTGAAGCTATCTGCTGGTCACCTGCAAAA 384
Db	93 GlyCysGlnGlyAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 112
RESULT 19	
ID	AAE27165
ID	AAE27165 standard; protein; 117 AA.
XX	
AC	AAE27165;
XX	
DT	13-DEC-2002 (first entry)
XX	
DE	Human gene 24 encoded secreted protein fragment #1.
XX	
KW	Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW	rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW	cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW	cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW	infection; corneal infection; skin aging; food additive; preservative;
KW	tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW	cardiant; vasotropic; cerebroprotective; antiproliferative; neuroprotective;
KW	antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW	vulnerary.
OS	Homo sapiens.
XX	
XX	US2002076756-A1.
PN	
XX	20-JUN-2002.
PD	
XX	
XX	11-MAY-2001; 2001US-00853161.
PR	
XX	02-FEB-2001; 2001US-0265583P.
XX	
PA	(RUBE/) RUBEN S M.
PA	(ROSE/) ROSEN C A.
PA	(LIY/) LI Y.
PA	(ZENG/) ZENG Z.
PA	(KYAW/) KYAW H.
PA	(FISC/) FISCHER C L.
PA	(LIHH/) LI H.
PA	(SOPP/) SOPPET D R.
PA	(GENT/) GENTZ R L.
PA	(WEIY/) WEI Y.
PA	(MOOR/) MOORE P A.
PA	(YOON/) YOUNG P E.
PA	(GREE/) GREENE J M.
PA	(FERR/) FERRIE A M.
XX	

DE Human secreted protein gene 24, protein #4.

XX Secreted protein; immunodeficiency; multiple sclerosis;

XX severe combined immunodeficiency; autoimmune disorder; cancer;

KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;

KW inflammatory condition; septic shock; inflammatory bowel disease;

KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;

KW gastrointestinal disorder; central nervous system disorder;

KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;

KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;

KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;

KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;

KW endocrine disorder; liver disease; reproductive system disorder;

KW endometriosis; infectious disease; pancreatic disorder; vaccine;

KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;

XX body height; hair colour; human.

XX Homo sapiens.

OS US2002172994-A1.

PN 21-NOV-2002.

XX 11-MAY-2001; 2001US-00852797.

XX 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.

PR 30-MAY-1997; 97US-0050934P.

PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.

PR 19-DEC-1997; 97US-0068368P.

PR 12-MAR-1998; 98WO-US004858.

PR 11-SEP-1998; 98US-0015206P.

PR 02-FEB-2001; 2001US-0265583P.

XX (RUBEN) RUBEN S M.

PA (ROSE) ROSEN C A.

PA (LIYI) LI Y.

PA (ZENG) ZENG Z.

PA (KYAW) KYAW H.

PA (FISC) FISCHER C L.

PA (LIH) LI H.

PA (SOPP) SOPPET D R.

PA (GENT) GENTZ R L.

PA (WEI) WEI Y.

PA (MOOR) MOORE P A.

PA (YOUN) YOUNG P E.

PA (GREEN) GREENE J M.

PA (FERR) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX WPI: 2003-310989/30.

XX New human secreted polypeptides and polynucleotides for diagnosing,

PT prognosing, preventing and treating immune, hyperproliferative, liver,

PT kidney, reproductive disorders and for identifying modulators of

PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

XX The invention relates to an isolated polypeptide comprising an amino acid

CC sequence at least 95% identical to sequence of 28 human secreted

CC proteins, their fragment, polypeptide domain, epitope, secreted form,

CC variant, allelic variant, or species homologue, or the encoded sequence

CC included in ATCC 97921 and 97922. Also included are the encoding nucleic

CC acids, recombinant vectors, host cells, antibodies, and genes. The

CC proteins and nucleic acids are useful for diagnosing, preventing,

CC

CC treating, prognosing or ameliorating a medical condition e.g.

CC immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell

CC immunodeficiencies, severe combined immunodeficiencies), autoimmune

CC disorders (e.g. systemic erythematosus, rheumatoid arthritis, multiple

CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,

CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),

CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,

CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),

CC respiratory disorders (e.g. asthma and allergy), gastrointestinal

CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and

CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain

CC injury and/or stroke, traumatic brain injury), neurodegenerative

CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related

CC dementia, and prion disease), cardiovascular disorders (e.g. atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary

CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,

CC pancreatitis, sarcoidosis, dermatitis, allergic transplant rejection),

CC blood-related disorders (thrombosis, arterial thrombosis),

CC hyperproliferative disorders, renal disorders (e.g. acute

CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,

CC hyperthyroidism, hyperpituitarism), liver diseases and disorders,

CC reproductive system disorders (e.g. endometriosis), infectious diseases,

CC and pancreatic disorders. Many other diseases and disorders are listed in

CC the specification. They also useful as a vaccine adjuvant. Further they

CC are useful to enhance or inhibit complement mediated cell lysis, for

CC stimulating wound and tissue repair, angiogenesis, and the repair of

CC vascular or lymphatic diseases or disorders. They are also useful to

CC prevent hair loss, to modulate mammalian characteristics such as body

CC height, weight, hair colour, and to increase or decrease storage

CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,

CC minerals, cofactors or other nutritional components. The proteins are

CC also useful for identifying binding partners. The present sequence

CC represents a secreted protein of the invention

XX

SQ Sequence 117 AA;

Alignment Scores:

Pred. No.: 8.57e-32 Length: 117

Score: 389.50 Matches: 65

Percent Similarity: 77.00% Conservative: 12

Best Local Similarity: 65.00% Mismatches: 22

Query Match: 50.98% Indels: 1

DB: 6 Gaps: 1

US-10-807-204-11 (1-396) x ABU65038 (1-117)

QY 85 CTTGGCAAGCCGTGTCCTCCAAATCAAGTGGAGTGGAGAGAAATAGACCACTGT 144

DB 14 LeuGlyArg---CysProLysIleArgGluGluCysGluPheGlnGluArgAspValCys 32

QY 145 ACCAAACCCAGAGATTGCCAGAAACATGAAGTGTTCGCCCTTCAGCCGTGGAAGAAA 204

DB 33 ThrLysArgArgGlnCysGlnAspAsnLysLysCysCysValPheSerCysGlyLysLys 52

QY 205 TGTTTAGACTTCAGAAAGATATATGTCAGTATGCCACAGGAGCTGGCCCTCTGCGCC 264

DB 53 CysLeuAspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAla 72

QY 265 TCCATACCACTGTGTGGTACAAATAAAACCTAAAGATCTGCTCGAAATCTATCTATGCG 324

DB 73 TyrPheLeuHisTrpIrrPyzAspLysLysAspAsnThrCysSerMetPheValTyrGly 92

QY 325 GGTTCGCCAGGGGAACAATAACAACTTCACAACTGAAGCTATCTGTGTGTCACCTGCAAA 384

DB 93 GlyCysGlnGlyAsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 112

RESULT 21

ADG89847

ID ADG89847 standard; protein; 117 AA.

XX

AC ADG89847;

XX

DT 11-MAR-2004 (first entry)

DE Human secreted protein #2.
XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
XX autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotropic; vulnary; cytotactic; nootropic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.
XX Homo sapiens.
XX US2002077287-A1.
XX 20-JUN-2002.
XX 11-MAY-2001; 2001US-00852659.
XX 11-SEP-1998; 98US-00152060.
XX (RUBE/) RUBEN S M.
XX (ROSE/) ROSEN C A.
XX (LIYV/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIH/) LI H.
XX (SOPP/) SOPPOT D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppot DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX WPI; 2002-598780/64.
XX Novel human secreted polypeptides and polynucleotides for diagnosing,
PT preventing, treating immune, hyperproliferative, cardiovascular, of
PT neurological, reproductive disorders and identifying modulators of
PT therapeutic use.
XX Disclosure; Page 16; 209pp; English.
XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
CC AAE27000-AAE27025 represent human secreted protein fragments or their
CC variants. The secreted proteins and genes are useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. Specific uses are described for each of the 28 genes, based on
CC the tissues in which they are most highly expressed and include
CC developing products for the diagnosis or treatment of immunodeficiencies,
CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
CC bowel disease, cancers e.g., gastric, ovarian, lung, liver, bladder and
CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
CC

CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
CC sarcoidosis and allergic transplant rejection, blood-related disorder
CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
CC lung cancer, allergic disorders, pneumonitis, renal disorders, e.g. acute
CC glomerulonephritis, neurological diseases, liver disorders, endocrine
CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
CC infectious diseases and reproductive system disorders e.g. endometriosis.
XX The present sequence represents a human secreted protein of the invention
XX
SQ Sequence 102 AA;
Alignment Scores:
Pred. NO.: 1.19e-31 Length: 102
Score: 388.00 Matches: 63
Percent Similarity: 77.08% Conservative: 11
Best Local Similarity: 65.62% Mismatches: 22
Query Match: 50.79% Indels: 0
DB: 5 Gaps: 0
US-10-807-204-11 (1-396) x AAE27095 (1-102)
QY 97 TGTCCCAAAATCAAGTGGATGCGAAGTGGAGAAATAGACAGTGTACCAACCCAGA 156
Db 2 CysProlysisleArgGluGluCysGluPheGlnGluArgAspValCysThrLysAspArg 21
QY 157 GATTGCCCAAAACATGAAGTGTGGCCGTTGACCGTGGAAAGAAATGTTTAGATTC 216
Db 22 GlnCysGlnAspAsnLysLysCysValPheSerCysGlyLysLysCysLeuAspLeu 41
QY 217 AGAAAGGATATATGAGTATGCCACAGAGAGCTGGCCCTGGCTCCATACCACAC 276
Db 42 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHis 61
QY 277 TGGTGGTACATAAAACAACTAAGATCTGCTCCGAATTCATCTATGGGGTGGCAGGG 336
Db 62 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 81
QY 337 AACATAACAACTTCCAAACTGAAGTATCTGTCTGTGTCACCTGCNAA 384
Db 82 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 97
RESULT 23
AAE28009
ID AAE28009 standard; protein; 102 AA.
XX AAE28009;
AC AAE28009;
XX 13-DEC-2002 (first entry)
XX Human gene 24 encoded secreted protein fragment #2.
XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnary.
XX Homo sapiens.
XX US2002076756-A1.
XX 20-JUN-2002.
XX 11-MAY-2001; 2001US-00853161.
XX 02-FEB-2001; 2001US-0265583P.
XX

PT New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

XX Disclosure; SEQ ID NO 121; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis, asthma,
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.

XX SQ Sequence 102 AA;

Alignment Scores:
Pred. No.: 1.19e-31 Length: 102
Score: 388.00 Matches: 63
Percent Similarity: 77.08% Conservative: 11
Best Local Similarity: 65.62% Mismatches: 22
Query Match: 80.79% Indels: 0
DB: Gaps: 0

US-10-807-204-11 (1-396) x ADG98848 (1-102)

Qy 97 TGTCCCAAAATCAAAATGGAATGCGAATGAGAACAAATAGACAGTGACCAACCCAGA 156
Db 2 CysProlysisleArgGluGluCysGluPheGlnGluArgaspValCysThrLysAspArg 21
Qy 157 GATTGCCAGAACATGAAGTGTTCGCCGTTCACGCGTGGAAAGAAATGTTTACATTC 216
Db 22 GlnCysGlnAseAsnLysLysCysCysValPheSerCysGlyLysLysCysLeuAspLeu 41
Qy 217 AGAAGATATATACGATATGCCACAGAGGCTGCCCGCTCCCTCCATACCCACAC 276
Db 42 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyPheLeuHis 61
Qy 277 TGTGGTGACATAAAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGGTTGCCAGGGG 336

Db 62 TptTptTyAspLysLysAspAsnThrCysSerMetPheValTyArgGlyGlyCysGlnGly 81
Qy 337 AACAAATCAACTCCAAACTGAAGCTATCTGTCTGCTACCTGCAAA 384
Db 82 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 97

RESULT 26

ADA19813 standard; protein; 134 AA.

XX ADA19813;

XX 20-NOV-2003 (first entry)

DE Mouse EPPIN protein SEQ ID NO:14.

DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
antibacterial; immunosuppressive; antirheumatic; antiarthritic;
nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
acute pancreatitis; pulmonary injury; allergy-induced protease release;
deep vein thrombosis; myocardial infarction; shock; septic shock;
hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
chronic inflammatory bowel disease; psoriasis; EPPIN.

OS Mus musculus.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

New engineered human Kunitz-type protease inhibitor for diagnosing,
preventing or treating conditions associated with excessive proteinase
activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
hemorrhage.
Disclosure; Fig 1; 87pp; English.
The present invention describes an isolated, purified or recombinant DJ11
polypeptide comprising a Kunitz-type protease inhibitor domain or its
biologically active portion. The polypeptide comprises at least 98 %
identity to residues 77-127 of a 131 amino acid sequence (S1, see
ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
activities, and can be used as a protease inhibitor and in gene therapy.
Composition and methods from the present invention can be used in
diagnosing, preventing or treating conditions associated with excessive
proteinase activity, such as acute pancreatitis, pulmonary injury,
allergy-induced protease release, deep vein thrombosis, myocardial
infarction, shock (including septic shock), hyperfibrinolytic
haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
be used in preserving platelet function, organ preservation or in wound
healing. The polynucleotide sequence encoding DJ11 may be used as
hybridisation probes, in chromosome and gene mapping, in the generation
of antisense RNA and DNA, and as targets for pharmaceutical intervention.
The present sequence represents a mouse EPPIN protein given in comparison
with DJ11 proteins in the exemplification of the present invention.


```
XX SQ Sequence 134 AA;
Alignment Scores:
Pred. No.: 2,05e-31 Length: 134
Score: 386.00 Matches: 66
Percent Similarity: 70.54% Conservative: 25
Best Local Similarity: 51.16% Mismatches: 38
Query Match: 50.52% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19813 (1-134)
QY 1 ATGGGACTCTCAGGACTTCTGCAATCTCTGGTACCATTTCCTTTTGGGGGACATCCAG 60
DB 1 MetLysLeuSerGlyPheValSerIleLeuValLeuPheGlyLeuLeuAlaArgValGln 20
QY 61 GAACCTGGGACGCTGAAGGCATCTCTGGCAAGCCGTGTCCAAATCAAAAGTGAATGC 120
DB 21 GlyProSerLeuAlaAspLeuLeuPheProArgArgCysProArgPheArgGluCys 40
QY 121 GAAGTGGAGAAATAGACAGGTGTACCAACCACAGATTCGCCAGAAACATGAAGTGT 180
DB 41 GluHisGlnGluArgAspLeuCysThrArgAspArgCysProLysLysGluLysCys 60
QY 181 TGCCCGTTCAGCGCTGGAAAGAAATGTTTAGACTTCAGAAAGATATATGTCAGTATGCCA 240
DB 61 CysValPheAsnCysGlyLysLysCysLeuAsnProGlnAsnIleCysSerLeuPro 80
QY 241 CAGGAGGCTGGCCCTGCTGCTGCCCTCCATACACACTGGTGATCAATAAAAACTAAG 300
DB 81 LysAspSerGlyTyrcysMetAlaTyrcysPheArgArgTrpPheAsnLysGluAsnSer 100
QY 301 ATCTGCTCGAATTATCTATCGCGGTTCAGGGGACAAATAACAACCTTCCAAACTGAA 360
DB 101 ThrCysGlnValPheIleTyrcysGlyGlyCysGlnGlyAsnAsnAsnPheGlnSerGln 120
QY 361 GCTATCTGTCTGCTACCTGCACCTGCAAAAAA 387
DB 121 SerIleCysGlnAsnAlaCysGluLys 129

RESULT 27
ADA19804
ID ADA19804 standard; protein; 43 AA.
XX AC ADA19804;
XX DT 20-NOV-2003 (first entry)
XX DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:5.
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003070770-A2.
XX PD 28-AUG-2003.
XX PF 18-FEB-2003; 2003WO-EP001629.
XX PR 21-FEB-2002; 2002US-0358683P.
XX PA (GENE-) GENEPROT INC.
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XX Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX hemorrhage.
XX Disclosure; Page 79; 87pp; English.
XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents a partial engineered human DJ11 protein
XX amino acid sequence from the present invention.
XX SQ Sequence 43 AA;
Alignment Scores:
Pred. No.: 9,96e-18 Length: 43
Score: 254.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.25% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19804 (1-43)
QY 94 CCGTGTCCCAAAATCAAAAGTGAATGCGAAGTGAAGAAATAGACCAGTGTACCAACCC 153
DB 1 ProCysProLysIleLysValGluCysGluValGluGluIleAspGlnCysThrLysPro 20
QY 154 AGAGATTGCCAGAAACATGAAGTGTTCGCGTTCACCGTGGGAAGAAATGTTTAGAC 213
DB 21 ArgAspCysProGluAsnMetLysCysCysProPheSerArgGlyLysLysCysLeuAsp 40
QY 214 TTCAGAAAG 222
DB 41 PheArgLys 43
RESULT 28
AAE13093
ID AAE13093 standard; peptide; 64 AA.
XX AC AAE13093;
XX DT 28-JAN-2002 (first entry)
XX DE Human serine proteinase inhibitor BTL.009 C-terminal peptide.
XX KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
XX nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
XX rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
```


KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.

XX Homo sapiens.

XX USG294648-B1.

XX 25-SEP-2001.

XX 20-JUL-1999; 99US-00358569.

XX 20-JUL-1999; 99US-00358569.

XX (FARB) BAYER CORP.

XX Delaria K, Rocznik S, Davies C;

XX WPI; 2001-662224/76.

XX New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.

XX Disclosure; Col 6; 16pp; English.

XX The invention relates to human BTL009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL009 C-terminal peptide containing Kunitz domain which is used in the
CC exemplification of the invention

XX Sequence 64 AA;

Alignment Scores:
Pred. No.: 1.95e-16 Length: 64
Score: 242.00 Matches: 38
Percent Similarity: 79.31% Conservative: 8
Best Local Similarity: 65.52% Mismatches: 12
Query Match: 31.68% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x ABL13093 (1-64)

Qy 211 GACTTCAGAAAGGATATATGAGTATGCGACAGGAGGTGGCCCTGCTGGCTCCATA 270

Db 1 AspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyPhe 20

Qy 271 CCACACTGGTGGTACATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGC 330

Db 21 LeuHisTrpTrpTyAspLysLeuAspAsnThrCysSerMetPheValTyGlyGlyCys 40

Qy 331 CAGGGGAACATAACAACCTCCAAACTGAACCTATCTGTCTGGTCACCTGCAAA 384

Db 41 GlnGlyAsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 58

RESULT 29

ADQ66734

ID ADQ66734 standard; protein; 101 AA.

XX ADQ66734;

XX 07-OCT-2004 (first entry)

XX Novel human protein sequence #1707.

DE osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.

XX Homo sapiens.

XX EPI440981-A2.

XX 28-JUL-2004.

XX 21-JAN-2004; 2004EP-00001196.

XX 21-JAN-2003; 2003JP-00102206.

PR 09-MAY-2003; 2003JP-00131392.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;

XX WPI; 2004-535376/52.

XX N-PSDB; ADQ64546.

XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX Claim 1; SEQ ID NO 3895; 2449pp; English.

XX The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a protein
CC sequence of the invention.

XX Sequence 101 AA;

Alignment Scores:
Pred. No.: 8.06e-16 Length: 101
Score: 236.50 Matches: 44
Percent Similarity: 61.46% Conservative: 15
Best Local Similarity: 45.83% Mismatches: 34
Query Match: 30.96% Indels: 3
DB: 8 Gaps: 1

US-10-807-204-11 (1-396) x ADQ66734 (1-101)

Qy 1 ATGGGACTCTCAGGACTTCTGCCAATCTCGTGTACCATTCATCTTTGGGGACATCCAG 60

Db 1 MetGlySerSerglyLeuLeuSerLeuLeuValLeuPheValLeuAlaAsnValGln 20

Qy 61 GAACCTGGGACCGCTGAGGCATCTCTGGCAACCGCTGCCAAATCAAGTGGATGC 120

Db 21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProLysIleArgGluGluCys 40

Qy 121 GAAGTGGAAAGATAGACCATGTGTACCAACCCAGAGATTGCCAGAAAACATGAAGTGT 180

Db 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60

Qy 181 TGCCCGTTACGCCGTGGAAAGAAATGTTAGACTTCAGAAAG-----GATATATGC 231

Db 61 CysValPheSerCysGluLysLysCysLeuAspLeuLysGlnGlyAsnIleGlnSerCys 80

Qy 232 AGTATGCCACAGGAGGTGGCCCTGCTGGCTCCATACACACTGG 279

Db 81 ArgIleThrAsnProSerProCysProHisLeuLeuProSerTrp 96

RESULT 30	
AAE13084	
ID	AAE13084 standard; peptide; 58 AA.
XX	
AC	AAE13084;
XX	
DT	28-JAN-2002 (first entry)
XX	
DE	Human serine proteinase inhibitor BTL.009 peptide.
XX	
KW	Human; BTL.009 protein; serine proteinase inhibitor; cystostatic;
KW	nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW	rheumatoid arthritis; adult respiratory distress syndrome; angiolasty;
KW	blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW	neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW	elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW	therapeutic.
XX	
OS	Homo sapiens.
XX	
XX	US6294648-B1.
PN	
XX	
PD	25-SEP-2001.
XX	
XX	20-JUL-1999; 99US-00358569.
XX	
PR	20-JUL-1999; 99US-00358569.
XX	
PA	(FARB) BAYER CORP.
XX	
PI	Delaria K, Rocznia S, Davies C;
XX	
XX	WPI; 2001-662224/76.
DR	
XX	New isolated protein for inhibiting human serine protease activity in the
PT	treatment of e.g. emphysema and adult respiratory distress syndrome.
XX	
PS	Claim 1; Col 15-16; 16pp; English.
XX	
CC	The invention relates to human BTL.009 protein, a serine proteinase
CC	inhibitor of the Kunitz family that exhibits greater potency towards
CC	neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC	elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC	protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC	adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC	arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC	and diseases involving lung and vascular injury. BTL.009 is also useful
CC	for preventing neutrophil and monocyte activation and formation of active
CC	oxygen species during the oxidative burst of stimulated granulocytes.
CC	BTL.009 is useful for reducing platelet activation and blood coagulation
CC	and for the prophylactic or therapeutic treatment of patients undergoing
CC	angioplasty. The present sequence is human serine proteinase inhibitor
CC	BTL.009 peptide corresponding to Kunitz domain used in the
CC	exemplification of the invention. Note: The present sequence shown in
CC	column 14 and sequence listing of the specification lacks 3 amino acid
CC	residues at the C-terminal end
XX	
SQ	Sequence 58 AA;
Alignment Scores:	
Pred. No.:	8, 07e-16
Score:	236.00
Percent Similarity:	80.36%
Best Local Similarity:	66.07%
Query Match:	30.89%
DB:	4
US-10-807-204-11 (1-396) x AAE13084 (1-58)	
QY	217 AGAAGAGTATATGTCAGTATGCCACAGGAGGCTGCGCCCTGCTCCATACACAC 276
DB	1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTrpPheLeuHis 20
QY	277 TGTGGTACAAATAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGG 336
DB	21 TrpTrpTyzAspLysLysAspAsnThrCysSerMetPheValTrGlyGlyCysGlnGly 40
QY	337 AACAAATCAACACTTCCAAACTGAAGCTATCTGCTGCTCACCTGCAAA 384
DB	41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56
RESULT 31	
AAE60630	
ID	AAE60630 standard; protein; 58 AA.
XX	
AC	AAE60630;
XX	
DT	27-APR-2001 (first entry)
XX	
DE	Kunitz domain, SEQ ID NO:8, used to identify BTL.010 protein.
XX	
KW	Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;
KW	proteinase-3 inhibitor; Kunitz domain; emphysema;
KW	idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
KW	cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
KW	platelet activation; blood coagulation; neutrophil activation;
KW	monocyte activation; angiolasty; inflammatory disease; lung injury;
KW	vascular injury; nephrotropic; antirheumatic; antiarthritic.
XX	
OS	Unidentified.
XX	
PN	US6180607-B1.
XX	
PD	30-JAN-2001.
XX	
XX	05-AUG-1999; 99US-00369494.
XX	
PR	05-AUG-1999; 99US-00369494.
XX	
PA	(DAVI/) DAVIES C.
PA	(CHEN/) CHEN D.
PA	(ROCZ/) ROCZNIAK S.
XX	
PI	Davies C, Chen D, Rocznia S;
XX	
DR	WPI; 2001-190860/19.
XX	
PT	Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful
PT	for treating emphysema, cystic fibrosis, adult respiratory distress
PT	syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
XX	
PS	Disclosure; Col 6; 17pp; English.
XX	
CC	The invention relates to a novel human serine protease inhibitor of the
CC	Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and
CC	AAB60634). The BTL.010 protein is thought to preferentially inhibit
CC	neutral serine proteases such as elastase and proteinase-3, relative to
CC	trypsin-like and chymotrypsin-like proteases. A substantial proportion of
CC	the BTL.010 protein Kunitz domain (AAB60631) was identified via homology
CC	searching in the GenBank high throughput genomic (HTG) DNA sequence
CC	database using the Kunitz domain sequences AAB60630, and was confirmed as
CC	being novel using the Kunitz domain sequences AAB60632, and AAB60633.
CC	This sequence information was extended to provide a larger region of
CC	BTL.010 protein sequence data (AAB60634) by identifying an open reading
CC	frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain
CC	fragment in a 399 bp fragment of human genomic DNA (AAAF59750),
CC	corresponding to bases 16016-16414 of GenBank accession number AC004846.
CC	The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from
CC	the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical
CC	compositions comprising it, may be used for inhibiting protease activity,
CC	particularly that of leukocyte elastase, in the prevention, treatment or
CC	amelioration of medical conditions such as emphysema, idiopathic
CC	pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,
CC	rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010
CC	compositions of the invention modulate at least one physiological

CC condition such as platelet activation, blood coagulation, neutrophil
CC activation, or monocyte activation. BTL010 is also useful for the
CC prophylactic or therapeutic treatment of patients undergoing angioplasty,
CC and for the treatment of inflammatory diseases and diseases involving
CC lung and vascular injury. The present sequence represents a Kunitz domain
CC sequence used to identify the BTL010 protein
XX
XX

SQ Sequence 58 AA;

Alignment Scores:
Pred. No.: 8.07e-16 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x AAB60630 (1-58)

QY 217 AGAAGGATATATGCAGTATGCCAGGAGGCTGCCCTCGCTCCATACCACAC 276
DB 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHis 20
QY 277 TGGTGGTACAAATAAAATAAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
DB 21 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 40
QY 337 AACATAAACAACCTCCAAACTGAAGCTATCTGTCTGCTACCTGCACAA 384
DB 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56

RESULT 32

ID ADF41997
ADP41997 standard; protein; 58 AA.

XX ADF41997;

DT 12-FEB-2004 (first entry)

DE Human CAB37 Kunitz domain peptide.

XX albumin fusion; Kunitz domain; cytostatic; haemostatic;

KW hereditary angioedema; cancer; bleeding; gene therapy; human; CAB37.

XX Homo sapiens.

XX WO2003066924-A2.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003616.

XX 07-FEB-2002; 2002US-0355547P.

XX (AVET) AVENTIS BEHRING GMBH.

PA (AVET) AVENTIS BEHRING LLC.

PA (DELZ) DELTA BIOTECHNOLOGY LTD.

PA (DYAX-) DYAX CORP.

XX Hauser H, Weimer T, Romberg V, Kee SM, sleep D, Ladner RC;

PI Ley AC;

XX WPI; 2003-731497/69.

XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.
XX

PS Disclosure; Page 20; 110pp; English.

XX The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates

CC cytostatic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the human Kunitz domain peptide of the invention.
XX
XX

SQ Sequence 58 AA;

Alignment Scores:
Pred. No.: 8.07e-16 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADF41997 (1-58)

QY 217 AGAAGGATATATGCAGTATGCCAGGAGGCTGCCCTCGCTCCATACCACAC 276

DB 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHis 20

QY 277 TGGTGGTACAAATAAAATAAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336

DB 21 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 40

QY 337 AACATAAACAACCTCCAAACTGAAGCTATCTGTCTGCTACCTGCACAA 384

DB 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56

RESULT 33

ID ADL16838
ADL16838 standard; peptide; 58 AA.

XX ADL16838;

DT 06-MAY-2004 (first entry)

DE Human Kunitz domain (KD) peptide.

XX BTL010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;

KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;

KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;

KW inflammatory disease; oxidative burst; platelet activation;

KW blood coagulation; gene therapy; human; KD.

XX Homo sapiens.

XX US6689582-B1.

XX 10-FEB-2004.

XX 12-MAY-2000; 2000US-00569670.

XX 05-AUG-1999; 99US-00369494.

XX (FARB) BAYER PHARM CORP.

XX Davies C, Chen D, Roczniak S;

XX WPI; 2004-141424/14.

XX New isolated polynucleotide encoding BTL010 serine proteinase, useful
PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
PT glomerulonephritis.
XX

PS Disclosure; SEQ ID NO 8; 17pp; English.

XX The invention relates to BTL010, a human serine proteinase inhibitor of

CC the Kunitz family and its corresponding nucleic acid sequence. The

CC sequences of the invention are useful for treating diseases, e.g.

CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress

CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
CC glomerulonephritis or inflammatory diseases. The BTL010 protein is also
CC useful for preventing neutrophil and monocyte activation and formation of
CC active oxygen species during the oxidative burst of stimulated
CC granulocytes. It is also useful for reducing platelet activation and
CC blood coagulation. BTL010 DNA is useful in gene therapy. The present
CC sequence is human kunitz domain (KD) peptide.

XX
SQ Sequence 58 AA;

Alignment Scores:
Pred. No.: 8.07e-16 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
DB: Gaps: 0

US-10-807-204-11 (1-396) x ADL16838 (1-58)

QY 217 AGAAAGGATATATGCAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACCACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyPheLeuHis 20
QY 277 TGGTGGTACAAATAAAAAAATAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 21 TrpTyrAspLysAspAsnThrCysSerMetPheValTyGlyGlyCysGlnGly 40
QY 337 AACATAACAACCTTCCAACTCAAGCTATCTGTCTGGTCACCTGCATA 384
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56

RESULT 34
ADR89980
ID ADR89980 standard; peptide; 58 AA.
AC ADR89980;
XX
XX
DT 18-NOV-2004 (first entry)
XX
XX Human CAB37 protein kunitz domain peptide.
DE
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytostatic; haemostatic; CAB37 protein; human.
XX
OS Homo sapiens.
XX
XX US2004171794-A1.
XX
XX 02-SEP-2004.
PD
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX (LADN/) LADNER R C.
PA (LEYA/) LEY A C.
XX
XX Ladhner RC, Ley AC;
XX
XX WPI; 2004-625120/60.
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
XX
XX Disclosure; SEQ ID NO 5; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including

CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cycostatic and haemostatic agent. The present sequence is the human CAB37
CC protein (A4) kunitz domain peptide. This sequence is used in the
CC invention.

XX
SQ Sequence 58 AA;

Alignment Scores:
Pred. No.: 8.07e-16 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
DB: Gaps: 0

US-10-807-204-11 (1-396) x ADR89980 (1-58)

QY 217 AGAAAGGATATATGCAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACCACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyPheLeuHis 20
QY 277 TGGTGGTACAAATAAAAAAATAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 21 TrpTyrAspLysAspAsnThrCysSerMetPheValTyGlyGlyCysGlnGly 40
QY 337 AACATAACAACCTTCCAACTCAAGCTATCTGTCTGGTCACCTGCATA 384
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56

RESULT 35
AAW75257
ID AAW75257 standard; protein; 51 AA.
XX
XX AC AAW75257;
XX
XX DT 29-JAN-1999 (first entry)
XX
XX DE Fragment of human secreted protein encoded by gene 24.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX OS Homo sapiens.
XX
XX PN WO9840483-A2.
XX
XX PD 17-SEP-1998.
XX
XX PF 12-MAR-1998; 98WO-US004858.
XX
XX PR 14-MAR-1997; 97US-0040710P.
XX PR 14-MAR-1997; 97US-0040762P.
XX PR 30-MAY-1997; 97US-0048100P.
XX PR 30-MAY-1997; 97US-0048189P.
XX PR 30-MAY-1997; 97US-0048357P.
XX PR 06-JUN-1997; 97US-0050934P.
XX PR 05-SEP-1997; 97US-0048970P.
XX PR 19-DEC-1997; 97US-0057765P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX

DR WPI; 1998-520811/44.
DR N-PSDB; AAV34309.
XX
PT Isolated human polynucleotide(s) encoding secretory peptide(s) - used to
PT develop products for the diagnosis and treatment of e.g. inflammation,
PT cancers, CNS disorders or immune system disorders.
XX
PS Disclosure; Page 24; 201pp; English.
XX
CC This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule designated Gene 24 (AAV34309). The gene can
CC be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 28 novel genes and their fragments (nucleic acid sequences:
CC AAV34286-V34325; amino acid sequences AAV75196-W5235) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 28 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV34286 for
CC described uses)
XX
SQ Sequence 51 AA;

Alignment Scores:
Pred. NO.: 4.69e-14 Length: 51
Score: 219.00 Matches: 35
Percent Similarity: 78.43% Conservative: 5
Best Local Similarity: 68.63% Mismatches: 11
Query Match: 28.66% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x AAV75257 (1-51)

Qy 229 TGCAGTATGCCACAGGAGCTGGCCCTGCTGCTCCATACCACACTGGTGTCACAT 288
Db 1 CysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHisIrrPirPyrAsp 20

Qy 289 AAAAAAAGTCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAAACAATAACAAC 348
Db 21 LysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGlyAsnAsnAsn 40

Qy 349 TTCCAAACTGAAGTACTCTGCTGCTACCTCC 381
Db 41 PheGlnSerLysAlaAsnCysLeuAsnThrCys 51

RESULT 36
AAE27025
ID AAE27025 standard; protein; 51 AA.
XX
AC AAE27025;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human gene 24 encoded secreted protein variant, SEQ ID NO:118.
XX
KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW hyperproliferative disorder; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotrophic; vulnary; cytostatic; nootropic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.
XX
OS Homo sapiens.
XX

PN US2002077287-A1.
XX
PD 20-JUN-2002.
XX
PF 11-MAY-2001; 2001US-00852659.
XX
PR 11-SEP-1998; 98US-00152060.
XX
PA (RUBE// RUBEN S M.
PA (ROSE// ROSEN C A.
PA (LIYY// LI Y.
PA (ZENG// ZENG Z.
PA (KYAW// KYAW H.
PA (FISC// FISCHER C L.
PA (LIHH// LI H.
PA (SOPP// SOPPET D R.
PA (GENT// GENTZ R L.
PA (WEIY// WEI Y.
PA (MOOR// MOORE P A.
PA (YOUN// YOUNG P E.
PA (GREE// GREENE J M.
PA (FERR// FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
DR WPI; 2002-598780/64.
XX
PT Novel human secreted polypeptides and polynucleotides for diagnosing,
PT preventing, treating immune, hyperproliferative, cardiovascular,
PT neurological, reproductive disorders and identifying modulators of
PT therapeutic use.
XX
PS Disclosure; Page 16; 209pp; English.
XX
CC AAD4636-AA044676 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
CC AAE27000-AAE27025 represent human secreted protein fragments or their
CC variants. The secreted proteins and genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Specific uses are described for each of the 28 genes, based on
CC the tissues in which they are most highly expressed and include
CC developing products for the diagnosis or treatment of immunodeficiencies,
CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
CC Grave's disease, diabetes mellitus, dermatitis, inflammatory bowel
CC including septic shock, sepsis, reperfusion injury, inflammatory disorders
CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
CC sarcoidosis and allogeneic transplant rejection, blood-related disorder
CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
CC lung cancer, allergic disorders, pneumonitis, renal disorders, endocrine
CC glomerulonephritis, neurological diseases, liver disorders, endocrine
CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
CC infectious diseases and reproductive system disorders e.g. endometriosis.
CC The present sequence represents a human secreted protein variant of the
CC invention
XX
SQ Sequence 51 AA;

Alignment Scores:
Pred. No.: 4.69e-14 Length: 51
Score: 219.00 Matches: 35

Percent Similarity:	78.43%	Conservative:	5
Best Local Similarity:	68.63%	Mismatches:	11
Query Match:	28.66%	Indels:	0
DB:	5	Gaps:	0
US-10-807-204-11 (1-396) x AAE27025 (1-51)			
QY	229	TGCAGTATGCCACAGAGCGTGGCCCTGCGCTCCATACACACTGGTGGTACAAAT	288
Db	1	CysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpTrpAsp	20
QY	289	AAAAAACTAAGATCTGCCGAATTCATCTATGCGGTTGCCAGGGAACATACAAAC	348
Db	21	LysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGlyAsnAsnAsnAsn	40
QY	349	TTCCAACTGAAGCTATCTGCTGCTCACCTGC	381
Db	41	PheGlnSerLysAlaAsnCysLeuAsnThrCys	51
RESULT 37			
AAE27163			
ID	AAE27163	standard; protein; 51 AA.	
XX	AC	AAE27163;	
XX	DT	13-DEC-2002 (first entry)	
DE	Human gene 24	encoded secreted protein fragment kunitz-type domain.	
KW	Human; secreted protein; autoimmune disease; hyperproliferative disorder;		
KW	rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;		
KW	cerebral ischaemia; cardiovascular disorder; nervous system disorder;		
KW	cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;		
KW	infection; corneal infection; skin aging; food additive; preservative;		
KW	tissue regeneration; immunosuppressive; antiproliferative; cytostatic;		
KW	cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;		
KW	antibacterial; virucide; fungicide; ophthalmological; gene therapy;		
XX	OS	Homo sapiens.	
XX	PN	US2002076756-A1.	
XX	PD	20-JUN-2002..	
XX	PF	11-MAY-2001; 2001US-00853161.	
XX	PR	02-FEB-2001; 2001US-0265583P.	
PA	(RUBE/) RUBEN S M.		
PA	(ROSE/) ROSEN C A.		
PA	(LIYY/) LI Y.		
PA	(ZENG/) ZENG Z.		
PA	(KYAW/) KYAW H.		
PA	(FISC/) FISCHER C L.		
PA	(LIHH/) LI H.		
PA	(SOPP/) SOPPET D R.		
PA	(GENT/) GENTZ R L.		
PA	(WEIY/) WEI Y.		
PA	(MOOR/) MOORE P A.		
PA	(YOUN/) YOUNG P E.		
PA	(GREE/) GREENE J M.		
PA	(FERR/) FERRIE A M.		
XX	Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;		
PI	Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;		
PI	Ferrie AM;		
XX	WPI; 2002-574454/61.		
XX	PT	New nucleic acid molecules encoding 28 human secreted proteins, useful	
PT	for diagnosing, preventing, treating or ameliorating medical conditions		
PT	and as food additives or preservatives.		
XX	XX	Disclosure; Page 16; 209pp; English.	
XX	PS	AD44854-AD44984 represent CDNA sequences corresponding to 28 human secreted	
CC	protein genes, and AAE27097-AAE27137 represent the proteins they encode.		
CC	AAE27138-AAE27164 represent human secreted protein fragments. The genes		
CC	and their corresponding secreted proteins are useful for preventing,		
CC	treating or ameliorating medical conditions, e.g., by protein or gene		
CC	therapy. Secreted protein sequences of the invention are useful for the		
CC	diagnosis or treatment of disorders such as autoimmune diseases (e.g.		
CC	rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of		
CC	the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,		
CC	angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous		
CC	system disorders (e.g. Alzheimer's disease), infections caused by fungi,		
CC	bacteria and viruses and ocular disorders (e.g. corneal infection). The		
CC	polypeptides can also be used to aid wound healing and epithelial cell		
CC	proliferation, to prevent skin aging due to sunburn, to maintain organs		
CC	before transplantation, for supporting cell culture of primary tissues,		
CC	to regenerate tissues and in chemotaxis. They can also be used as food		
CC	additives or preservative to increase or decrease storage capabilities,		
CC	fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors		
CC	and other nutritional components. The present sequence represents a human		
CC	secreted protein fragment kunitz-type domain referred to in the		
CC	disclosure of the invention		
XX	XX	Sequence 51 AA;	
SQ	Alignment Scores:		
	Pred. No.:	4,69e-14	Length: 51
	Score:	219.00	Matches: 35
	Percent Similarity:	78.43%	Conservative: 5
	Best Local Similarity:	68.63%	Mismatches: 11
	Query Match:	28.66%	Indels: 0
	DB:	5	Gaps: 0
US-10-807-204-11 (1-396) x AAE27163 (1-51)			
QY	229	TGCAGTATGCCACAGAGCGTGGCCCTGCGCTCCATACACACTGGTGGTACAAAT	288
Db	1	CysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpTrpAsp	20
QY	289	AAAAAACTAAGATCTGCCGAATTCATCTATGCGGTTGCCAGGGAACATACAAAC	348
Db	21	LysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGlyAsnAsnAsnAsn	40
QY	349	TTCCAACTGAAGCTATCTGCTGCTCACCTGC	381
Db	41	PheGlnSerLysAlaAsnCysLeuAsnThrCys	51
RESULT 38			
ADG89845			
ID	ADG89845	standard; protein; 51 AA.	
XX	AC	ADG89845;	
XX	DT	11-MAR-2004 (first entry)	
XX	DE	Human secreted protein gene 24 protein #3.	
XX	KW	Secreted protein; gene therapy; neural disorder; immune system disorders;	
XX	KW	muscular disorder; reproductive disorder; gastrointestinal disorder;	
XX	KW	pulmonary disorder; cardiovascular disorder; renal disorder;	
XX	KW	proliferative disorder; cancer; systemic lupus erythematosus;	
XX	KW	rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;	
XX	KW	Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;	
XX	KW	Parkinson's disease; Alzheimer's disease; atherosclerosis;	
XX	KW	myocardial infarction; AIDS; infection; human.	
XX	OS	Homo sapiens.	
XX	PN	US2003225009-A1.	
XX	PD	04-DEC-2003.	

Thu Sep 22 07:16:43 2005

XX PS Disclosure; Page 27-29; 39pp; English.
 XX CC An anticoagulant was isolated from extracts of adult hookworm
 CC (Ancylostoma caninum). Preliminary sequencing identified 2 internal
 CC peptide fragments (AAR62521-22). The protein sequence of the
 CC anticoagulant, predicted from a 2.3 kb clone isolated from a cDNA library
 CC of adult hookworm, is given in AAR62523. The protein sequence exhibited
 CC homology to the pancreatic trypsin-inhibitor (AAR62524), green mamba
 CC venom (AAR62525) and tissue factor pathway inhibitors (AAR62526-8),
 CC suggesting the anticoagulant to be a Kunitz-type serine protease-
 CC inhibitor. (Updated on 25-MAR-2003 to correct FN field.)
 XX SQ Sequence 560 AA;

Alignment Scores: 5,12e-10 Length: 560
 Pred. No.: 182.50 Matches: 46
 Score: 182.50
 Percent Similarity: 41.94% Conservative: 19
 Best Local Similarity: 29.68% Mismatches: 57
 Query Match: 23.89% Indels: 33
 DB: Gaps: 3

US-10-807-204-11 (1-396) x AAR62523 (1-560)

QY 20 TGCCAACTCTGTACCAATTCCTTTGGGGGACATCCAGGAACCTGGGCACGCTGAAG 79
 DB 166 CysLysSerPhePheGlyCysGlyGlyAenGlyAenAenPheMetThrLysAla 185
 QY 80 GCATCTCTGGCAAGCGTGTCCAAA---ATCAAGTGGATGCGAAGTGAAGAATAG 136
 DB 186 LysCysMet--GluThrCysSerLysHisIleLysProGluThrGluGlnAsePValCys 205
 QY 137 ACCAGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGTGGCCGCTC---AGCC 193
 DB 205 exGlnProIleLysAlaGlyProCysMetAlaMetLeuLysArgTyrAlaTyrAsePhe 225
 QY 194 GTGGAAAGAAATGTTAGACTTC--- 216
 DB 225 ysLysLysArgCysValGlnPheIleTyrGlyGlyCysLysGlyAenLysAenAsePhe 245
 QY 217 -----AGAAAGGATA 226
 DB 245 IuSerMetGluGluCysThrArgThrCysLysLysAlaValProGluProGluGlnAseP 265
 QY 227 TATGCAGTATGCACAGGAGGCTGCCCTGCTGCTCCATACACACACTGGTGTACA 286
 DB 265 hrCysSerGlnProIleGluValGlyProCysLysAlaMetLeuLysArgTyrAlaTyrA 285
 QY 287 ATAAAAAACTAAGATCTCTCCGAATTCATCTATGGCGGTGGCCAGGGGAACAATAACA 346
 DB 285 sPAsnLysLysAenLysCysValArgPheIleTyrGlyGlyCysLysGlyAenLysAenA 305
 QY 347 ACTTCCAACTAAGCTATCTCTGGTGCACCTGCAAAAAA 387
 DB 305 snPheGluSerMetGluGluCysThrTyrThrCysLysLys 318

RESULT 40
 ABB71150
 ID ABB71150 standard; protein; 2858 AA.
 XX AC ABB71150;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 40242.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.

XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-658860/75.
 XX DR N-PSDB; ABL15253.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX PS Disclosure; SEQ ID NO 40242; 2lpp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABBS72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 2858 AA;

Alignment Scores: 1.04e-09 Length: 2858
 Pred. No.: 181.00 Matches: 36
 Score: 181.00
 Percent Similarity: 42.98% Conservative: 13
 Best Local Similarity: 31.58% Mismatches: 35
 Query Match: 23.69% Indels: 30
 DB: Gaps: 3

US-10-807-204-11 (1-396) x ABB71150 (1-2858)

QY 136 GACCACTGTACCAACCCAGG-----GATTGCCAGAAACATGAAGTGTGCCCG 186
 DB 1748 AsparGysAlaLeuProLysGlnThrGlyAspCysSerGlyLysAlaLeuAlalysTrpHis 1767
 QY 187 TTCAGCCGTGA---AGAAATGTTAGACTTC----- 216
 DB 1768 PheSerGluSerGluLysArgCysValProPheTyrTyrSerGlyCysGlyAenLys 1787
 QY 217 -----AGAAAGGAT 225
 DB 1788 AsnAenPheProThrLeuGluSerCysGluAsePheCysProArgGlnValalalysAseP 1807
 QY 226 ATATGCAGTATGCCACAGAGGCTGGCCCTGCTGCTCCATACACACTGGTGTAC 285
 DB 1808 IleCysGluIleProAlaGluValGlyCysAlaAenTyrValThrSerTrpTyrTyr 1827
 QY 286 AATAAAAACTAAGATCTCTCCGAATTCATCTATGGCGGTGGCCAGGGGAACAATAAC 345
 DB 1828 AspThrGlnAsePheGlnAlaCysArgGlnPheTyrTyrGlyCysGlyAenGluAen 1847
 QY 346 AACTTCCAACTGAAGCTATCTGTGCTGCTACCTGCAAAAAA 387
 DB 1848 ArgPheProThrGluGluSerCysLeuAlaArgCysAseParg 1861

RESULT 41
 ABB58064
 ID ABB58064 standard; protein; 3060 AA.
 XX AC ABB58064;
 XX PN

CC differentiation factor)-associated serum protein (GASP)

XX Sequence 571 AA;

Alignment Scores:
Pred. No.: 8.31e-10 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 7 Gaps: 3

US-10-807-204-11 (1-396) x AAE39498 (1-571)

QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 322 GluCysLeuLysProProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
QY 175 -----AAGTGTGCCGCTTCCAGCGCTGGAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisHisAsnLeuAsn 361
QY 202 -----AAATGTTTAGACTTCAGAAAGATATATGC 231
Db 362 HisPheGluThrTyrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGAGGCTGGCCCTCGCTCCATACACACATCGTGGTGATACAAATAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrValProArgTrpAlaTyrAsnSer 401
QY 292 AAACTAAGATCTGCTCCGAATTCATCTATGCGCGTTCAGCGGGAACAATAACACTTC 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyrGlyGlyCysGluGlyAsnGlyAsnAsnPhe 421
QY 352 CAAACTGAAGCTATCTGCTGCTACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431

RESULT 43

AAE39459

ID AAE39459 standard; protein; 571 AA.

AC AAE39459;

DT 18-DEC-2003 (first entry)

XX Mouse GDF-associated serum protein (GASP)1 protein.

XX Mouse; GDF-associated serum protein; GASP; amyotrophic lateral sclerosis;
growth and differentiation factor; GDF; chronic glucocorticoid therapy;
familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;
androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;
metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
myotonia; neuroprotective; obesity; immunomodulator; diabetes.

XX Mus sp.

XX Key Location/Qualifiers

FT 105..170

FT /note= "Follistatin domain"

XX US2003162714-A1.

XX 28-AUG-2003.

XX 21-FEB-2003; 2003US-00369736.

XX 21-FEB-2002; 2002US-0357845P.

PR

PR 20-DEC-2002; 2002US-0434644P.

XX (AMHP) WYETH.

XX Hill JJ, Wolfman NM;

XX WPI; 2003-756055/71.

XX N-PSDB; AAD59923.

XX Composition containing growth and differentiation factor-associated serum
protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
for diagnosis.

XX Disclosure; Fig 6C; Opp; English.

XX The present invention relates to the use of a protein GDF (growth and
differentiation factor)-associated serum protein (GASP) 1 comprising
at least one follistatin domain to modulate the level or activity of
growth and differentiation factor (GDF) -8. Administration of GASP1 is
used to modulate GDF-8 for treatment of muscular disorders such as
muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
congestive obstructive pulmonary disease, congenital myopathy (myotonia),
familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
and other muscle wasting syndromes such as diabetes types 1 or 2, impaired
muscle, metabolic disorders such as diabetes types 1 or 2, impaired
glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
induced by trauma and obesity, adipose tissue disorder such as obesity,
and bone degenerative conditions such as osteoporosis, osteopaenia,
osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
premature gonadal failure, vitamin D deficiency, androgen suppression,
secondary hyperparathyroidism, nutritional deficiencies and anorexia
nervosa. The present sequence is mouse GDF (growth and differentiation
factor)-associated serum protein (GASP)

XX Sequence 571 AA;

Alignment Scores:

Pred. No.: 8.31e-10 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 7 Gaps: 3

US-10-807-204-11 (1-396) x AAE39459 (1-571)

QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 322 GluCysLeuLysProProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
QY 175 -----AAGTGTGCCGCTTCCAGCGCTGGAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisHisAsnLeuAsn 361
QY 202 -----AAATGTTTAGACTTCAGAAAGATATATGC 231
Db 362 HisPheGluThrTyrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGAGGCTGGCCCTCGCTCCATACACACATCGTGGTGATACAAATAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrValProArgTrpAlaTyrAsnSer 401
QY 292 AAACTAAGATCTGCTCCGAATTCATCTATGCGCGTTCAGCGGGAACAATAACACTTC 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyrGlyGlyCysGluGlyAsnGlyAsnAsnPhe 421
QY 352 CAAACTGAAGCTATCTGCTGCTACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431

PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.

XX Disclosure; Page 80; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antibacterial, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antipapillary, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and in gene therapy.
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.

XX Sequence 33 AA;

Alignment Scores:
Pred. No.: 5.08e-10 Length: 33
Score: 180.00 Matches: 32
Percent Similarity: 96.97% Conservative: 0
Best Local Similarity: 96.97% Mismatches: 1
Query Match: 23.56% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19806 (1-33)

QY 295 ACTAAGATCTGCTCCGAATTCATCTATGCGGTGCCAGGGAACAATAACACTTCCAA 354
Db 1 ThrLysIleCysSerGluPheIleTyrglyGlySerGlnGlyAsnAsnAsnAsnGln 20

QY 355 ACTGAAGCTATCTGCTGCTACCTGCAAAAATACCAT 393
Db 21 ThrGluAlaIleCysLeuValThrCysLysLysTyrrHis 33

RESULT 46

ADA19809

ID ADA19809 standard; peptide; 33 AA.

XX ADA19809;

XX 20-NOV-2003 (first entry)

DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:10.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiarthritic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.

OS Homo sapiens.

XX

PN WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,

XX preventing or treating conditions associated with excessive proteinase

XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or

XX hemorrhage.

XX Disclosure; Page 82-83; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11

XX polypeptide comprising a Kunitz-type protease inhibitor domain or its

XX biologically active portion. The polypeptide comprises at least 98 %

XX identity to residues 77-127 of a 131 amino acid sequence (S1, see

XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see

XX ADA19801). DJ11 has antiinflammatory, antibacterial, thrombolytic,

XX anticoagulant, cardiant, vasotropic, antipapillary, immunosuppressive,

XX antirheumatic, antiarthritic, nephrotropic, antipsoriatic and in gene therapy.

XX activities, and can be used as a protease inhibitor and in gene therapy.

XX Composition and methods from the present invention can be used in

XX diagnosing, preventing or treating conditions associated with excessive

XX proteinase activity, such as acute pancreatitis, pulmonary injury,

XX allergy-induced protease release, deep vein thrombosis, myocardial

XX infarction, shock (including septic shock), hyperfibrinolytic

XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,

XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,

XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may

XX be used in preserving platelet function, organ preservation or in wound

XX healing. The polynucleotide sequence encoding DJ11 may be used as

XX hybridisation probes, in chromosome and gene mapping, in the generation

XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.

XX The present sequence represents a partial engineered human DJ11 protein

XX amino acid sequence from the present invention.

XX Sequence 33 AA;

Alignment Scores:

Pred. No.: 5.08e-10 Length: 33

Score: 180.00 Matches: 32

Percent Similarity: 96.97% Conservative: 0

Best Local Similarity: 96.97% Mismatches: 1

Query Match: 23.56% Indels: 0

DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19809 (1-33)

QY 295 ACTAAGATCTGCTCCGAATTCATCTATGCGGTGCCAGGGAACAATAACACTTCCAA 354

Db 1 ThrLysIleCysSerGluPheIleTyrglyGlySerGlnGlyAsnAsnAsnAsnGln 20

QY 355 ACTGAAGCTATCTGCTGCTACCTGCAAAAATACCAT 393

Db 21 ThrGluAlaIleCysLeuValThrCysLysLysTyrrHis 33

RESULT 47

AAR99146

ID AAR99146 standard; protein; 58 AA.

XX AAR99146;

XX 12-FEB-1997 (first entry)

XX

XX

DE Aprotinin-like Kunitz domain.
XX
KW Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alaph antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX
OS Synthetic.
XX
XX WO9620278-A2.
XX
XX 04-JUL-1996.
XX
XX 15-DEC-1995; 95WO-US016349.
XX
XX 16-DEC-1994; 94US-00358160.
XX
XX (PROT-) PROTEIN ENG CORP.
XX
XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX WPI; 1996-321851/32.
XX
XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
XX -like Kunitz domain for treating, e.g. cystic fibrosis or other
XX respiratory disorders.
XX
XX Example 23; Page 47; 105pp; English.
XX
XX Genetically engineered human derived Kunitz domains can be used to
XX inhibit human neutrophil elastase, an enzyme involved in the elimination
XX of pathogens and the restructuring of connective tissue. In cases of
XX reduction of the circulating alpha-1-protease inhibitor (API or alpha
XX antitrypsin), or the inactivation of API by oxidation (smokers
XX emphysema), extensive destruction of the lung tissue may result from
XX uncontrolled elastolytic activity of human neutrophil elastase. Other
XX respiratory disorders such as cystic fibrosis are thought to be caused by
XX human neutrophil elastase release by neutrophils. The genetically
XX engineered human derived Kunitz domains can be used to treat such
XX respiratory disorders. See AAR99146-R99211
XX
SQ Sequence 58 AA;

Alignment Scores:
Pred. No.: 1.18e-09 Length: 58
Score: 177.00 Matches: 21
Percent Similarity: 65.43% Conservative: 5
Best Local Similarity: 56.36% Mismatches: 19
Query Match: 23.17% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x AAR99146 (1-58)

Qy 217 AGAAGGNATATGCAATATCCAGAGAGCTGCGCCCTCGCTCCATACCAAC 276
Db 1 ArgProAspPheCysLeuLeuProAlaGluThrGlyProCysArgAlaMetIleProArg 20

Qy 277 TGGTGGTACATAAAAACTAAGATCTGCTCCGAAATTCATCTATGGCGGTGCCAGGG 336
Db 21 PheTyrTyrAsnAlaLysSerGlyLysCysGluProPheIleTyrGlyGlyCysGlyGly 40

Qy 337 AACCAATACAACTTCCAACTGAAGCTATCTGCTGGTGCACCTGC 381
Db 41 AsnAlaAsnAsnPheLysThrGluGluGluCysArgArgThrCys 55

RESULT 48
AAE13096
ID AAE13096 standard; peptide; 43 AA.
XX
XX AAE13096;
XX
XX 28-JAN-2002 (first entry)
XX

DE Human serine proteinase inhibitor BTL.009 peptide fragment #2.
XX
XX Human: BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angiodiastis;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
XX Homo sapiens.
OS
XX US6294648-B1.
XX
XX 25-SEP-2001.
XX
XX 20-JUL-1999; 99US-00358569.
XX
XX 20-JUL-1999; 99US-00358569.
XX
XX (FARB) BAYER CORP.
XX
XX Delaria K, Roczniaak S, Davies C;
PI
XX WPI; 2001-662224/76.
XX
XX New isolated protein for inhibiting human serine protease activity in the
XX treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
XX Disclosure; Col 5-6; 16pp; English.
XX
XX The invention relates to human BTL.009 protein, a serine proteinase
XX inhibitor of the Kunitz family that exhibits greater potency towards
XX neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
XX elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
XX protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
XX adult respiratory distress syndrome, cystic fibrosis, rheumatoid
XX arthritis, organ failure, glomerulonephritis, other inflammatory diseases
XX and diseases involving lung and vascular injury. BTL.009 is also useful
XX for preventing neutrophil and monocyte activation and formation of active
XX oxygen species during the oxidative burst of stimulated granulocytes.
XX BTL.009 is useful for reducing platelet activation and blood coagulation
XX and for the prophylactic or therapeutic treatment of patients undergoing
XX angioplasty. The present sequence is human serine proteinase inhibitor
XX BTL.009 peptide fragment related to the invention
XX
SQ Sequence 43 AA;

Alignment Scores:
Pred. No.: 1.79e-09 Length: 43
Score: 175.00 Matches: 29
Percent Similarity: 78.57% Conservative: 4
Best Local Similarity: 69.05% Mismatches: 9
Query Match: 22.91% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x AAE13096 (1-43)

Qy 259 CTGGCCCTCCATACCACTGGTGGTACATAAAAACTAAGATCTGCTCGAATTCATC 318
Db 1 LeuAlaTyrPheLeuHisTrpTrpTyrAspLysLysAspAsnThrCysSerMetPheVal 20

Qy 319 TATGGCGGTGCCAGGGGAACAATAACAACCTCCAACTCAAGCTATCTCTGGTCACC 378
Db 21 TyrGlyGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThr 40

Qy 379 TGCAAA 384
Db 41 CysLys 42

RESULT 49
AAE13092
ID AAE13092 standard; peptide; 54 AA.

—


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; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8

Alignment Scores:
Pred. No.: 2,32e-17 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x US-09-569-670-8 (1-58)
QY 217 AGAAGGATATATGACAGTATGCCAGGAGCTGCCCTGGCTCCATACCACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaIaTy:PheLeuHis 20
QY 277 TGGTGGTACATAAAAAAAGTATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGG 336
Db 21 TrpTrpTyAspLysAspAsnThrCysSerMetPheValTyGlyGlyCysGlnGly 40
QY 337 AACATAACAATTCCTCAAGCTATCTGTCTGGTCACCTGCAC 384
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56

RESULT 5
US-09-358-569D-8
; Sequence 8, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-8

Alignment Scores:
Pred. No.: 4.8e-17 Length: 54
Score: 233.00 Matches: 37
Percent Similarity: 79.63% Conservative: 6
Best Local Similarity: 68.52% Mismatches: 11
Query Match: 30.50% Indels: 0
DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-358-569D-8 (1-54)
QY 223 GATATGAGTATGCCAGGAGCTGCCCTGGCTCCATACCACACTGGTGG 282
Db 1 AspValCysGluMetProLysGluThrGlyProCysLeuAlaIaTy:PheLeuHisTrpTrp 20
QY 283 TACAATAAAAAAAGTATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAAAT 342
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaIaTy:PheLeuHis 20

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Db 21 TyrAspLysLysAspAsnThrCysSerMetPheValTyGlyGlyCysGlnGlyAsnAsn 40
QY 343 AACAACTCCAACTGAAGCTATCTGTCTGCTACCTGCACAA 384
Db 41 AsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 54

RESULT 6
US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Alignment Scores:
Pred. No.: 7.95e-17 Length: 55
Score: 231.00 Matches: 36
Percent Similarity: 80.00% Conservative: 8
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 30.24% Indels: 0
DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-358-569D-1 (1-55)
QY 217 AGAAGGATATATGACAGTATGCCAGGAGCTGCCCTGGCTCCATACCACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaIaTy:PheLeuHis 20
QY 277 TGGTGGTACATAAAAAAAGTATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGG 336
Db 21 TrpTrpTyAspLysLysAspAsnThrCysSerMetPheValTyGlyGlyCysGlnGly 40
QY 337 AACATAACAATTCCTCAAGCTATCTGTCTGGTCACCTGC 381
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCys 55

RESULT 7
US-08-358-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:

```


Db 44 AsnLysAsnAenPheLysThrLysAlaGluCysValArgAlaCysArg 59

RESULT 10

US-08-358-160-71

; Sequence 71, Application US/08358160

; Patent No. 5663143

; GENERAL INFORMATION:

; APPLICANT: LEY, Arthur C.

; APPLICANT: LADNER, Robert C.

; APPLICANT: GUTERMAN, Sonia K.

; APPLICANT: ROBERTS, Bruce L.

; APPLICANT: MARKLAND, William

; APPLICANT: KENT, Rachel B.

; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

; NUMBER OF SEQUENCES: 234

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W. Suite 300

; CITY: Washington

; STATE: District of Columbia

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/358,160

; FILING DATE: 16-DEC-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/133,031

; FILING DATE: 13-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/009,319

; FILING DATE: 26-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/664,989

; FILING DATE: 01-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/487,063

; FILING DATE: 02-MAR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/240,160

; FILING DATE: 02-SEP-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Cooper, Iver P.

; REGISTRATION NUMBER: 28,005

; REFERENCE/DOCKET NUMBER: LEV=1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 58 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-358-160-71

Alignment Scores:

Pred. No.: 5,71e-11 Length: 58

Score: 177.00 Matches: 31

Percent Similarity: 65.45% Conservative: 5

Best Local Similarity: 56.36% Mismatches: 19

Query Match: 23.17% Indels: 0

DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-71 (1-58)

QY 217 AGAAGGATATATGCAGTATGCCACAGAGGCTGGCCCTGCTCCATACCACAC 276

Db 1 ArgProAspPheCysLeuLeuProAlaGluThrGlyProCysArgAlaMetIleProArg 20

QY 277 TGGTGGTACATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGCCAGGGG 336

Db 21 PheTyrTyrAenAlaLysSerGlyLysCysGluProPheIleTyrGlyCysGlyGly 40

QY 337 AACATAACAACTTCCAACTGAAGCTATCTGTCTGGTCACTGC 381

Db 41 AsnAlaAenAenPheLysThrGluGluCysArgArgThrCys 55

RESULT 11

US-09-358-569D-13

; Sequence 13, Application US/09358569D

; Patent No. 6294648

; GENERAL INFORMATION:

; APPLICANT: Delaria, Kathy

; APPLICANT: Rocznik, Steve

; APPLICANT: Davies, Christopher

; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

; FILE REFERENCE: MSB-7259

; CURRENT APPLICATION NUMBER: US/09/358,569D

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 13

; LENGTH: 43

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Artificial

; OTHER INFORMATION: sequence derived from EST database

US-09-358-569D-13

Alignment Scores:

Pred. No.: 8.7e-11 Length: 43

Score: 175.00 Matches: 29

Percent Similarity: 78.57% Conservative: 4

Best Local Similarity: 69.05% Mismatches: 9

Query Match: 22.91% Indels: 0

DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-358-569D-13 (1-43)

QY 259 CTGGCTCCATACCACTGGTGTAACAATAAAAACTAGATCTGCTCCGAATTCATC 318

Db 1 LeuAlaTyrPheLeuHisTyrTyrAspLysAspAenThrCysSerMetPheVal 20

QY 319 TATGCGGTTCGAGGGGAACAATAACAACTTCCAACTGAAGCTATCTGTCTGGTCA 378

Db 21 TyrGlyGlyCysGlnGlyAenAenAenAenPheGlnSerLysAlaAenCysLeuAenThr 40

QY 379 TGC AAA 384

Db 41 CysLys 42

RESULT 12

US-09-358-569D-9

; Sequence 9, Application US/09358569D

; Patent No. 6294648

; GENERAL INFORMATION:

; APPLICANT: Delaria, Kathy

; APPLICANT: Rocznik, Steve

; APPLICANT: Davies, Christopher

; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

; FILE REFERENCE: MSB-7259

; CURRENT APPLICATION NUMBER: US/09/358,569D

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 9


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; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-9

Alignment Scores:
Pred. No.: 9.23e-11 Length: 54
Score: 175.00 Matches: 27
Percent Similarity: 68.52% Conservative: 10
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 22.91% Indels: 0
DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-358-569D-9 (1-54)
Qy 223 GATATATGACGATGTCACAGGAGGCTGGCCCTGCTGCTCCATACACACTGGTGG 282
Db 1 AspleuCysGlnLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 20
Qy 283 TACAATAAAAACTAAGATCTGCTCGAATTCATCTATGCGGTGCGAGGGGAACAAT 342
Db 21 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 40
Qy 343 AACAACTTCCAACTGAAGCTATCTGCTGCTCACCTGCAAA 384
Db 41 AsnAsnPheGluThrThrGluMetCysLeuArgIleCysGlu 54

RESULT 13
; Sequence 123, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-123

Alignment Scores:
Pred. No.: 9.77e-11 Length: 67
Score: 175.00 Matches: 27
Percent Similarity: 68.52% Conservative: 10
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 22.91% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-123 (1-67)
Qy 223 GATATATGACGATGTCACAGGAGGCTGGCCCTGCTGCTCCATACACACTGGTGG 282
Db 6 AspleuCysGlnLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 25
Qy 283 TACAATAAAAACTAAGATCTGCTCGAATTCATCTATGCGGTGCGAGGGGAACAAT 342
Db 26 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 45
Qy 343 AACAACTTCCAACTGAAGCTATCTGCTGCTCACCTGCAAA 384
Db 46 AsnAsnPheGluThrThrGluMetCysLeuArgIleCysGlu 59

RESULT 14
; Sequence 17, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
```



```
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-17

Alignment Scores:
Pred. No.: 1.55e-10 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-17 (1-58)

QY 217 AGAAGGATATATGCAGTATGCCAGGAGGCTGCGCCCTGCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACAATAAAAAAAGTATCGCTCCGAATTCATCTATGGGGTGGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAACCTCCAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 15
US-08-358-160-18
; Sequence 18, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESS: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004

; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-17

Alignment Scores:
Pred. No.: 1.55e-10 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-18 (1-58)

QY 217 AGAAGGATATATGCAGTATGCCAGGAGGCTGCGCCCTGCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACAATAAAAAAAGTATCGCTCCGAATTCATCTATGGGGTGGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAACCTCCAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 16
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chien, Kretzmer, Kuniko K. Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
```


RESULT 21
US-07-664-989B-48
; Sequence 48, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Suite 300
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-48
Alignment Scores:
Pred. No.: 8.89e-10 Length: 58
Score: 166.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.73% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-07-664-989B-48 (1-58)
Qy 217 AGAAGATATATGAGTATGCCAGAGGCTGCGCCCTCGCTGCATACACAC 276
Db 1 ArgProaspPheCysLeuGluProProTyrThrGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATATAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 21 TyrPheTyrAenAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly 40

Qy 337 AACAAATAACAACCTCCAAACTGAAGCTATCTGTCTGTGTCACCTGC 381
Db 41 AsnGlyAenAenPheLysSerAlaGluAspCysMetArgThrCys 55
RESULT 22
US-07-664-989B-51
; Sequence 51, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Suite 300
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-51
Alignment Scores:
Pred. No.: 8.89e-10 Length: 58
Score: 166.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.73% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-07-664-989B-51 (1-58)
Qy 217 AGAAGATATATGAGTATGCCAGAGGCTGCGCCCTCGCTGCATACACAC 276
Db 1 ArgProaspPheCysLeuGluProProTyrThrGlyProCysValAlaMetPheProArg 20

us-10-807-204-11.std.ra1

Qy 277 TGGTGGTACATAAATAAAGTATGCTCCGAATTCTATCTATGCGGTTGCCAGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly 40

Qy 337 AACATAACAATCTCCAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 41 AsnGlyAsnAenPheLysSerAlaGluAepCysMetArgThrCys 55

RESULT 23
US-08-358-160-1
; Sequence 1, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-1

Alignment Scores: 8.89e-10 Length: 58
Pred. No.: 166.00 Matches: 26
Score:

us-10-807-204-11 (1-396) x US-08-358-160-1 (1-58)

Qy 217 AGAAGGATATATGACAGTATGCCACAGAGGCTGGCCCTGCCTGCCTCCATACCACAC 276
Db 1 ArgProAspPheCysLeuGluProTyrThrGlyProCysValAlaMetPheProArg 20

Qy 277 TGGTGGTACATAAATAAAGTATGCTCCGAATTCTATCTATGCGGTTGCCAGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly 40

Qy 337 AACATAACAATCTCCAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 41 AsnGlyAsnAenPheLysSerAlaGluAepCysMetArgThrCys 55

RESULT 24
US-08-358-160-15
; Sequence 15, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-15

Percent Similarity: 61.82%
Best Local Similarity: 47.27%
Query Match: 21.73%
Conservative: 8
Mismatch: 21
Indels: 0
Gaps: 0


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-15

Alignment Scores:
Pred. No.: 8.89e-10 Length: 58
Score: 166.00 Matches: 27
Percent Similarity: 62.50% Conservative: 8
Best Local Similarity: 48.21% Mismatches: 21
Query Match: 21.73% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-15 (1-58)
Qy 217 AGAAGGATATATGAGTATGCCAGAGGCTGCCCTCGCTCCATACCACAC 276
Db 1 LysGluaspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGTATGCTCCGAATTCTATGCGGGTTGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheGlnTyrGlyGlyCysMetGly 40
Qy 337 AACAAATACAACTCCAACTGAAGCTATCTGTCTGTCACTGCATAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 25
; Sequence 26, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-26

Alignment Scores:
Pred. No.: 8.89e-10 Length: 58
Score: 166.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.73% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-26 (1-58)
Qy 217 AGAAGGATATATGAGTATGCCAGAGGCTGCCCTCGCTCCATACCACAC 276
Db 1 ArgProaspPheCysLeuGluProProTyrThrGlyProCysAlaAlaPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGTATGCTCCGAATTCTATGCGGGTTGCCAGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACAAATACAACTCCAACTGAAGCTATCTGTCTGTCACTGC 381
Db 41 AsnGlyAsnAsnPheLysSerAlaGluAspCysMetArgThrCys 55

RESULT 26
; Sequence 27, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
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Thu Sep 22 07:16:44 2005

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; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-27

Alignment Scores:
Pred. No.: 9,048-10 Length: 62
Score: 166.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.73% Indels: 0
Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-27 (1-62)
QY 217 AGAAGGATATATGAGTATGCCAGAGGCTGCCCTCGCTCCATACCAC 276
Db 5 ArgProaspPheCysLeuGluProProTyrThrGlyProCysIleAlaPheProArg 24
QY 277 TGGTGGTACATAAATAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGCCAGGG 336
Db 25 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyCysMetGly 44
QY 337 AACATAACAACCTCCAACTGAAGCTATCTGCTGGTCCACTGC 381
Db 45 AsnGlyAsnAsnPheLysSerAlaGluAspCysMetArgThrCys 59

RESULT 27
; Sequence 49, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Lev, Arthur Charles
; APPLICANT: Kent, Rachel Barbault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA

; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-49

Alignment Scores:
Pred. No.: 1,148-09 Length: 58
Score: 165.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.60% Indels: 0
Gaps: 0

US-10-807-204-11 (1-396) x US-07-664-989B-49 (1-58)
QY 217 AGAAGGATATATGAGTATGCCAGAGGCTGCCCTCGCTCCATACCAC 276
Db 1 ArgProaspPheCysLeuGluProProTyrThrGlyProCysValAlaIlePheProArg 20
QY 277 TGGTGGTACATAAATAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGCCAGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAACCTCCAACTGAAGCTATCTGCTGGTCCACTGC 381
Db 41 AsnGlyAsnAsnPheLysSerAlaGluAspCysMetArgThrCys 55

RESULT 28
; Sequence 24, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
```


;
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-24

Alignment Scores:
Pred. No.: 1.14e-09 Length: 58
Score: 165.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.60% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-24 (1-58)

Qy 217 AGAAGGATATATGCAGTATGCCACAGAGCTGGCCCTGCCTCCATACCAC 276
Db 1 ArgProaspPheCysLeuGluProProTyrThrGlyProCysValAlaIlePheProArg 20
Qy 277 TGGTGGTACATAAATAAAGTATGCTCCGAATTCATCTATGGCGGTGCGAGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACAACTCAACTCCAAAGTATGCTGTGTGTCACCTGC 381
Db 41 AsnGlyAsnAsnPheLysSerAlaGluAspCysMetArgThrCys 55

RESULT 29

US-08-358-160-9

; Sequence 9, Application US/08358160

; Patent No. 5663143

; GENERAL INFORMATION:

; APPLICANT: LEY, Arthur C.

;
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-9

Alignment Scores:
Pred. No.: 1.46e-09 Length: 58
Score: 164.00 Matches: 27
Percent Similarity: 62.50% Conservative: 8
Best Local Similarity: 48.21% Mismatches: 21
Query Match: 21.47% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-9 (1-58)

Qy 217 AGAAGGATATATGCAGTATGCCACAGAGCTGGCCCTGCCTCCATACCAC 276
Db 1 LysGluaspSerCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAATAAAGTATGCTCCGAATTCATCTATGGCGGTGCGAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheGlnTyrGlyGlyCysMetGly 40

Qy 337 AACAAATCAACTTCCAAACTGAAGCTATCTGTCTGTGGTCACTGCAAA 384
Db 41 AsnGlyAsnAsnPhValThrGluLysAspCysLeuGlnThrCysArg 56
RESULT 30
US-08-829-876-211
; Sequence 211, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-211
Alignment Scores:
Pred. No.: 1.48e-09 Length: 61
Score: 164.00 Matches: 25
Percent Similarity: 62.96% Conservative: 9
Best Local Similarity: 46.30% Mismatches: 20
Query Match: 21.47% Indels: 0
DB: 2 Gaps: 0
US-10-807-204-11 (1-396) x US-08-829-876-211 (1-61)
Qy 220 AAGGATATATGAGTATGCCACAGAGGCTGCGCCCTGCCTCCATACCACCTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaLeuIleProArgTrp 23
Qy 280 TGGTACAATAAAAAAACAATCAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAAC 339
Db 24 TyrPheAspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsn 43
Qy 340 AATAACAACCTTCCAAACTGAAGCTATCTGTCTGTGGTCACTGC 381
Db 44 ArgAsnAsnPhAspThrGluGluTyrCysMetalAlaValCys 57
RESULT 32

Db 44 ArgAsnAsnPhAspThrGluGluTyrCysMetalAlaValCys 57
RESULT 31
US-08-829-876-214
; Sequence 214, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-214
Alignment Scores:
Pred. No.: 1.48e-09 Length: 61
Score: 164.00 Matches: 25
Percent Similarity: 62.96% Conservative: 9
Best Local Similarity: 46.30% Mismatches: 20
Query Match: 21.47% Indels: 0
DB: 2 Gaps: 0
US-10-807-204-11 (1-396) x US-08-829-876-214 (1-61)
Qy 220 AAGGATATATGAGTATGCCACAGAGGCTGCGCCCTGCCTCCATACCACCTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaLeuIleProArgTrp 23
Qy 280 TGGTACAATAAAAAAACAATCAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAAC 339
Db 24 TyrPheAspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysArgGlyAsn 43
Qy 340 AATAACAACCTTCCAAACTGAAGCTATCTGTCTGTGGTCACTGC 381
Db 44 ArgAsnAsnPhAspThrGluGluTyrCysMetalAlaValCys 57
RESULT 32

Lesikar, David D.
McFadden, Kathleen
Garrick, Brett L.
TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,873A
FILING DATE: 21-Jan-1999
PRIOR APPLICATION NUMBER: 08/829,876
FILING DATE: 02-APR-1997
APPLICATION NUMBER: 08/436,555
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 056324/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 211:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-234-873A-211

Alignment Scores:
Pred. No.: 1.48e-09 Length: 61
Score: 164.00 Matches: 25
Percent Similarity: 62.96% Conservative: 9
Best Local Similarity: 46.30% Mismatches: 20
Query Match: 21.47% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x US-09-234-873A-211 (1-61)

QY 220 AAGGATATATGAGTATGCCACAGGAGGCTGCCCTGCCTCCATACACACTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaAlaIleGlnHisTrp 23
QY 280 TGGTACAATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAC 339
Db 24 TyrPheAspValThrGluGlyLysCysAlaProPhePheTyrglyCysGlyGlyAen 43
QY 340 AATAACAATCCAACTCAAGCTATCTGTGGTCACCTGC 381
Db 44 ArgAsnAsnPheAspThrGluGluTyrCysMetAlaValCys 57

RESULT 35

US-09-234-873A-214
; Sequence 214, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damir, Deborah
; Lesikar, David D.

McFadden, Kathleen
Garrick, Brett L.
TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,873A
FILING DATE: 21-Jan-1999
PRIOR APPLICATION NUMBER: 08/829,876
FILING DATE: 02-APR-1997
APPLICATION NUMBER: 08/436,555
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 056324/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-234-873A-214

Alignment Scores:
Pred. No.: 1.48e-09 Length: 61
Score: 164.00 Matches: 25
Percent Similarity: 62.96% Conservative: 9
Best Local Similarity: 46.30% Mismatches: 20
Query Match: 21.47% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x US-09-234-873A-214 (1-61)

QY 220 AAGGATATATGAGTATGCCACAGGAGGCTGCCCTGCCTCCATACACACTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaAlaIleProargTrp 23
QY 280 TGGTACAATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAC 339
Db 24 TyrPheAspValThrGluGlyLysCysAlaProPhePheTyrglyCysArgGlyAen 43
QY 340 AATAACAATCCAACTCAAGCTATCTGTGGTCACCTGC 381
Db 44 ArgAsnAsnPheAspThrGluGluTyrCysMetAlaValCys 57

RESULT 36

US-07-664-989B-84
; Sequence 84, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William

APPLICANT: Ley, Arthur Charles
APPLICANT: Kent, Rachel Baribault
TITLE OF INVENTION: Directed Evolution of No. 5223409el
TITLE OF INVENTION: Binding Proteins
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
SUITE: Suite 300
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 4.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/664,989B
FILING DATE: 19910301
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005

REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 84:

SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-664-989B-84
Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.34% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-07-664-989B-84 (1-58)
Qy 217 AGAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTCCATACCACAC 276
Db 1 ArgProaspPheCysLeuGluProProTyrThrGlyProCysValAlaMetPheProArg 20

Qy 277 TGGTGGTACATAAAAAAAGTATGCTGCCGAATTCATCTATGGCGGTGCCAGGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheMetTyrGlyGlyCysGlnGly 40
Qy 337 AACAAATCAACTCCAAAGCTATCTGTCTGGTCACTGC 381
Db 41 LysGlyAsnAsnPheLysSerAlaGluAspCysMetArgThrCys 55

RESULT 37
US-08-358-160-12
; Sequence 12, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-358-160-12
Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 27
Percent Similarity: 58.93% Conservative: 6
Best Local Similarity: 48.21% Mismatches: 23
Query Match: 21.34% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-12 (1-58)
Qy 217 AGAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTCCATACCACAC 276
Db 1 ArgProaspPheCysGlnLeuGlyTyrSerThrGlyProCysValAlaMetPheProArg 20

Qy 277 TGGTGGTACATAAAAAAAGTATCTGTCTGGTCACTGC 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheMetTyrGlyGlyCysGlnGly 40
Qy 337 AACAAATCAACTCCAAAGCTATCTGTCTGGTCACTGC 381
Db 41 LysGlyAsnAsnPheLysSerAlaGluAspCysMetArgThrCys 55

RESULT 37
US-08-358-160-12
; Sequence 12, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:

Db 21 TyrPheTyraenGlyThrSerMetAlaCysGluThrPheGlnTyrglyGlyCysMetGly 40
Qy 337 AACAAATCAACTCCAACTGAAGCTATCTGCTGGTCACTGCAAA 384
Db 41 AenGlyAenAenPheValThrGluLysaspCysLeuGlnThrCysarg 56

RESULT 38
US-08-358-160-61
; Sequence 61, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-358-160-61
Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21

Query Match: 21.34% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-08-358-160-61 (1-58)
Qy 217 AGAAAGGATATATGACGTATGCCACAGAGGCTGGCCCTGCTGCTCCATACCACAC 276
Db 1 ArgProaspPheCysLeuGluProProTyThrGlyProCysValAlaMetPheProarg 20
Qy 277 TGGTGTACAAATAAAAACTAAGATCTGTCCGAATTCATCTATGCGGGTTCAGGGG 336
Db 21 TyrPheTyraenAlaLysAlaGlyLeuCysGlnThrPheMetTyrglyGlyCysGlnGly 40
Qy 337 AACAAATCAACTCCAACTGAAGCTATCTGCTGGTCACTGCG 381
Db 41 LysGlyAenAenPheLysSerAlaGluaspCysMetArgThrCys 55

RESULT 39
US-08-463-155A-56
; Sequence 56, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,155A
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-155A-56

Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 26
Percent Similarity: 62.96% Conservative: 8
Best Local Similarity: 48.15% Mismatches: 20
Query Match: 21.34% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-08-463-155A-56 (1-58)
Qy 220 AAGGATATATGACGTATGCCACAGAGGCTGGCCCTGCTGCTCCATACCACACTGG 279
Db 2 ArgGluValCysSerGluGlnAlaGluaspGlyProCysArgAlaAlaIleProargTrp 21
Qy 280 TGGTACAAATAAAAACTAAGATCTGCTCCGAAATTCATCTATGCGGGTTCAGGGGGAAC 339

Db 22 TyrPheAspValThrGluGlyLysCysAlaProPheIleTyrGlyGlyCysGlyGlyAsn 41
Qy 340 AATAACAACTTCCAAACTGAAGCTATCTGTCTGGTCACTGC 381
Db 42 ArgAenAenPheAspThrGluGluTyrCysAlaLaValCys 55
RESULT 40
US-08-463-432B-56
; Sequence 56, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKEIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463.432B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-432B-56
Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 26
Percent Similarity: 62.96% Conservative: 8
Best Local Similarity: 48.15% Mismatches: 20
Query Match: 21.34% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-08-463-432B-56 (1-58)
Qy 220 AAGATATATGCAGTATCCACAGAGCTGGCCCTGCTGCCTCATACCACTGG 279
Db 2 ArgGluValCysSerGluGlnAlaGluAspGlyProCysArgAlaAlaIleProArgTrp 21
Qy 280 TGGTACATAAAAAAACTAAGATCTGCTCGAAATTCATCTATGCGGTTCAGGGGAAC 339
Db 22 TyrPheAspValThrGluGlyLysCysAlaProPheIleTyrGlyGlyCysGlyGlyAsn 41
Qy 340 AATAACAACTTCCAAACTGAAGCTATCTGTCTGGTCACTGC 381
Db 42 ArgAenAenPheAspThrGluGluTyrCysAlaLaValCys 55
RESULT 41
US-08-676-124-69
; Sequence 69, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:

; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,124
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,658
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,265
; FILING DATE: 10-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: MARKLAND=3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-676-124-69
Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 25
Percent Similarity: 62.26% Conservative: 8
Best Local Similarity: 47.17% Mismatches: 20
Query Match: 21.34% Indels: 0
DB: 3 Gaps: 0
US-10-807-204-11 (1-396) x US-08-676-124-69 (1-58)
Qy 223 GATATATGCAGTATGCCACAGGAGCTGGCCCTGCTGCCTCATACCACTGGTGG 282
Db 3 AspIleCysLysLeuProLysAspThrGlyProCysArgAlaArgPheAspLysTrpTyr 22
Qy 283 TACAATAAAAAAACTAAGATCTGCTCGAAATTCATCTATGCGGTTCAGGGGAACAAAT 342
Db 23 TyrAspProAsnThrLysSerCysGluGluPheValTyrGlyGlyCysGlyGlyAsnGlu 42
Qy 343 AACAACTTCCAAACTGAAGCTATCTGTCTGGTCACTGC 381
Db 43 AsnLysPheGlySerGlnLysGluCysGluLysValCys 55
RESULT 42
US-09-414-878-69
; Sequence 69, Application US/09414878
; Patent No. 6071723
; GENERAL INFORMATION:

APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plamin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-414-878-69

Alignment Scores:
Pred. No.: 1,88e-09 Length: 58
Score: 163.00 Matches: 25
Percent Similarity: 62.26% Conservative: 8
Best Local Similarity: 47.17% Mismatches: 20
Query Match: 21.34% Indels: 0
Gaps: 0
DB:

US-10-807-204-11 (1-396) x US-09-414-878-69 (1-58)

QY 223 GATATATGAGTATGCCACAGAGGCTGGCCCTGCTCCATACACACTGGTGG 282
Db 3 AspIleCysLeuProlAspThrGlyProCysArgAlaArgPheAspLysTyrTyr 22
QY 283 TACAATAAAAAAATGATCTGCTCCGAATTCATCTGCGGTTGCCAGGGGAACAT 342
Db 23 TyrAspProAsnThrLysSerCysGluGluPheValTyrGlyGlyCysGlyAenGlu 42

QY 343 AACAACTTCCAAACTGAAGCTATCTGTCTGGTGCACCTGC 381
Db 43 AsnLysPheGlySerGlnLysGluCysGluLysValCys 55
RESULT 43
US-09-240-136-69
Sequence 69, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plamin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,136
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-69

Alignment Scores:
Pred. No.: 1,88e-09 Length: 58
Score: 163.00 Matches: 25
Percent Similarity: 62.26% Conservative: 8
Best Local Similarity: 47.17% Mismatches: 20
Query Match: 21.34% Indels: 0
Gaps: 0
DB:

US-10-807-204-11 (1-396) x US-09-240-136-69 (1-58)

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Qy 283 TACAATAAAAAAAGTATGCTCCGAATTCATCTATGCGGTGCGAGGGGAACAAT 342
Db 23 TyrAspProAnthrLysSerCysGluGluPheValTyrGlyGlyCysGlyGlyAsnGlu 42
Qy 343 AACAACTTCCAAACTGAAGCTATCTGCTGCTGCACCTGC 381
Db 43 AsnLysPheGlySerGlnLysGluCysGluLysValCys 55
RESULT 44
US-09-638-770A-69
; Sequence 69, Application US/09638770A
; Patent No. 6423498
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; MARKLAND, William
; LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; From The Kunitz Domains
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankeech & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,770A
; FILING DATE: 15-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-638-770A-69
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Query Match: 21.34% Indels: 0
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Db 3 AspileCysLysLeuProLysAspThrGlyProCysArgAlaAaPheAspLysTrpTyr 22
Qy 283 TACAATAAAAAAAGTATGCTCCGAATTCATCTATGCGGTGCGAGGGGAACAAT 342
Db 23 TyrAspProAnthrLysSerCysGluGluPheValTyrGlyGlyCysGlyGlyAsnGlu 42
Qy 343 AACAACTTCCAAACTGAAGCTATCTGCTGCTGCACCTGC 381
Db 43 AsnLysPheGlySerGlnLysGluCysGluLysValCys 55
RESULT 45
US-08-829-876-180
; Sequence 180, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-180
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Score: 163.00 Matches: 25
Percent Similarity: 61.11% Conservative: 8
Best Local Similarity: 46.30% Mismatches: 21
Query Match: 21.34% Indels: 0
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US-09-234-873A-218
; Sequence 218, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-873A-218

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US-10-807-204-11 (1-396) x US-09-234-873A-218 (1-61)

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QY	340	ATAACAACTTCCAACTGAAGCTATCTGTCTGTCACCTGC	381
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	739	96.7	131	16	US-10-807-204-15 Sequence 15, Appl
4	613	80.2	106	16	US-10-807-204-2 Sequence 2, Appl
5	559	73.2	98	16	US-10-807-204-9 Sequence 9, Appl
6	480	62.8	136	16	US-10-807-204-16 Sequence 16, Appl
7	455	59.6	133	9	US-09-853-161-75 Sequence 75, Appl
8	455	59.6	133	9	US-09-852-659A-75 Sequence 75, Appl
9	455	59.6	133	9	US-09-852-797-75 Sequence 75, Appl
10	455	59.6	133	15	US-10-058-993-75 Sequence 75, Appl
11	455	59.6	133	16	US-10-807-204-13 Sequence 13, Appl
12	412	53.9	86	17	US-10-480-988-21 Sequence 21, Appl
13	412	53.9	101	15	US-10-276-774-2606 Sequence 2606, Ap
14	399.5	51.0	117	9	US-09-852-659A-119 Sequence 119, App
15	388.5	51.0	117	15	US-10-058-993-120 Sequence 120, App
16	388	50.8	102	9	US-09-852-659A-120 Sequence 120, App
17	388	50.8	102	15	US-10-058-993-121 Sequence 121, App
18	386	50.5	134	16	US-10-807-204-14 Sequence 14, Appl
19	246	32.2	43	16	US-10-807-204-5 Sequence 5, Appl
20	236	30.9	58	17	US-10-361-997-5 Sequence 21, Appl
21	236	30.9	58	17	US-10-331-153-21 Sequence 118, App
22	219	28.7	51	15	US-10-058-993-118 Sequence 48, Appl
23	189.5	24.8	759	17	US-10-825-692-48 Sequence 160, App
24	184	24.1	64	10	US-09-896-095-160 Sequence 103, App
25	184	24.1	64	14	US-10-038-722-103 Sequence 17, Appl
26	184	24.1	64	15	US-10-115-134-17 Sequence 3, Appl
27	180.5	23.6	571	14	US-10-369-736-3 Sequence 49, Appl
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30	180.5	23.6	571	14	US-10-369-738-3 Sequence 3, Appl
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33	180	23.6	33	16	US-10-807-204-7 Sequence 10, Appl
34	180	23.6	33	16	US-10-807-204-10 Sequence 5, Appl
35	177	23.2	58	14	US-10-038-722-5 Sequence 147, App
36	175	22.9	67	10	US-09-896-095-147 Sequence 90, Appl
37	175	22.9	67	14	US-10-038-722-90 Sequence 4, Appl
38	175	22.9	67	15	US-10-115-134-4 Sequence 17, Appl
39	173	22.6	58	14	US-10-038-722-17 Sequence 18, Appl
40	173	22.6	58	14	US-10-038-722-18 Sequence 19, Appl
41	173	22.6	58	14	US-10-038-722-18 Sequence 88, Appl
42	173	22.6	58	15	US-10-115-134-88 Sequence 89, Appl
43	173	22.6	58	15	US-10-115-134-89 Sequence 90, Appl
44	173	22.6	58	15	US-10-456-986A-42 Sequence 42, Appl
45	173	22.6	58	15	US-10-456-986A-43 Sequence 43, Appl
46	173	22.6	58	15	US-10-456-986A-44 Sequence 44, Appl
47	173	22.6	58	15	US-10-953-902A-42 Sequence 42, Appl
48	173	22.6	58	18	US-10-953-902A-43 Sequence 43, Appl
49	173	22.6	58	18	US-10-953-902A-43 Sequence 44, Appl
50	173	22.6	58	18	US-10-953-902A-44 Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Annes
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18


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; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
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; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
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; OTHER INFORMATION: predicted by SignalP 2.0
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
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; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
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; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
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; NAME/KEY: DISULFID
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Score: 741.00 Matches: 130
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Query Match: 96.99% Indels: 0
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Db 101 IleCysSerGluPheIleTyrGlyGlyCysGlnGlyAsnAsnAsnAsnPheGlnThrGlu 120
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RESULT 2
US-10-807-204-12
; Sequence 12, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
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; SOFTWARE: FastSeq for Windows Version 4.0
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; US-10-807-204-12

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Query Match: 96.99% Indels: 0
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; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
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US-10-807-204-15

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US-10-807-204-11 (1-396) x US-10-807-204-15 (1-131)

Qy 1 ATGGGACTCTCAGGACTCTGCAATCTCTGTACCATTCATCTTTTGGGGACATCCAG 60
Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
Qy 61 GAACCTGGGCACGCTGAGGACATCTCTTGGCAAGCCGTGTCCAAATCAAACTGGAATGC 120
Db 21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysIleLysValGluCys 40
Qy 121 GAATGGGAATAATAGACAGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
Db 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
Qy 181 TCCCGCTTCAGCGCTGGAAGAAATCTTTAGACTTCAGAAAGATATATGCAATGCA 240
Db 61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
Qy 241 CAGGAGGCTGGCCCTGCTGCTCCATACACACTGGTGGTACATAAATAAATAAG 300
Db 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTyrIleTyrAsnLysLysThrLys 100
Qy 301 ATCTGCTCCGAATTCATCTATGGCGTTGCCAGGGGAACAATAACAACCTTCCAAACTGAA 360
Db 101 IleCysSerGluPheIleTyrGlyGlySerGlnGlyAsnAsnAsnGlnThrGlu 120
Qy 361 GCTATCTCTCTGGTCACCTGCAGAAAAATACCAT 393
Db 121 AlaIleCysLeuValThrCysLysLysTyrHis 131

RESULT 4

US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (23)...(35)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-2

Alignment Scores:
Pred. No.: 1.07e-56 Length: 106
Score: 613.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 80.24% Indels: 0
DB: 16 Gaps: 0

US-10-807-204-11 (1-396) x US-10-807-204-2 (1-106)

Qy 76 GAAGCCTCTTGGCAAGCCGTGTCCAAATCAAACTGGAATGCGAAGTGAAGATA 135
Db 1 GluGlyIleLeuGlyLysProCysProLysIleLysValGluCysGluValGluGluIle 20

FILE REFERENCE: P2003P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 75
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
US-09-853-161-75

Alignment Scores:
Pred. No.: 133
Score: 455.00
Percent Similarity: 74.22%
Best Local Similarity: 60.16%
Query Match: 59.55%
DB: 0

US-10-807-204-11 (1-396) x US-09-853-161-75 (1-133)

QY 1 ATGGGACTCTCAGGACTCTGCAATCTCTGGTACCATTATCTCTTTGGGGACATCCAG 60
Db 1 MetGlySerSerGlyLeuLeuSerLeuLeuValLeuPheValLeuLeuAlaAsnValGln 20
QY 61 GAACCTGGGCACGCTGAAGGCATCTTGGCAAGCGGTGTCCTCCAAATCAAAGTGAATGC 120
Db 21 GlyProGlyLeuThrAspTrpLeuPheProArgArgCysProLysIleArgGluGluCys 40
QY 121 GAAGTGGAAAGAAATAGACAGGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
Db 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60
QY 181 TGCCCGTTCAGCGTGAAGAAATGTTAGACTTCCAGAAAGATATATGAGTATGCCA 240
Db 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
QY 241 CAGGAGGCTGGCCCTCGCTGCTCCATACCACTGGTGTGTACAAATAAAAAACTAAG 300
Db 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTyrTrpTyrAspLysLysAspAsn 100
QY 301 ATCTGCTCCGAATTCATATGCGGTTCAGGGGAAACAATAACAACTTCCAAACTGAA 360
Db 101 ThrCysSerMetPheValTyrGlyGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerLys 120
QY 361 GCTATCTGCTGTGTACCTGCAGAA 384
Db 121 AlaAsnCysLeuAsnThrCysLys 128

RESULT 8
US-09-852-659A-75
Sequence 75, Application US/09852659A
Patent No. US20020077287A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 75
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-659A-75

Alignment Scores:
Pred. No.: 133
Score: 455.00
Percent Similarity: 74.22%
Best Local Similarity: 60.16%
Query Match: 59.55%
DB: 0

US-10-807-204-11 (1-396) x US-09-852-659A-75 (1-133)

QY 1 ATGGGACTCTCAGGACTCTGCAATCTCTGGTACCATTATCTCTTTGGGGACATCCAG 60
Db 1 MetGlySerSerGlyLeuLeuSerLeuLeuValLeuPheValLeuLeuAlaAsnValGln 20
QY 61 GAACCTGGGCACGCTGAAGGCATCTTGGCAAGCGGTGTCCTCCAAATCAAAGTGAATGC 120
Db 21 GlyProGlyLeuThrAspTrpLeuPheProArgArgCysProLysIleArgGluGluCys 40
QY 121 GAAGTGGAAAGAAATAGACAGGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
Db 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60
QY 181 TGCCCGTTCAGCGTGAAGAAATGTTAGACTTCCAGAAAGATATATGAGTATGCCA 240
Db 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
QY 241 CAGGAGGCTGGCCCTCGCTGCTCCATACCACTGGTGTGTACAAATAAAAAACTAAG 300
Db 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTyrTrpTyrAspLysLysAspAsn 100
QY 301 ATCTGCTCCGAATTCATATGCGGTTCAGGGGAAACAATAACAACTTCCAAACTGAA 360

Pred. No.:	3.63e-35	Length:	86
Score:	412.00	Matches:	74
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	93.93%	Indels:	0
DB:	17	Gaps:	0

US-10-807-204-11 (1-396) x US-10-480-988-21 (1-86)

1	ATGGGACTCTCAGGACTTCTGCCAATCTCTGTACGATTCATCTCTTTGGGGGAGATCCAG	60
Qy		
1	MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln	20
Db		
61	GAACCTGGGCACGCTGAAGGCATCTTCGGCAAGCGGTCTCCAAAAATCAAAAGTGGAAATGC	120
Qy		
21	GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProIlySerIleLysValGluCys	40
Db		
121	GAAGTGGAGAAATAGACAGGTGTACCAAAACCCAGAGATTGCCCCAGAGAAAACATGAAGTGT	180
Qy		
41	GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys	60
Db		
181	TGCCCGTTTCAGCCGTGGAAAGAAATGTTTTAGATCTCAGAAG	222
Qy		
61	CysProPheSerArgGlyLysLysCysLeuAspPheArgLys	74
Db		

RESULT 13

```

US-10-276-774-2606
; Sequence 2606, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2606
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2606

```

Alignment Scores:	3.74e-35	Length:	101
Pred. No.:	412.00	Matches:	74
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	53.93%	Gaps:	0
DB:	15		

US-10-807-204-11 (1-396) x US-10-276-774-2606 (1-101)

1	ATGGAGCTCTCAGGACTTCTGCCAATCTCGTGTACATTCATCTCTTTTGGGGGACATCCAG	60	QY
16	MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln	35	Db
61	GAACCTGGGCACGCTGAAGGCATCTTCGGCAAGCGGTCTCCCAAAATCAAAAGTGGAAATGC	120	QY
36	GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProIlyIleLysValGluCys	55	Db
121	GAAGTGGAGAAATAGACAGTGTACCAAAACCCAGAGATTGCCACAGAAAACATGAAGTGT	180	QY
56	GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys	75	Db
181	TGCCCGTTCAGCCGTGGAAAGAAATGTTTTAGACTTCAGAAG	222	QY
76	CysProPheSerArgGlyLysLysCysLeuAspPheArgLys	89	Db

RESULT 14

US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-119

Alignment Scores:	9.92e-33	Length:	117
Pred. No.:	Score:	Matches:	65
	389.50	Conservative:	12
Percent Similarity:	77.00%	Mismatches:	22
Best Local Similarity:	65.00%	Indels:	1
Query Match:	50.98%	Gaps:	1
DB:	9		

US-10-807-204-11 (1-396) x US-09-852-659A-119 (1-117)

Qy	85	CTTGGAGACCGTGTGCCAAATCAAAAGTGCAGAGTGGAGAAATAGACCAAGTGT	144
Db	14	LeuGlyArg--CysProLysIleArgGluGluCysGluPheGlnGluArgAspValCys	32
Qy	145	ACCAAAACCAGAGATTGCCAGAAAACATGAAGTGTTCGCCCTTCAGCCGTGCAAAAGAA	204
Db	33	ThrLysAspArgGlnCysGlnAspAsnLysCysCysValPheSerCysGlyLysLys	52
Qy	205	TGTTTAGACTTCAGAAAGGATATATGCAGTATGCCACAGAGAGCTGGCCCTCGCTGGCC	264
Db	53	CysLeuAspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAla	72
Qy	265	TCCATACCACTGCTGTGTGACAAATAAAAACCTAAGATCTGCTCCGAATTCATCTATGGC	324
Db	73	TyrPheLeuHisIleTrpIlyAspLysLysAspAsnThrCysSerMetPheValTyrGly	92
Qy	325	GGTGTCCAGGGGAACAATAACAACTTCCAACTGAAGCTATCTGTCTGGTCACCTGCAAA	384
Db	93	GlyCysGlnGlyAsnAspAsnAspPheGlnSerLysAlaAsnCysLeuAsnThrCysLys	112

RESULT 15
 US-10-058-993-120
 ; Sequence 120, Application US/10058993
 ; Publication No. US20030225009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: P2003P5
 ; CURRENT APPLICATION NUMBER: US/10/058,993
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: 09/852,659
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/852,797
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/853,161
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/265,583
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/152,060
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/04858
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-05
 ; PRIOR APPLICATION NUMBER: 60/050,934
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,100
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,357
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/040,710
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/040,762
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 120
 ; LENGTH: 117
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-058-993-120
 Alignment Scores:
 Pred. No.: 9,92e-33 Length: 117
 Score: 389.50 Matches: 65
 Percent Similarity: 77.00% Conservative: 12
 Best Local Similarity: 65.00% Mismatches: 22
 Query Match: 50.98% Indels: 1
 DB: 15 Gaps: 1
 US-10-807-204-11 (1-396) x US-10-058-993-120 (1-117)
 QY 85 CTGTGGCAAGCGGTGTCACAAATCAAGTGGATGCGAATGGAAGAAATAGACCAAGTCT 144
 Db 14 LeuGlyArg---CysProLysIleAe:ggluGluCysGluPheGlnGluArgAspValCys 32
 QY 145 ACCAAACCCAGAGATTGCCCCAGAAAACATCAAGTGTGGCCGTTACAGCCGTGGAAGAAA 204
 Db 33 ThrLysAspArgGlnCysGlnAspAsnLysLysCysValPheSerCysGlyLysLys 52
 QY 205 TGTTTAGACTTCAAGAGATATATGCAAGTATGCCACAGGAGCTGCCCTCGTGGCC 264
 Db 53 CysLeuAspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAla 72
 QY 265 TCCATACCACTGGTGGTACATAAATAAATACTAAGATCTGCTCCGAATTCATCTATGCG 324
 Db 73 TyrPheLeuHisTrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGly 92


```

US-10-807-204-5
; Sequence 5, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015, US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-5
Alignment Scores:
Pred. No.: 2e-17 Length: 43
Score: 246.00 Matches: 42
Percent Similarity: 97.6% Conservative: 0
Best Local Similarity: 97.6% Mismatches: 1
Query Match: 32.20% Indels: 0
Gaps: 16
DB:

US-10-807-204-11 (1-396) x US-10-807-204-5 (1-43)
QY 94 CGGTGTCACCAATCAAGTGAAGTGGAGAAATAGACAGTGTACCAACCC 153
Db 1 ProCysProLysLeuValGluCysGluValGluGluLeuAspGlnCysThrLysPro 20
QY 154 AGAGATTGCCAGAAACATGAAGTGTGCGCGTTTCAGCGGTGGAAAGAAATGTTAGAC 213
Db 21 ArgAspCysProGluAsnMetLysCysCysProPheSerCysGlyIleValCysLeuAsp 40
QY 214 TTCAGAAAG 222
Db 41 PheArgLys 43
RESULT 20
US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5
Alignment Scores:
Pred. No.: 2.5e-16 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
Gaps: 0

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DB: 16 Gaps: 0
US-10-807-204-11 (1-396) x US-10-361-997-5 (1-58)
QY 217 AGAAGGATATATGCAGTATGCCACAGAGAGGCTGCCCTCGCTCCATACCACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHis 20
QY 277 TGGTGGTACAATAAAAAAATAAGATCTGCTCCGAAATTCATCTATGGCGGTGCCAGGG 336
Db 21 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 40
QY 337 AACATAACAACCTCCAAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56
RESULT 21
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-PEGYLATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21
Alignment Scores:
Pred. No.: 2.5e-16 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
Gaps: 0
DB:

US-10-807-204-11 (1-396) x US-10-931-153-21 (1-58)
QY 217 AGAAGGATATATGCAGTATGCCACAGAGAGGCTGCCCTCGCTCCATACCACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHis 20
QY 277 TGGTGGTACAATAAAAAAATAAGATCTGCTCCGAAATTCATCTATGGCGGTGCCAGGG 336
Db 21 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 40
QY 337 AACATAACAACCTCCAAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56
RESULT 22
US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30

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; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-118
Alignment Scores:
Pred. No.: 1.62e-14 Length: 51
Score: 219.00 Matches: 35
Percent Similarity: 78.43% Conservative: 5
Best Local Similarity: 68.63% Mismatches: 11
Query Match: 28.66% Indels: 0
DB: 15 Gaps: 0
US-10-807-204-11 (1-396) x US-10-058-993-118 (1-51)
Qy 229 TGCAGTATGCCACAGGAGGCTGGCCCTGCTGGCTCCATACCACACTGGTGGTACAAT 288
Db 1 CysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTyrAsp 20
Qy 289 AAAAAAATAAGATCTGCTCGGAATTCATCTATCGCGGTGCCAGGGGAACAATAACAAC 348
Db 21 LysLysAspAenThrCysSerMetPheValTyrGlyCysGlnGlyAsnAsnAsn 40
Qy 349 TTCCAACTGAAGTATCTGCTGCTGCTACCTGC 381
Db 41 PheGlnSerLysAlaAsnCysLeuAsnThrCys 51
RESULT 23
US-10-825-692-48
; Sequence 48, Application US/10825692
; Publication No. US2005004223A1
; GENERAL INFORMATION:
; APPLICANT: Hotez, Peter
; APPLICANT: Ashcom, James
; APPLICANT: Bdamchian, Mahnaz
; APPLICANT: Zhan, Bin
; APPLICANT: Wang, Yan
; APPLICANT: Hawdon, John
; APPLICANT: Loukas, Alexander
; APPLICANT: Williamson, Angela
; APPLICANT: Jones, Brian
; APPLICANT: Bethony, Jeffrey
; APPLICANT: Goud, Gaddam
; APPLICANT: Botazzi, Maria E.
; APPLICANT: Mendez, Subana
; TITLE OF INVENTION: Hookworm Vaccine
; FILE REFERENCE: 03740007aa
; CURRENT APPLICATION NUMBER: US/10/825,692
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/329,533
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 60/332,007
; PRIOR FILING DATE: 2001-11-23
; PRIOR APPLICATION NUMBER: US 60/375,404
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: PCT US02/33106
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Ancylostoma caninum
US-10-825-692-48
Alignment Scores:
Pred. No.: 3.83e-11 Length: 759
Score: 189.50 Matches: 42
Percent Similarity: 40.71% Conservative: 15
Best Local Similarity: 30.00% Mismatches: 30
Query Match: 24.80% Indels: 53
DB: 17 Gaps: 4
US-10-807-204-11 (1-396) x US-10-825-692-48 (1-759)
Qy 127 GAAGAAATAGACCAGTGTACAAA-----CCAGAGATTGCCAGAA 168
Db 496 GluSerMetGluGluCysThrArgThrCysLysLysAlaValProGluProGluProGlu 515
Qy 169 AACATGAAGTGTGC---CCGTCAGCCGTGGA----- 198
Db 516 LysGluThrCysSerGlnProLleGluAlaGlyProCysLysAlaMetValArgPhe 535
Qy 199 -----AAGAAATGTTAGACTTC----- 216
Db 536 AlaTyrAspAsnAlaLysGluLysCysValGluPhePheTyrGlyCysLysGlyAsn 555
Qy 216 ----- 216
Db 556 LysAsnAsnPheGluThrMetGluAspCysThrPheThrCysGluGlnArgLeuAlaLys 575
Qy 217 -----AGAAAGATATATCCAGTATGCCACAGAGAGCTGGCCCTGCGCTCC 267
Db 576 ProGluLeuGluLysAspValCysSerGlnProIleThrAlaGlyProCysArgAlaSer 595
Qy 268 ATACCACACTGGGTGACATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGT 327
Db 596 IleProArgTyrGlyTyrAspSerLysLysArgLysCysValLysPheThrTyrGlyGly 615
Qy 328 TGCAGGGGAACAATAACAACTTCCAAACTGAAGACTATCTGCTGGTCCACCTGCAAAAAA 387
Db 616 CysLysGlyAsnGlyAsnArgPheProThrLysAsnGluCysGluLysThrCysLysArg 635
RESULT 24
US-09-896-095-160
; Sequence 160, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEV, Arthur C.
```


; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Caretta sp.
US-09-896-095-160

Alignment Scores:
Pred. No.: 9.55e-11 Length: 64
Score: 184.00 Matches: 27
Percent Similarity: 73.21% Conservative: 14
Best Local Similarity: 48.21% Mismatches: 15
Query Match: 24.08% Indels: 0
DB: 10 Gaps: 0

US-10-807-204-11 (1-396) x US-09-896-095-160 (1-64)

QY 217 AGAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTGCCCTCCATACACAC 276
Db 4 LysArgAspIleCysArgLeuProGluGlnGlyProCysGlyArgLeuProArg 23
QY 277 TGGTGTACAAATAAAAAAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 24 TyrPheTyrAsnProAlaSerArgMetCysGluSerPheIleTyrGlyGlyCysGly 43
QY 337 AACATAACAATTCCTCAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 44 AsnLysAsnAsnPhelYsThrLysAlaGluCysValArgAlaCysArg 59

RESULT 25
US-10-038-722-103
; Sequence 103, Application US/10038722
; Publication No. US2003017591A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS mHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Caretta sp.
US-10-038-722-103

Alignment Scores:

Pred. No.: 9.55e-11 Length: 64
Score: 184.00 Matches: 27
Percent Similarity: 73.21% Conservative: 14
Best Local Similarity: 48.21% Mismatches: 15
Query Match: 24.08% Indels: 0
DB: 10 Gaps: 0

US-10-807-204-11 (1-396) x US-10-038-722-103 (1-64)

QY 217 AGAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTGCCCTCCATACACAC 276
Db 4 LysArgAspIleCysArgLeuProGluGlnGlyProCysGlyArgLeuProArg 23
QY 277 TGGTGTACAAATAAAAAAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 24 TyrPheTyrAsnProAlaSerArgMetCysGluSerPheIleTyrGlyGlyCysGly 43
QY 337 AACATAACAATTCCTCAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 44 AsnLysAsnAsnPhelYsThrLysAlaGluCysValArgAlaCysArg 59

RESULT 26
US-10-115-134-17
; Sequence 17, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Caretta sp.
US-10-115-134-17

Alignment Scores:
Pred. No.: 9.55e-11 Length: 64
Score: 184.00 Matches: 27
Percent Similarity: 73.21% Conservative: 14
Best Local Similarity: 48.21% Mismatches: 15
Query Match: 24.08% Indels: 0
DB: 15 Gaps: 0

US-10-807-204-11 (1-396) x US-10-115-134-17 (1-64)

QY 217 AGAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTGCCCTCCATACACAC 276
Db 4 LysArgAspIleCysArgLeuProGluGlnGlyProCysGlyArgLeuProArg 23
QY 277 TGGTGTACAAATAAAAAAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 24 TyrPheTyrAsnProAlaSerArgMetCysGluSerPheIleTyrGlyGlyCysGly 43
QY 337 AACATAACAATTCCTCAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 44 AsnLysAsnAsnPhelYsThrLysAlaGluCysValArgAlaCysArg 59

RESULT 27
US-10-369-736-3
; Sequence 3, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:


```
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-736-3

Alignment Scores:
Pred. No.: 3.36e-10 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 14 Gaps: 3

US-10-807-204-11 (1-396) x US-10-369-736-49 (1-571)
QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 322 GluCysLeuLysProProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
QY 175 -----AAGTGTGCCGTTCCAGCGTGGAAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn 361
QY 202 -----AAATGTTTACACTTCAGAAAGGATATATGC 231
Db 362 HisPheGluThrTyrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGGAGGCTGCCCTGCCTCCATACACACTGGTGATACAATAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrValProArgTrpAlaTyrAsnSer 401
QY 292 AAAACTAAGATCTCTCCGAATTCATCTATGGCGGTTGCCAGGGGAAACAATAA 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyrGlyCysGluGlyAsnGlyAsnAsnPhe 421
QY 352 CAAACTGAAGCTATCTCTGTGTCACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431

RESULT 29
US-10-369-738-3
; Sequence 3, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-12-20
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-738-3

Alignment Scores:
Pred. No.: 3.36e-10 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 14 Gaps: 3

US-10-807-204-11 (1-396) x US-10-369-738-3 (1-571)
QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 322 GluCysLeuLysProProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
QY 175 -----AAGTGTGCCGTTCCAGCGTGGAAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn 361
QY 202 -----AAATGTTTACACTTCAGAAAGGATATATGC 231
Db 362 HisPheGluThrTyrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGGAGGCTGCCCTGCCTCCATACACACTGGTGATACAATAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrValProArgTrpAlaTyrAsnSer 401
QY 292 AAAACTAAGATCTCTCCGAATTCATCTATGGCGGTTGCCAGGGGAAACAATAA 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyrGlyCysGluGlyAsnGlyAsnAsnPhe 421
QY 352 CAAACTGAAGCTATCTCTGTGTCACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431

RESULT 28
US-10-369-736-49
; Sequence 49, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-12-20
; PRIOR FILING DATE: 2002-12-20
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
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QY 175 -----AAGTGTGGCCGTTACGCCGTGGAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn 361
QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
Db 362 HisPheGluThrTyxGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGAGGCTGGCCCTGCCTCCATACACACACTGGTGGTACAAATAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyxValProArgTrpAlaTyxAsnSer 401
QY 292 AAACTAAGATCTGCTCCGAATTATCATATGCGGTGCCAGGGGAAACAATAACAATTC 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyxGlyGlyCysGluGlyAsnGlyAsnAsnPhe 421
QY 352 CAAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431
RESULT 30
US-10-369-738-49
; Sequence 49, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-738-49
Alignment Scores:
Pred. No.: 3 36e-10 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 14 Gaps: 3
US-10-807-204-11 (1-396) x US-10-369-738-49 (1-571)
QY 139 CAGTGTACCAACCC-----AGAGATTGCCCAAGAAACATG----- 174
Db 322 GluCysLeuLysProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
QY 175 -----AAGTGTGGCCGTTACGCCGTGGAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn 361
QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
Db 362 HisPheGluThrTyxGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGAGGCTGGCCCTGCCTCCATACACACACTGGTGGTACAAATAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyxValProArgTrpAlaTyxAsnSer 401
QY 292 AAACTAAGATCTGCTCCGAATTATCATATGCGGTGCCAGGGGAAACAATAACAATTC 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyxGlyGlyCysGluGlyAsnGlyAsnAsnPhe 421
QY 352 CAAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431
RESULT 32
US-11-028-058-49
; Sequence 49, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058

QY 352 CAAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431
RESULT 31
US-11-028-058-3
; Sequence 3, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-3
Alignment Scores:
Pred. No.: 3 36e-10 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 19 Gaps: 3
US-10-807-204-11 (1-396) x US-11-028-058-3 (1-571)
QY 139 CAGTGTACCAACCC-----AGAGATTGCCCAAGAAACATG----- 174
Db 322 GluCysLeuLysProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
QY 175 -----AAGTGTGGCCGTTACGCCGTGGAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn 361
QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
Db 362 HisPheGluThrTyxGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGAGGCTGGCCCTGCCTCCATACACACACTGGTGGTACAAATAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyxValProArgTrpAlaTyxAsnSer 401
QY 292 AAACTAAGATCTGCTCCGAATTATCATATGCGGTGCCAGGGGAAACAATAACAATTC 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyxGlyGlyCysGluGlyAsnGlyAsnAsnPhe 421
QY 352 CAAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431
RESULT 32
US-11-028-058-49
; Sequence 49, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058


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; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-49

Alignment Scores:
Pred. No.:      3,36e-10      Length:      571
Score:          180.50        Matches:     35
Percent Similarity: 42.73%    Conservative: 12
Best Local Similarity: 31.82% Mismatches:   34
Query Match:    23.63%       Indels:      29
DB:              19         Gaps:       3

US-10-807-204-11 (1-396) x US-11-028-058-49 (1-571)
Qy      139 CAGTGTACCAAAACC-----AGAGATTGCCCAGAAAACATG----- 174
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      322 GluCysLeuLysProAspSerGluAapCysGlyGluGlunThrArgTrpHisPhe 341
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      175 -----AAGTGTCCTCCCGTGCAGCCGTGGGAAG----- 201
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      342 AspAlaGlnAlaAenAenCysLeuThrPheThrPheGlyHisCysHisAenLeuAen 361
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      362 HisPheGluThrTyrgluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      232 AGTATGCCACGAGGCGTGCCTCCCTCCATACCACACTGGTGGTACAAATAA 291
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyValProArgTrpAlaTyrsnSer 401
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      292 AAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGGCAGGGGAACAATAAACATTC 351
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      402 GlnThrGlyLeuCysGlnSerPheValTyrglyGlyCysgluGlyAenGlyAenAenPhe 421
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      352 CAAACTGAAGCTATCTGCTGGTCACTGC 381
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      422 GluSerArgGluAlaCysGluSerCys 431
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 33
US-10-807-204-7
; Sequence 7, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-10

Alignment Scores:
Pred. No.:      2,27e-10      Length:      33
Score:          180.00        Matches:     32
Percent Similarity: 96.97%    Conservative: 0
Best Local Similarity: 96.97% Mismatches:   1
Query Match:    23.56%       Indels:      0
DB:              16         Gaps:       0

US-10-807-204-11 (1-396) x US-10-807-204-10 (1-33)
Qy      295 ACTAAGATCTGCTCCGAATTCATCTATGGCGGTGGCAGGGGAACAATAAACATTCCAA 354
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 ThrLysIleCysSerGluPheIleTyrglyGlySerGlnGlyAenAenAenAenPheGln 20
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      355 ACTGAAGCTATCTGCTGGTCACTGCACCTGCAAAAAATACCAT 393
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      21 ThrGluAlaIleCysLeuValThrCysLysLysTyrrHis 33
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 34
US-10-807-204-10
; Sequence 10, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-10

Alignment Scores:
Pred. No.:      2,27e-10      Length:      33
Score:          180.00        Matches:     32
Percent Similarity: 96.97%    Conservative: 0
Best Local Similarity: 96.97% Mismatches:   1
Query Match:    23.56%       Indels:      0
DB:              16         Gaps:       0

US-10-807-204-11 (1-396) x US-10-807-204-7 (1-33)
Qy      295 ACTAAGATCTGCTCCGAATTCATCTATGGCGGTGGCAGGGGAACAATAAACATTCCAA 354
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 ThrLysIleCysSerGluPheIleTyrglyGlySerGlnGlyAenAenAenAenPheGln 20
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      355 ACTGAAGCTATCTGCTGGTCACTGCACCTGCAAAAAATACCAT 393
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      21 ThrGluAlaIleCysLeuValThrCysLysLysTyrrHis 33
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 35
US-10-038-722-5
; Sequence 5, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEV, Arthur C.
; APPLICANT: CUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.

```



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; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5

Alignment Scores:
Pred. No.: 5 28e-10 Length: 58
Score: 177.00 Matches: 31
Percent Similarity: 65.43% Conservative: 5
Best Local Similarity: 56.36% Mismatches: 19
Query Match: 23.17% Indels: 0
DB: 14 Gaps: 0

US-10-807-204-11 (1-396) x US-10-038-722-5 (1-58)
QY 217 AGAAGGATATATGAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACACAC 276
Db 1 ArgProaspPheCysLeuLeuProAlaGluThrGlyProCysArgAlaMetileProArg 20
QY 277 TGGTGTACAAATAAAAACTAAGATCTCTCCGATTCATCTATGCGGTTGCCAGGG 336
Db 21 PheTyrTyrAsnAlaLysSerGlyLysCysGluProPheIleTyrGlyGlyCysGlyGly 40
QY 337 ACAATAACAATTCACAACTGAAGCTATCTGTGTCACCTGC 381
Db 41 AsnAlaAsnAsnPheLysThrGluGluGluCysArgArgThrCys 55

RESULT 36
US-09-896-095-147
; Sequence 147, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER=7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 147
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-896-095-147
```

```

Alignment Scores:
Pred. No.: 8 88e-10 Length: 67
Score: 175.00 Matches: 27
Percent Similarity: 68.52% Conservative: 10
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 22.91% Indels: 0
DB: 10 Gaps: 0

US-10-807-204-11 (1-396) x US-09-896-095-147 (1-67)
QY 223 GATATATGAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACACACTGGTGG 282
Db 6 AspLeuCysGlnLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 25
QY 283 TACAATAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAACAAT 342
Db 26 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 45
QY 343 AACAACTTCCAACTGAAGCTATCTGTGTCACCTGCAAA 384
Db 46 AsnAsnPheGluThrThrGluMetCysLeuArgIleCysGlu 59

RESULT 37
US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Alignment Scores:
Pred. No.: 8 88e-10 Length: 67
Score: 175.00 Matches: 27
Percent Similarity: 68.52% Conservative: 10
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 22.91% Indels: 0
DB: 14 Gaps: 0

US-10-807-204-11 (1-396) x US-10-038-722-90 (1-67)
QY 223 GATATATGAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACACACTGGTGG 282
Db 6 AspLeuCysGlnLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 25
QY 283 TACAATAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAACAAT 342
Db 26 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 45
QY 343 AACAACTTCCAACTGAAGCTATCTGTGTCACCTGCAAA 384
Db 46 AsnAsnPheGluThrThrGluMetCysLeuArgIleCysGlu 59
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; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 88
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-115-134-88

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 14 Gaps: 0

US-10-807-204-11 (1-396) x US-10-038-722-19 (1-58)
QY 217 AGAAAGGATATATGCGAGTATGCCACAGGAGGCTGCGCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACAAATAAATAAAGTATCTCTCGAATTCATCTATGCGCGGTGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAATCTCCAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 41
US-10-038-722-19
; Sequence 19, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-038-722-19

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 14 Gaps: 0

US-10-807-204-11 (1-396) x US-10-038-722-19 (1-58)
QY 217 AGAAAGGATATATGCGAGTATGCCACAGGAGGCTGCGCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACAAATAAATAAAGTATCTCTCGAATTCATCTATGCGCGGTGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAATCTCCAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 42
US-10-115-134-88
; Sequence 88, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
```

```

; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 88
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-115-134-88

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0

US-10-807-204-11 (1-396) x US-10-115-134-88 (1-58)
QY 217 AGAAAGGATATATGCGAGTATGCCACAGGAGGCTGCGCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACAAATAAATAAAGTATCTCTCGAATTCATCTATGCGCGGTGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGlnThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAATCTCCAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 43
US-10-115-134-89
; Sequence 89, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 89
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-115-134-89

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0

US-10-807-204-11 (1-396) x US-10-115-134-89 (1-58)
```



```
Qy 217 AGAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTGCCTCCATACCAC 276
Db 1 ArgProaspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGTATCTGCTCCGAATTCATCTATGGCGGTGCCAGGG 336
Db 21 TyrPheTyrAsnGlyAlaSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACCAATAACAACCTCCAACTGAAGCTATCTGCTGGTCACCTGCATA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 44
US-10-115-134-90
; Sequence 90, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-115-134-90
Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0
US-10-807-204-11 (1-396) x US-10-115-134-90 (1-58)
Qy 217 AGAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTGCCTCCATACCAC 276
Db 1 ArgProaspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGTATCTGCTCCGAATTCATCTATGGCGGTGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACCAATAACAACCTCCAACTGAAGCTATCTGCTGGTCACCTGCATA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 45
US-10-456-986A-42
; Sequence 42, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Lev, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A Sequence
US-10-456-986A-42
Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0
US-10-807-204-11 (1-396) x US-10-456-986A-43 (1-58)
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```
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITI-E7-141 Sequence
US-10-456-986A-42
Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0
US-10-807-204-11 (1-396) x US-10-456-986A-42 (1-58)
Qy 217 AGAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTGCCTCCATACCAC 276
Db 1 ArgProaspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGTATCTGCTCCGAATTCATCTATGGCGGTGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACCAATAACAACCTCCAACTGAAGCTATCTGCTGGTCACCTGCATA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 46
US-10-456-986A-43
; Sequence 43, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Lev, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A Sequence
US-10-456-986A-43
Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0
US-10-807-204-11 (1-396) x US-10-456-986A-43 (1-58)
```


; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-42

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: Gaps: 0

US-10-807-204-11 (1-396) x US-10-953-902A-42 (1-58)

QY 217 AGAAGGATATATGCAGTATGCCACAGGAGGCTGCCCTGCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACATAAAAAAAGCTATCTGCTCGAATTCATCTATGGCGGTGCCAGGGG 336
Db 21 TyrPheTyraSnGlyThrSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly 40
QY 337 AACATAACAACCTCCAAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 49
US-10-953-902A-43
; Sequence 43, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-43

QY 217 AGAAGGATATATGCAGTATGCCACAGGAGGCTGCCCTGCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACATAAAAAAAGCTATCTGCTCGAATTCATCTATGGCGGTGCCAGGGG 336
Db 21 TyrPheTyraSnGlyThrSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly 40
QY 337 AACATAACAACCTCCAAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 47
US-10-456-986A-44
; Sequence 44, Application US/10456986A
; Publication No. US2004003893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE Sequence
US-10-456-986A-44

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: Gaps: 0

US-10-807-204-11 (1-396) x US-10-456-986A-44 (1-58)

QY 217 AGAAGGATATATGCAGTATGCCACAGGAGGCTGCCCTGCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACATAAAAAAAGCTATCTGCTCGAATTCATCTATGGCGGTGCCAGGGG 336
Db 21 TyrPheTyraSnGlyThrSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly 40
QY 337 AACATAACAACCTCCAAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 48
US-10-953-902A-42
; Sequence 42, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2005, 16:50:52 ; Search time 22 Seconds
(without alignments)
3463.803 Million cell updates/sec

Title: US-10-807-204-11
Perfect score: 764
Sequence: 1 atgggactctcaggactctt.....cctgcaaaaaataaccattaa 396

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Command line parameters: -DEV=xlh

-MODE=frame+n2p,model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10807204/runat_20092005_162900_29238/app_query.fasta_1.583
-DB=PIR_79 -QFMT=fastan -SUFFIX=std.rpr -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=51 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=50
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10807204 @C@N 1 1 25 @runat_20092005_162900_29238 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	24.3	110	1 TITTOR	basic proteinase i
2	185.5	24.3	1522	2 H88380	protein T22F7.3 (i
3	173.5	22.7	1599	2 T16210	hypothetical prote
4	172	22.5	67	1 TIBOC	trypsin inhibitor,
5	171	22.4	1416	2 E88550	protein ZC84.1 (im
6	171	22.4	2844	2 S28291	hypothetical prote
7	168	22.0	1743	2 T26859	hypothetical prote
8	167.5	21.9	922	2 T23573	hypothetical prote
9	167.5	21.9	1474	2 D88550	protein ZC84.6 (im
10	165.5	21.7	337	1 TIBGBI	alpha-1-microglobu
11	161.5	21.1	747	2 JH0773	Alzheimer's diseas
12	161	21.1	62	2 A44180	taicatoxin serine
13	161	21.1	751	2 A49974	beta-amyloid precu
14	160	20.9	57	2 A59204	basic proteinase i

15	160	20.9	252	2	JG0185	hepatocyte growth
16	157	20.5	58	1	TIHABK	isoinhibitor K (BP
17	157	20.5	111	2	S41082	amyloid precursor
18	157	20.5	763	2	A49321	amyloid beta (A4)
19	157	20.5	765	2	S42880	amyloid precursor-
20	154.5	20.2	300	2	S12143	lipoprotein-associ
21	154	20.2	484	4	A32761	hypothetical Alzhe
22	154	20.2	770	1	QRH044	Alzheimer's diseas
23	153	20.0	62	2	S19327	venom basic protei
24	153	20.0	299	2	I46937	tissue factor path
25	153	20.0	352	1	TI0801	alpha-1-microglobu
26	152	19.9	62	2	S07451	proteinase inhibit
27	152	19.9	76	2	S06678	Alzheimer's diseas
28	152	19.9	76	2	S03607	Alzheimer's diseas
29	152	19.9	352	1	HCHU	alpha-1-microglobu
30	151.5	19.8	372	2	JC2556	venom basic protei
31	151	19.8	65	1	TIIVVC	Alzheimer's diseas
32	151	19.8	100	2	A32282	hypothetical prote
33	151	19.8	2150	2	T32497	hypothetical prote
34	150.5	19.7	1043	2	TI9734	hypothetical prote
35	149.5	19.6	62	2	S01802	chymotrypsin inhib
36	149	19.5	57	1	TI0FBP	proteinase inhibit
37	149	19.5	76	2	S04855	Alzheimer's diseas
38	149	19.5	123	2	A29652	inter-alpha-trypsi
39	148.5	19.4	62	2	S01803	chymotrypsin inhib
40	148.5	19.4	249	2	T32060	hypothetical prote
41	147.5	19.3	349	2	S21089	alpha-1-microglobu
42	147	19.2	125	1	TI0HBI	alpha-1-microglobu
43	146	19.1	100	1	TI0B	basic proteinase i
44	146	19.1	1558	2	C89114	protein C37C3.6a (
45	146	19.1	2167	2	T34395	hypothetical prote
46	145	19.0	122	1	A55115	uterine plasmin/tr
47	145	19.0	805	2	T34212	hypothetical prote
48	144	18.8	57	2	B59399	short epsilon-dend
49	144	18.8	59	1	TI0EPD	venom basic protei
50	144	18.8	59	2	S00371	isoaptrotinin G1 -

ALIGNMENTS

RESULT 1

TITTOR

Basic proteinase inhibitor - loggerhead

C:Species: Carretta caretta (loggerhead)

C>Date: 31-May-1979 #sequence_revision 23-Oct-1991 #text_change 09-Jul-2004

C:Accession: A01224

R:Kato, I.; Tominaga, N.

Fed. Proc. 38, 832, 1979

A:Title: Trypsin--subtilisin inhibitor from red sea turtle eggwhite consists of two tand

A:Reference number: A01224

A:Accession: A01224

A:Molecule type: protein

A:Residues: 1-110 <KAT>

A:Cross-references: UNIPROT:P00993

C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inhi

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:63-105/Domain: antileukoproteinase repeat homology <ALP>

F:1/Modified site: pyroglutamic acid (Gln) #status experimental

F:8-58,17-41,33-54,67-93,76-97,80-92,86-101/disulfide bonds: #status predicted

F:18/Inhibitory site: Lys (trypsin) #status predicted

Alignment Scores:

Pred. No.:	3,748-10	Length:	110
Score:	186.00	Matches:	28
Percent Similarity:	73.21%	Conservative:	13
Best Local Similarity:	50.00%	Mismatches:	15
Query Match:	24.35%	Indels:	0
DB:	1	Gaps:	0

US-10-807-204-11 (1-396) x TITTOR (1-110)

F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:8-58,17-41,33-54/Diulfide bonds: #status experimental
F:18/Inhibitory site: Lys (trypsin) #status experimental
F:27/Binding site: carbohydrate (Aen) (covalent) #status experimental

Alignment Scores:
Pred. No.: 9.22e-09 Length: 67
Score: 172.00 Matches: 26
Percent Similarity: 68.52% Conservatve: 11
Best Local Similarity: 48.15% Mismatches: 17
Query Match: 22.51% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x TIBOC (1-67)

QY 223 GATATGTCAGTATCCAGAGGCTGGCCCTGCTGCCTCCATACCACCTGGTG 282
DB 6 AspLeuGluLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 25
QY 283 TACAATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGTTGCCAGGGGAACAAT 342
DB 26 TyrAenSerThrSerAenAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAenAen 45
QY 343 AACAACTCCAACTGAAGTATCTGTCTGTGTCACCTGCMAA 384
DB 46 ***AenPheGluThrThrGluMetCysLeuArgIleCysGlu 59

RESULT 5
E88550
protein ZC84.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E88550
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: E88550
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1416 <STO>
A:Cross-references: UNIPROT:003610; GB:chr III; PIDN:CAA79569.1; PID:g3881446; GSPDB:GND
A:Note: similar to Serine protease inhibitor, Kunitz type
C:Genetics:
A:Gene: ZC84.1
A:Map position: 3

Alignment Scores:
Pred. No.: 9.57e-09 Length: 1416
Score: 171.00 Matches: 35
Percent Similarity: 46.30% Conservatve: 15
Best Local Similarity: 32.41% Mismatches: 40
Query Match: 22.38% Indels: 18
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x E88550 (1-1416)

QY 109 AAAGTGAATGCGAAGTG----- 126
DB 380 LysHisGluCysGluMetTyrCysAlaArgLeuGlnCysGluArgGlySerProLeuArg 399
QY 127 -----GAAGAATACACCGTGTACCAACCCAGAGATGCCAGAAAACATGAAGTGT 180
DB 400 IleGlyGluGluAlaGlnArgCysGlnAenAlaGlnCysProSerSerHisGlu--- 418
QY 181 TGCCCGTTCCAGCGTGAAGAAATGTTTAGACTTCAGAAAGGATATATGCAGTATGCCA 240
DB 419 CysLysAlaAaspGlnGly---ValCysCysProArgLysGlnThrIleCysAlaGlnPro 437
QY 241 CAGGAGCTGGCCCTGCCTCCATACCACACTGGTGTACATAAAAACTAAG 300

Db 438 LeuArgIleGlyAaspCysThrGluAenValLysArgTyrTrrTyrAenAlaArgThrArg 457
QY 301 ATCTGCTCCGAATTCATCTATGGCGTTGCCAGGGGAACAATAACAATTCCTCAAACTGAA 360
Db 458 GlnCysGlnMetPheGluTyrThrGlyCysGlnGlyAenAaspAenAenPheAaspSerIle 477
QY 361 GCTATCTGTCTGGTCACCTGCMAA 384
Db 478 MetAaspCysGlnAenPheCysLys 485

RESULT 6
S28291
hypotheical protein ZC84.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S28291
R:Thomas, K.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28285
A:Accession: S28291
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2844 <THO>
A:Cross-references: UNIPROT:003610; EMBL:Z19157
C:Genetics:
A:Introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 1244/3; 2555/1; 2720/1; 2739/3; 2819/1
F:220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>
F:343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F:442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>
F:546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPI4>
F:654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI5>
F:1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BPI6>
F:1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BPI7>
F:1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BPI8>
F:1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>
F:2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BPI0>

Alignment Scores:
Pred. No.: 9.17e-09 Length: 2844
Score: 171.00 Matches: 35
Percent Similarity: 46.30% Conservatve: 15
Best Local Similarity: 32.41% Mismatches: 40
Query Match: 22.38% Indels: 18
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x S28291 (1-2844)

QY 109 AAAGTGAATGCGAAGTG----- 126
DB 388 LysHisGluCysGluMetTyrCysAlaArgLeuGlnCysGluArgGlySerProLeuArg 407
QY 127 -----GAAGAATACACCGTGTACCAACCCAGAGATGCCAGAAAACATGAAGTGT 180
DB 408 IleGlyGluGluAlaGlnArgCysGlnAenAlaGlnCysProSerSerHisGlu--- 426
QY 181 TGCCCGTTCCAGCGTGAAGAAATGTTTAGACTTCAGAAAGGATATATGCAGTATGCCA 240
DB 427 CysLysAlaAaspGlnGly---ValCysCysProArgLysGlnThrIleCysAlaGlnPro 445
QY 241 CAGGAGCTGGCCCTGCCTCCATACCACACTGGTGTACATAAAAACTAAG 300
DB 446 LeuArgIleGlyAaspCysThrGluAenValLysArgTyrTrrTyrAenAlaArgThrArg 465
QY 301 ATCTGCTCCGAATTCATCTATGGCGTTGCCAGGGGAACAATAACAATTCCTCAAACTGAA 360
DB 466 GlnCysGlnMetPheGluTyrThrGlyCysGlnGlyAenAaspAenAenPheAaspSerIle 485
QY 361 GCTATCTGTCTGGTCACCTGCMAA 384
DB 486 MetAaspCysGlnAenPheCysLys 493

RESULT 7


```

||||| ||||| ||||| ||||| |||||
369 ProPheThrTyrLeuGly-----AlaGlyGlyAsnTyrAsnAsnPheLeuSer--- 384
QY 94 CCGTGTCCTCCAAATCAAGTGAATGCGAAGT----- 126
Db 385 -----ArgilleAspCysGluLeuTyrCysAlaArgLeuGlnCysAspArg 399
QY 127 -----GAGAAATAGACAGGTGTACCAAAACCCAGAGATTGCCCA 165
Db 400 GlyAsnProLeuArgIleGlyAspValThrGlnSerCysAlaSerAsnAsnAspCysPro 419
QY 166 GAAACATGAAG-----TGTTCCCGCTTCAGCCGCTGGGAAAGAAA 204
Db 420 SerSerHisGluCysLeuMetAspGlnAlaValCysCysPro----- 433
QY 205 TGTTAGACTTCAGAAAGGATATGCGAGTATGCCACAGGAGGCTGGCCCTGCTGCC 264
Db 434 -----ArgMetGlnThrIleCysThrGlnProLeuArgValGlyAsnCysAspArg 450
QY 265 TCCATACCACACTGGTGTACATAAAAAAACTAAGATCTGCTCGAATTTCATCTATGCC 324
Db 451 SerValArgArgTyrTrpTyrSerAlaAlaThrArgGluCysGlnSerPheGluTyrThr 470
QY 325 GGTTCGCCAGGGAACAATAACAACTTCCAACTGAAGCTATCTGTCTGGTCACTGCAAA 384
Db 471 GlyCysGlnGlyAsnAsnAsnPhedGluThrLeuValAspCysGlnThrPheCysArg 490

RESULT 10
TIPGBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
N:Alternate names: bikunin; ITI; PI-14 (inhibitory fragment of ITI)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 30-Jun-1987 #sequence revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: S11066; S13493; A01208
R:Gebhard, W.; Schreiffmuller, T.; Vetr, H.; Wachter, E.; Hochstrasser, K.
FEBS Lett. 269, 32-36, 1990
A:Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microglobulin
A:Reference number: S11066; MUID:90353595; PMID:1696914
A:Accession: S11066
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-337 <GES>
A:Cross-references: UNIPROT:P04366; EMBL:X53685; NID:g1877; PIDN:CAA37725.1; PID:g1878
R:Tavakkol, A.
Biochim. Biophys. Acta 1088, 47-56, 1991
A:Title: Molecular cloning of porcine alpha (1)-microglobulin/HI-30 reveals developmental
A:Reference number: S13493; MUID:91113729; PMID:1703444
A:Accession: S13493
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 'W',3-48,'M',50-337 <TAV>
A:Cross-references: GB:X52087; NID:g1891; PIDN:CAA36306.1; PID:g1882
R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A:Reference number: A90685; MUID:85225367; PMID:2408637
A:Accession: A01208
A:Molecule type: protein
A:Residues: 212-258,'Q',260-269,'S',271-277,'Q',279-282,'A',284,'IR',287-292,'A',294-310
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis
first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
C:Comment: The amino acid at position P2 (228-Met) appears to determine the specificity
nd elastase; those with leucine interact strongly.
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:20-173/Domain: lipocalin homology <LIP>
F:216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:216-266,225-249,241-262,272-322,281-305,297-318/Disulfide bonds: #status predicted
F:226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:235/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:282/Inhibitory site: Arg (trypsin) #status predicted

```

Alignment Scores:

```

Pred. No.: 3,64e-08 Length: 337
Score: 165.50 Matches: 51
Percent Similarity: 37.50% Conservative: 15
Best Local Similarity: 28.98% Mismatches: 51
Query Match: 21.66% Indels: 59
DB: 7

```

US-10-807-204-11 (1-396) x TIPGBI (1-337)

```

QY 32 TACCATTCATCTTTTGGGGACA----- 55
Db 94 TyrHisLysSerLysTyrPheAsnIleThrMetGluSerTyrValValHisThrAsnTyrAsp 113
QY 56 -----TCCAGGAACCTGGGC-----ACCTCGAAGGCA 82
Db 114 GluTyrAlaIlePheLeuThrLysLysPheSerArgHisGlyProThrLeuThrAla 133
QY 83 TCCTTGGCAAGCCGTGTCCCAAAATCAAGTGGAAATGCGAAGTGGAGAAATAGACCAAGT 142
Db 134 LysLeuTyrGlyArgGluProGlnLeuArg--GluSerLeuLeuGluGluPheArgGluV 153
QY 143 GTACAAA-----CCCAGAGAT-----TGCCCAAAAACATGAAGT 178
Db 153 alAlaLeuGlyValGlyIleProGluAspSerIlePheThrMetProAspArgGlyGluC 173
QY 179 GTTCCCG-----TTCCAGCGCTGGAAAGAAATGTTTAA- 210
Db 173 ysValProGlyGluGlnGluProGluProThrLeuLeuSerArgAlaArgAlaValL 193
QY 211 -----GACTTCAGAAAG----- 222
Db 193 euProGlnGluGluGlySerGlyAlaGlyGlnProValAlaAspPheSerLysLysG 213
QY 223 --GATATATGAGTATGCCACAGAGGCTGCCCTGCTGCCCTCCATACCACTGGT 280
Db 213 luAspSerCysGlnLeuGlyTyrSerGlnGlyProCysLeuGlyMetIleLysArgTyrP 233
QY 281 GGTACATAAAATAAAGATCTCGCAATTCATCTATGGCGGTTCGCCAGGAACA 340
Db 233 heTyrAsnGlySerSerMetAlaCysGluThrPheHisTyrGlyCysMetGlyAsnG 253
QY 341 ATAACAATTCCTCAAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 253 lyAsnAsnPheValSerGluLysGluCysLeuGlnThrCysArg 267

```

RESULT 11

```

JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AAE24853.1; PID:g263151
C:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

```

Alignment Scores:

```

Pred. No.: 8,58e-08 Length: 747
Score: 161.50 Matches: 33
Percent Similarity: 44.76% Conservative: 14
Best Local Similarity: 31.43% Mismatches: 43
Query Match: 21.14% Indels: 15
DB: 2 Gaps: 1

```


US-10-807-204-11 (1-396) x JH0773 (1-747)

Qy 112 GTGGAATGCGAAGTGGGAAGTAATAGACACGAGTGTACCAAAACCAGAGATTGCCCAAGAAAC 171
|||
Db 233 ValGluValGluGluGluGluThrAspAspGluAspGlyAspGluAlaGluGlu 252
|||
Qy 172 ATGAAGTGTTCGCCCGTTCCAGCCGTGGA----- 198
|||
Db 253 GluProGluGluProTyrgluGluAlaThrGluArgThrThrSerIleAlaThrThr 272
|||
Qy 199 -----AAGAAATGTTTAGACTTCAGAAGGATATATCCAGTATGCCACAGAG 246
|||
Db 273 ThrThrThrThrGluSerValGluGluValValArgGluValCysSerGluGluAlaGlu 292
|||
Qy 247 GCTGCGCCCTGCTGCTCCATCCACACACTGGTGTACATAAAAAAATAAGATCTGC 306
|||
Db 293 ThrGlyProCysArgAlaMetIleSerArgTrpTyrgluAspValThrGluSerLysCys 312
|||
Qy 307 TCCGAATTCATCTATGCGGTTGCCAGGGGAACAATAACAACTTCCAACTGAAGCTATC 366
|||
Db 313 AlaglnPheIleTyrglyGlyCysGlyGlyAsnArgAsnAsnPheGluSerAspAspTyr 332
|||
Qy 367 TGCTGCTGTCACCTGC 381
|||
Db 333 CysMetalAlaValCys 337
|||

RESULT 12

A44180

taicatoxin serine proteinase inhibitor component - Australian taipan

C;Species: Oxyuranus scutellatus scutellatus (Australian taipan)

C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A44180

R;Possani, L.D.; Martin, B.M.; Yatani, A.; Mocheca-Morales, J.; Zamudio, F.Z.; Gurrola, G

Toxicol 30, 1343-1364, 1992

A;Title: Isolation and physiological characterization of taicatoxin, a complex toxin with

A;Reference number: A44180; MUID:93134601; PMID:1485334

A;Accession: A44180

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-62 <POS>

A;Cross-references: UNIPROT:Q7LZE4

A;Experimental source: subsp. scutellatus, venom

A;Note: sequence extracted from NCBI backbone (NCBIP:122482)

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C;Keywords: serine proteinase inhibitor

F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:

Pred. No.: 1.12e-07 Length: 62

Score: 161.00 Matches: 27

Percent Similarity: 63.64% Conservative: 8

Best Local Similarity: 49.09% Mismatches: 20

Query Match: 21.07% Indels: 0

DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x A44180 (1-62)

Qy 217 AGAAGATATATGCAATGTCAGTATGCCAGAGAGCTGGCCCTGCTCCATACCACAC 276
|||
Db 3 ArgProLysPheCysHisLeuProLysProGlyProCysArgAlaAlaIleProArg 22
|||
Qy 277 TGGTGGTACATAAAAAAATAAGATCTGCCGAATTCATCTATGCGGTTGCCAGGG 336
|||
Db 23 PheTyrgluAsnProHisSerLysGlnCysGluLysPheIleTyrglyGlyCysHisGly 42
|||
Qy 337 AACATAACAACTTCCAACTGAAGCTATCTGTGTCACCTGC 381
|||
Db 43 AsnAlaAsnLysPheLysThrProAspGluCysAsnTyrrThrCys 57
|||

RESULT 13

A49974

beta-amyloid precursor protein 2 homolog APLP2 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A49974

R;Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.

J. Biol. Chem. 269, 2637-2644, 1994

A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid i

A;Reference number: A49974; MUID:94132029; PMID:8300594

A;Accession: A49974

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-751 <SU>

A;Cross-references: UNIPROT:Q60709; GB:U15571; NID:G558467; PIDN:AAA50603.1; PID:G5584646

A;Note: sequence extracted from NCBI backbone (NCBIP:144636)

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:

Pred. No.: 9.61e-08 Length: 751

Score: 161.00 Matches: 40

Percent Similarity: 44.07% Conservative: 12

Best Local Similarity: 33.90% Mismatches: 48

Query Match: 21.07% Indels: 18

DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x A49974 (1-751)

Qy 52 GACATCCAGGAACCTGGGCACGCTGGAAGGCATCTTGGCAAGCGGTGTCCTCCAAATCAAA 111
|||
Db 255 AspGluGluGluGluAspGluGluGly----- 264
|||

Qy 112 GTGGAATGCGAAGTGGGAAGAAATAGACAGTGTACCAAAACC-----AGAGATTGC 162
|||
Db 265 ---GluGluValValGluAspArgAspTyrTyrrAspProPheLysGlyAspAspTyr 283
|||

Qy 163 CCAGAAACATGAAGTGTTCCTCCGTTCCAGCGTGA-----AAGAAATGTTTA 210
|||

Db 284 AsnGluGluAsnProThrGluProSerSerGluGlyThrIleSerAspLysGluIleVal 303
|||

Qy 211 GACTTCAGAAAGGATATATGCAATGTCAGAGAGCTGGCCCTGCTCCATCA 270
|||

Db 304 HisAspValLysAlaValCysSerGlnGluAlaMetThrGlyProCysArgAlaValMet 323
|||

Qy 271 CCACACTGGTGTACATAAAAAAATAAGATCTGCCGAATTCATCTATGCGGTTGC 330
|||

Db 324 ProArgTrpTyrrPheAspLeuSerLysGlyLysCysValArgPheIleTyrglyGlyCys 343
|||

Qy 331 CAGGGGACATAACAACTTCCAACTGAGACTATCTGTGCTCACCTGCACA 384
|||

Db 344 GlyGlyAsnArgAsnAsnPheGluSerGluAspTyrCysMetalAlaValCysLys 361
|||

RESULT 14

A59204

basic proteinase inhibitor - great pond snail

N;Alternate names: trypsin inhibitor

C;Species: Lymnaea stagnalis (great pond snail)

C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004

C;Accession: A59204

R;Nagle, G.

submitted to the Protein Sequence Database, March 2000

A;Description: Lymnaea trypsin inhibitor.

A;Reference number: A59204

A;Accession: A59204

A;Molecule type: protein

A;Residues: 1-57 <NAG>

A;Cross-references: UNIPROT:Q7M411

A;Experimental source: albumen gland

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor

C;Keywords: glycoprotein; serine proteinase inhibitor

F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;5-55.14-28.30-51/Disulfide bonds: #status predicted

F;15/Inhibitory site: Lys (trypsin) #status predicted

F;24/Binding site: carbohydrate (Asn) (covalent) #status experimental

Db 96 ArgAsnAsnPheGluSerGluAspTyrCysMetAlaValCysLys 110

RESULT 18

A49321

amyloid beta (A4) homolog 2 precursor - human

N;Alternate names: CDEI-binding protein

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A49321; S34644; S40519

R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster, R. *Biochemistry* 32, 4481-4486, 1993

A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: evidence for a novel protein family

A;Reference number: A49321; MUID:93250009; PMID:8485127

A;Accession: A49321

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <SPR>

A;Cross-references: UNIPROT:Q06481; GB:S60099; NID:G300168; PIDN:AAC60589.1; PID:G300169

A;Experimental source: placenta

A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P:131199)

A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney

R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H. *submitted to the EMBL Data Library, April 1993*

A;Description: The human homologue of the murine CDEI binding protein is an amyloid precursor protein

A;Reference number: S34644

A;Accession: S34644

A;Molecule type: mRNA

A;Residues: 1-763 <VON>

A;Cross-references: EMBL:222572; NID:G394763; PIDN:CAA80295.1; PID:G394764

R;Waco, W.; Gurbhagavatlula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T. *Nature Genet.* 5, 95-99, 1993

A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's A2 protein

A;Reference number: S40519; MUID:94035131; PMID:8220435

A;Accession: S40519

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <WAS>

A;Cross-references: GB:L27631; NID:G450391; PIDN:AAC41701.1; PID:G450392

C;Genetics:

A;Gene: GDB:APLP2; APLP2

A;Cross-references: GDB:139159; OMIM:104776

A;Map position: 11q23-11q25

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor

C;Keywords: alternative splicing; transmembrane protein

F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:

Pred. No.:	2.38e-07	Length:	763
Score:	157.00	Matches:	25
Percent Similarity:	60.00%	Conservative:	8
Best Local Similarity:	45.45%	Mismatches:	22
Query Match:	20.55%	Indels:	0
DB:	2	Gaps:	0

US-10-807-204-11 (1-396) x A49321 (1-763)

Qy 220 AAGGATATGTCAGTATGCCACAGAGCGCTGCGCTCCATACCACTGG 279

Db 307 LysAlaValCysSerGlnGluAlaMetThrGlyProCysArgAlaValMetProArgTrp 326

Qy 280 TGGTACAAATAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAAC 339

Db 327 TyrPheAspLeuSerLysGlyCysValArgPheIleTyrGlyGlyCysGlyGlyAsn 346

Qy 340 AATAACAACTTCCAACTGAAGCTATCTGCTGTCACCTGCACAA 384

Db 347 ArgAsnAsnPheGluSerGluAspTyrCysMetAlaValCysLys 361

RESULT 19

amyloid precursor-like protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S42880; S47528

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K. *submitted to the EMBL Data Library, March 1994*

A;Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid precursor protein

A;Reference number: S42880

A;Accession: S42880

A;Molecule type: mRNA

A;Residues: 1-765 <SAN>

A;Cross-references: UNIPROT:P15943; EMBL:X77934

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K. *Biochim. Biophys. Acta* 1219, 167-170, 1994

A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor

A;Reference number: S47528; MUID:94368849; PMID:8086458

A;Accession: S47528

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-765 <SA2>

A;Cross-references: EMBL:X77934

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor

C;Keywords: alternative splicing

F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:

Pred. No.:	2.38e-07	Length:	765
Score:	157.00	Matches:	25
Percent Similarity:	60.00%	Conservative:	8
Best Local Similarity:	45.45%	Mismatches:	22
Query Match:	20.55%	Indels:	0
DB:	2	Gaps:	0

US-10-807-204-11 (1-396) x S42880 (1-765)

Qy 220 AAGGATATGTCAGTATGCCACAGAGCGCTGCGCTCCATACCACTGG 279

Db 309 LysAlaValCysSerGlnGluAlaMetThrGlyProCysArgAlaValMetProArgTrp 328

Qy 280 TGGTACAAATAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAAC 339

Db 329 TyrPheAspLeuSerLysGlyCysValArgPheIleTyrGlyGlyCysGlyGlyAsn 348

Qy 340 AATAACAACTTCCAACTGAAGCTATCTGCTGTCACCTGCACAA 384

Db 349 ArgAsnAsnPheGluSerGluAspTyrCysMetAlaValCysLys 363

RESULT 20

S12143

lipoprotein-associated coagulation inhibitor precursor - rabbit

N;Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor inhibitor

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999

C;Accession: S12143; A61373

R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J. *Nucleic Acids Res.* 18, 6440, 1990

A;Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.

A;Reference number: S12143; MUID:91057146; PMID:2136251

A;Accession: S12143

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-300 <WES>

A;Cross-references: EMBL:X54708; NID:G1612; PIDN:CAA38515.1; PID:G1613

R;Colburn, P.; Crabb, J.W.; Buonassisi, V. *J. Cell. Physiol.* 148, 320-326, 1991

A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell

A;Reference number: A61373; MUID:91349227; PMID:1880157

A;Accession: A61373

A;Molecule type: protein

A;Residues: 25-33, 'X', 35-46 <COL>

C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

C;Keywords: anticoagulant; glycoprotein

F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Alignment Scores:

```
Pred. No.: 4.44e-07 Length: 300
Score: 154.50 Matches: 48
Percent Similarity: 42.42% Conservative: 22
Best Local Similarity: 29.09% Mismatches: 50
Query Match: 20.22% Indels: 45
DB: 2 Gaps: 8

US-10-807-204-11 (1-396) x S12143 (1-300)

QY 7 CTCTCAGGACTTCTGCCATCTCTGTA-----CCATTTCATC 42
Db 14 LeuLeuGlyLeuValProAlaProValSerSerAlaAlaGluGluAspGluPheThr 33
QY 43 CTTTTCGGGGACATC-----CAGGAACCTGGCCACGCT----- 75
Db 34 AsnIleThrAspIleLysProLeuGlnLysProThrHisSerPheCysAlaMetLys 53
QY 76 -----GAAGGC-----ATCCTTGGCCAG 93
Db 54 ValAspAspGlyProCysArgAlaTyrIleLysArgPhePhePheAsnIleLeuAlaHis 73
QY 94 CCGTGTCCCAAA---ATCAAAGTGGATCGGA-----GTGGAAGAATA 135
Db 74 GlnCysGluGluPheIleTyrGlyGlyCysGluGlyAsnGluAsnArgPheGluSerLeu 93
QY 136 GACCAGTGTACCAA-----CCAGAGATTGCCAGAAACATGAAGTGTGCCCGTTC 189
Db 94 GluGluCysLysGluLysCysAlaArgAspTyrProLysMetThrThrLysLeuThrPhe 113
QY 190 AGCCGTGGAAGAAATGTTTAGACTTCACAAAGGATATATGTCAGTATGACACAGAGGCT 249
Db 114 GlnLysGlyLys-----ProAspPheCysPheLeuGluGluAspPro 127
QY 250 GGCCTCTGCTGCTCCATCCACACTGGTGTACAAATAAATAAACTAAGTCTCTCC 309
Db 128 GlyIleCysArgGlyTyrIleThrArgTyrPheTyrAsnAsnGlnSerLysGlnCysGlu 147
QY 310 GAATTCATCTATGGCGGTGGCCAGGGGAAACAATAACAACCTTCCAAACTGAAGTCTCTCT 369
Db 148 ArgPheLysTyrGlyGlyCysLeuGlyAsnLeuAsnAsnPheGluSerLeuGluCys 167
QY 370 CTGGTCACCTGCAAA 384
Db 168 LysAsnThrCysGlu 172

RESULT 21
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (fra
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C:Accession: A32761
R:de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted pe
A:Reference number: A32761; MUID:89346754; PMID:2569763
A:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A:Note: The authors translated the codon ATG for residue 433 as Leu
C:Comment: This is the hypothetical translation of a sequence believed to contain clonin
C:Keywords: cloning artifact

Alignment Scores:
Pred. No.: 4.83e-07 Length: 484
Score: 154.00 Matches: 24
Percent Similarity: 59.26% Conservative: 8
Best Local Similarity: 44.44% Mismatches: 22
Query Match: 20.16% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x A32761 (1-484)
```

```
QY 220 AAGGATATATGTCAGTATGCCACAGAGGCTGGCCCTGCTGCTGCTCCATACCACACTGG 279
Db 209 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetIleSerArgTrp 228
QY 280 TGGTACATAAAAAAATAAGATCTCTCCCAATCTATCTATGGCGGTGCCAGGGGAAC 339
Db 229 TyrPheAspValThrGluGlyLysCysAlaProPhePheTyrGlyCysGlyAsn 248
QY 340 AATAACAACCTCCAAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 249 ArgAsnAsnPheAspThrGluGluTyrCysMetalAlaValCys 262
```

RESULT 22

ORHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; A44
4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S3
R:Leinmair, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4 [695] precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEMI>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP (695)
R:Leinmair, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VM', 17-288, 'V', 365-770 <LEW2>
A:Cross-references: EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:9871360
A:Note: alternative splice form APP(695)
R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakia, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:G341202; PIDN:AAC13654.1; PID:9516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:G178863; PIDN:AAA51768.1; PID:G178865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:190321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:G178616

A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-530, 'QMLMPVIPAFWEAKVGR' <Y052>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AA859501.1; PID:g178615
R;Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 688-716, 'P' 718-737 <MUR>
A;Cross-references: GB:S57665; NID:9236720; PIDN:AA819991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijisman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93033397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692, 'G' 694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AA823645.1; PID:g257378
A;Experimental source: GB:M15315; NID:g257378
A;Note: sequence extracted from NCBI backbone (NCBI:P:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AA823646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBI:P:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288, 'V', 365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A;Cross-references: GB:M16785; NID:g178539; PIDN:AA851722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756, 'S', 758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707

A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ken
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
R;Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muellem
EMBO J. 7, 949-957, 1988
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precu
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve,
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g292612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Dav
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibito
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g9929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, P.
Brain Res. Mol. Brain Res. 4, 121-133, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three bra
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 132-288, 'V', 365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease bra
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.

QY 223 GATATATGAGTATGCCAGAGAGCTGGCCCTGCTGGCTCATACACACTGTGG 282
Db : : : : :
1 GluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetIleSerArgTrpTyr 20
QY 283 TACAATAAAAACTAAGATCTGCTCCCAATTCATCTATGCGGTGCCAGGGGAACAAT 342
Db : : : : :
21 PheAspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsnArg 40
QY 343 AACAACTTCCAACTGAAGCTATCTGCTGGTGCACCTGC 381
Db : : : : :
41 AsnAsnPheAspThrGluGluTyrCysMetAlaValCys 53
RESULT 28
S03607
Alzheimer's disease amyloid A4 protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S03607
R:Kang, J.; Mueller-Hill, B.
Nucleic Acids Res. 17, 2130, 1989
A:Title: The sequence of the two extra exons in rat preA4.
A:Reference number: S03607; MUID:89183625; PMID:2648331
A:Accession: S03607
A:Molecule type: mRNA
A:Residues: 1-76 <KAN>
A:Cross-references: UNIPROT:P08592; EMBL:X14066; NID:g56957; PID:g93026
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Alignment Scores:
Pred. No.: 8.53e-07 Length: 76
Score: 152.00 Matches: 24
Percent Similarity: 58.4% Conservative: 7
Best Local Similarity: 45.2% Mismatches: 22
Query Match: 19.9% Indels: 0
DB: 2 Gaps: 0
US-10-807-204-11 (1-396) x S03607 (1-76)
QY 223 GATATATGAGTATGCCAGAGAGCTGGCCCTGCTGGCTCATACACACTGTGG 282
Db : : : : :
1 GluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetIleSerArgTrpTyr 20
QY 283 TACAATAAAAACTAAGATCTGCTCCCAATTCATCTATGCGGTGCCAGGGGAACAAT 342
Db : : : : :
21 PheAspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsnArg 40
QY 343 AACAACTTCCAACTGAAGCTATCTGCTGGTGCACCTGC 381
Db : : : : :
41 AsnAsnPheAspThrGluGluTyrCysMetAlaValCys 53
RESULT 29
HCHU
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human
N:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) pH
rich protein
N:Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1982 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; P90450; B39079; A61580; B25
3217
R:Vetr, H.; Gebhard, W.
Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
A:Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
A:Reference number: S13433; MUID:91214554; PMID:1708673
A:Accession: S13433
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <VET1>
A:Cross-references: UNIPROT:P02760; EMBL:X54816; NID:g24475; PID:CAA38585.1; PID:g82561
R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Salier, J.P.; Leveillard, T.; Mart
Eur. J. Biochem. 191, 131-139, 1990

A:Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene
A:Reference number: S10778; MUID:90336621; PMID:1696200
A:Accession: S10778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <DIA>
R:Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
Nucleic Acids Res. 14, 7839-7850, 1986
A:Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-
A:Reference number: A93642; MUID:87040757; PMID:2430261
A:Accession: A93642
A:Molecule type: mRNA
A:Residues: 1-352 <KAU>
A:Cross-references: GB:X0494; NID:g24478; PID:CAA28182.1; PID:g24479
R:Lopez Otin, C.; Grubb, A.O.; Mendez, E.
Arch. Biochem. Biophys. 228, 544-554, 1984
A:Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge
A:Reference number: A90074; MUID:84126849; PMID:6198962
A:Accession: A90074
A:Molecule type: protein
A:Residues: 20-56,58-202 <LOP>
A:Experimental source: individual with tubular proteinuria
A:Note: no evidence of sequence heterogeneity could be found, in spite of persistent het
R:Takagi, T.; Takagi, K.; Kawai, T.
Biochem. Biophys. Res. Commun. 98, 997-1001, 1981
A:Title: Complete amino acid sequence of human alpha-1-microglobulin.
A:Reference number: A90225; MUID:81184038; PMID:6164372
A:Accession: A90225
A:Molecule type: protein
A:Residues: 20-47,58-136,138-141,'T',143-144,146-198 <TAK>
A:Experimental source: pooled urine of patients with tubular proteinuria
R:Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempert, K.; Salier, J.P.
Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
A:Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in
A:Reference number: A90686; MUID:85225968; PMID:2408638
A:Accession: A90686
A:Molecule type: protein
A:Residues: 206-290,'VI',293-342,'E',344-350 <REI>
R:Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueeke, T.; Daudon, M.
Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
A:Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ca
A:Reference number: P90450; MUID:93221481; PMID:8466493
A:Accession: P90450
A:Molecule type: protein
A:Residues: 206-214,'X' <ATM1>
R:Engchild, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.
J. Biol. Chem. 266, 747-751, 1991
A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot
A:Reference number: A39079; MUID:91093267; PMID:1898736
A:Accession: A39079
A:Molecule type: protein
R:Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
Int. J. Biochem. 23, 1201-1203, 1991
A:Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inh
A:Reference number: A61580; MUID:92175157; PMID:1794445
A:Accession: A61580
A:Molecule type: protein
A:Residues: 214,'X',216-222,'X' <CHI>
R:McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.
J. Biol. Chem. 261, 5378-5383, 1986
A:Title: Two apparent human endothelial cell growth factors from human hepatoma cells a
A:Reference number: A92583; MUID:86168278; PMID:3007499
A:Accession: A92583
A:Molecule type: protein
A:Residues: 206-225 <ENGL>
R:Engchild, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-a
A:Reference number: A92736; MUID:89380192; PMID:2476436
A:Accession: A92736
A:Molecule type: protein
A:Residues: 206-225 <ENG2>

R;Traboni, C.; Cortese, R.
Nucleic Acids Res. 14, 6340, 1986
A>Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobulin)
A:Reference number: A25303; MUID:86312901; PMID:2428011
A:Accession: A25303
A:Molecule type: mRNA
A:Residues: 1-218,'HW' <TRA>
A>Note: this mRNA sequence appears to contain errors after residue 218
R;Calero, M.; Escibano, J.; Grubb, A.; Mendez, E.
J. Biol. Chem. 269, 384-389, 1994
A>Title: Location of a novel type of interpolypeptide chain linkage in the human protein
A:Reference number: A53110; MUID:94103241; PMID:7506257
A:Accession: A53110
A:Molecule type: protein
A:Residues: 45-57 <CAL1>
R;Ver, H.; Koeglzer, M.; Gebhard, W.
FEBS Lett. 245, 137-140, 1989
A>Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inhibitor
A:Reference number: S03552; MUID:89171290; PMID:2466696
A:Accession: S03552
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 206-352 <VET2>
R;Malik, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fournet
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A>Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation
A:Reference number: S28928; MUID:93039735; PMID:1384548
A:Accession: S28930
A>Status: preliminary
A:Molecule type: protein
A:Residues: 206-215 <MAL>
R;Morelle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalecki, C.; Fournet
Eur. J. Biochem. 221, 881-888, 1994
A>Title: Chondroisin sulfate covalently cross-links the three polypeptide chains of inter
A:Reference number: S43466; MUID:94229087; PMID:7513643
A:Accession: S43466
A>Status: preliminary
A:Molecule type: protein
A:Residues: 206-221 <WOR>
R;Wianiewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
Biochemistry 33, 7423-7429, 1994
A>Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex
A:Reference number: A53642; MUID:94271799; PMID:7516184
A:Accession: A53642
A>Status: preliminary
A:Molecule type: protein
A:Residues: 206-217 <WIS>
R;Calero, M.; Mendez, E.; Garcia, E.
Biochim. Biophys. Acta 1249, 91-99, 1995
A>Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)
A:Reference number: S55688; MUID:95284116; PMID:7539295
A:Accession: S55688
A:Molecule type: protein
A:Residues: 20-24 <CAL2>
R;Bourguignon, J.; Diarra-Mehrpour, M.; Sesboue, R.; Frain, M.; Sala-Trepat, J.M.; Marti
Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
A>Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide sequence
A:Reference number: 152208; MUID:86025577; PMID:2413856
A:Accession: 152208
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 302-352 <BOU>
R;Wojcik, E.G.C.; van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Berti
Biochem. J. 311, 753-759, 1995
A>Title: Factor IX Zuthphen: a Cys(18) -> Arg mutation results in formation of a heterodimer
A:Reference number: S59509; MUID:96067589; PMID:7487929
A:Accession: S59509
A:Molecule type: protein
A:Residues: 27-35,'Y',37 <WOJ>
R;Atmani, F.; Mizon, J.; Khan, S.R.
Eur. J. Biochem. 236, 984-990, 1996
A>Title: Identification of uronic-acid-rich protein as urinary bikunin, the light chain

A:Reference number: S66434; MUID:96270753; PMID:8665922
A:Accession: S66434
A:Molecule type: protein
A:Residues: 206-214,'X',216-230 <ATM2>
R;Akerstroem, B.; Bratt, T.; Enghild, J.J.
FEBS Lett. 362, 50-54, 1995
A>Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect cells
A:Reference number: S68728; MUID:95212582; PMID:7535251
A:Accession: S68728
A:Molecule type: protein
A:Residues: 89-100 <AKE>
R;Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A>Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a novel
A:Reference number: S02431; MUID:88167187; PMID:2450785
A:Accession: S02431
A:Molecule type: protein
A:Residues: 206-214,'X',216-217 <JES>
R;Lopez, C.; Grubb, A.; Mendez, E.
FEBS Lett. 144, 349-353, 1982
A>Title: Human protein HC displays variability in its carboxyl-terminal amino acid sequence
A:Reference number: A91304
A:Contents: annotation; variant of alpha-1-microglobulin
A>Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys and
R;Hochstrasser, K.; Schonberger, O.L.; Rosemanith, I.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
A>Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-1
by affinity chromatography.
A:Reference number: A91698; MUID:82074265; PMID:6171497
A:Contents: annotation; carbohydrate binding sites
R;Morii, M.; Travis, J.
Biol. Chem. Hoppe-Seyler 366, 19-21, 1985
A>Title: The reactive site of human inter-alpha-trypsin inhibitor is in the amino-terminal
A:Reference number: A90882; MUID:85255940; PMID:3890890
A:Contents: annotation; inhibitory site
A>Note: in vitro, the first twelve residues of the amino end of the inhibitor appear to
C:Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolytically p
C:Comment: Alpha-1-microglobulin occurs in many physiological fluids including plasma, u
It contains at least one brown-yellow chromophore.
Alignment Scores:
Pred. No.: 7,75e-07 Length: 352
Score: 152.00 Matches: 25
Percent Similarity: 58.93% Conservative: 8
Best Local Similarity: 44.64% Mismatches: 23
Query Match: 19.90% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x HCHU (1-352)
Qy 217 AGAAAGGATATATGCAGTAGTGCACAGAGGCTGGCCCTCTGGCTCCATACCACAC 276
Db 227 LyeGluAaspSerCysGlnLeuGlyTyrSerAlaGlyProCysMetGlyMetThrSerArg 246
Qy 277 TGGTGGTACAAATAAAAAATTCATGCTCCGAATTCATCTATGCGGTTCGCGGG 336
Db 247 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheGlnTyrGlyGlyCysMetGly 266
Qy 337 AACAAATAACAACCTCCAAACTGAAGCTATCTGTCTGTGTACCTGCAAA 384
Db 267 AsnGlyAasnAenPheValThrGluLysGluCysLeuGlnThrCysArg 282
RESULT 30
JC2556
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - Atlantic salmon (fragment
N;Alternate names: bikunin
C;Species: Salmo salar (Atlantic salmon)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: JC2556
R;Hanley, S.; Powell, R.
Gene 147, 297-298, 1994
A>Title: Sequence of a cDNA clone encoding the Atlantic salmon alpha1-microglobulin/bikun

A:Reference number: JC2556; MUID:95011634; PMID:7523247
A:Accession: JC2556
A:Molecule type: mRNA
A:Residues: 1-372 <HAN>
A:Cross-references: UNIPROT:Q91484; GB:L26598; NID:q433806; PIDN:AAA72048.1; PID:q433807
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precursor
C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; serine proteinase inhibitor
F:1-19/Domain: signal sequence (fragment) #status predicted <SIG>
F:20-372/Product: alpha-1-microglobulin/inter-alpha-trypsin inhibitor #status predicted
F:34-187/Domain: lipocalin homology <LIP>
F:235-285/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:291-341/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:190-187/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F:222/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F:254/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 8,658-07 Length: 372
Score: 151.50 Matches: 38
Percent Similarity: 45.22% Conservativeness: 14
Best Local Similarity: 33.04% Mismatches: 38
Query Match: 19.83% Indels: 25
DB: 2 Gaps: 6

US-10-807-204-11 (1-396) x JC2556 (1-372)

QY 64 CTGGGACGCTGAAGGCATCTTGGCAAGCGTCTGCCAAATCAAAATCAAGTGAATGCGAA 123
DB 189 ProGly---ThrGluProValAlaGluProGlnProGluLe-----202
QY 124 GTGGAAGAANTAGACAGGTGTACCAAAACCCAGAGAT-----TGCCACGAA 168
DB 203 -----ThraProAArgAlaLysArgAsnIleValLeuProGlu 215
QY 169 AACATGAAGTGTGGCCGTTACCGCTGCAAGAGAATGT-----TTAGACTTACA--- 219
DB 216 -----LeuProAlaGluGlySerGlyAlaGlyIleMetMetPheArgSer 231
QY 220 AAGATATATGCAGTATGCCACAGAGCGTGGCCCTGCTGCTGCCATACACACTGG 279
DB 232 GluGluSerCysAsnAlaGluProAlaGluProCysPheGlyThrValGlnArgHis 251
QY 280 TGGTACAATAAATAAATAAGATCTGCTCCGAATTCATCTATGGCGTTGCCAGGGGAAC 339
DB 252 PheTyrAsnSerSerSerMetAlaCysGlnLeuPheThrTyrGlyGlyCysMetGlyAsn 271
QY 340 AATAACAACCTTCAAACTGAAGTATCTCTGCTGGTCACCTGCAA 384
DB 272 GlnAsnAsnPheValThrGluArgGluCysLeuGlnSerCysArg 286

RESULT 31
TIVIVC
venom basic proteinase inhibitor III - sand viper
N:Alternate names: venom chymotrypsin inhibitor
C:Species: Vipera ammodytes (sand viper)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A01223
R:Ritonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 746, 138-145, 1983
A:Title: The primary structure Of Vipera ammodytes venom chymotrypsin inhibitor.
A:Reference number: A01223
A:Molecule type: protein
A:Residues: 1-65 <RIT>
A:Cross-references: UNIPROT:P00992
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology
C:Keywords: serine proteinase inhibitor; venom
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:7-57,16-40,32-53/Disulfide bonds: #status predicted
F:17/Inhibitory site: Leu (chymotrypsin) #status predicted

Alignment Scores:
Pred. No.: 1,086-06 Length: 65

Score: 151.00 Matches: 26
Percent Similarity: 63.64% Conservativeness: 9
Best Local Similarity: 47.27% Mismatches: 20
Query Match: 19.76% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x TIVIVC (1-65)

QY 217 AGAAGGATATATGCGATGATCCACAGAGAGCTGGCCCTGCTGCCATACACAC 276
DB 3 ArgProLysPheCysTyrLeuProAlaAspProGlyArgCysLeuAlaTyrMetProArg 22
QY 277 TGGTGGTACATAAATAAATAAGATCTGCTCCGAATTCATCTATGGCGTTGCCAGGG 336
DB 23 PheTyrTyrAsnProAlaSerAsnLysCysGluLysPheIleTyrGlyGlyCysArgGly 42

QY 337 AACATAACAACCTTCAAACTGAAGCTATCTGCTGGTCACCTGC 381
DB 43 AsnAlaAsnAsnPheLysThrTrpAspGluCysArgHisThrCys 57

RESULT 32

A32282
Alzheimer's disease amyloid beta protein precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 09-Jul-2004
C:Accession: A32282
R:Yamada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 158, 906-912, 1989
A:Title: Structure and expression of the alternatively-spliced forms of mRNA for the mouse
A:Reference number: A32282; MUID:89149813; PMID:2493250
A:Accession: A32282
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <YAM>
A:Cross-references: UNIPROT:P12023; GB:M24397; NID:q200350; PIDN:AAA39929.1; PID:q200351
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing
F:11-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
Pred. No.: 1,058-06 Length: 100
Score: 151.00 Matches: 24
Percent Similarity: 57.41% Conservativeness: 7
Best Local Similarity: 44.44% Mismatches: 23
Query Match: 19.76% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x A32282 (1-100)

QY 220 AAGGATATATGCGATGATCCACAGAGAGCTGGCCCTGCTGCCATACACACTGG 279
DB 8 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetIleSerArgTrp 27
QY 280 TGGTACAATAAATAAATAAGATCTGCTCCGAATTCATCTATGGCGTTGCCAGGGGAAC 339
DB 28 TyrPheAspValThrGluGlyLysCysValProPhePheTyrGlyGlyCysGlyGlyAsn 47
QY 340 AATAACAACCTTCAAACTGAAGCTATCTGCTGGTCACCTGC 381
DB 48 ArgAsnAsnPheAspThrGluGluTyrCysMetAlaValCys 61

RESULT 33

T32497
hypothetical protein C08G9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32497
R:Geisel, C.; Stellies, L.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid C08G9.
A:Reference number: Z21179
A:Accession: T32497
A:Status: preliminary; translated from GB/EMBL/DBJ

A;Cross-references: UNIPROT:P26228
A;Experimental source: hemolymph
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;6-56,15-39,31-52/Disulfide bonds: #status predicted
F;16/Inhibitory site: Arg (chymotrypsin) #status predicted

Alignment Scores:
Pred. No.: 1,71e-06 Length: 57
Score: 149.00 Matches: 26
Percent Similarity: 61.11% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 21
Query Match: 19.50% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x TIFHP (1-57)

QY 220 AAGGATATATGAGTATGCCAGAGGCTGGCCCTGCTGCCTCCATACCACACTGG 279
Db 3 LysSerAlaCysLeuGlnProLysGluValGlyProCysArgLysSerAspPheValPhe 22
QY 280 TGGTACATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGAAC 339
Db 23 PheTyrAsnAlaAspThrLysAlaCysGluGluPheLeuTyrGlyGlyCysArgGlyAsn 42

QY 340 AATAACAACCTTCCAACTGAAGCTATCTGCTGGTCACCTGC 381
Db 43 AspAsnArgPheAsnThrLysGluGluCysGluLysLeuCys 56

RESULT 37

S04855
Alzheimer's disease amyloid A4 protein - mouse (fragment)
C;Species: Mus musculus domesticus (western European house mouse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
A;Accession: S04855
R;Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.
Nucleic Acids Res. 17, 5396, 1989
A;Title: Sequence of the protease inhibitor domain of the A4 amyloid protein precursor
A;Reference number: S04855; MUID:89345111; PMID:2569710
A;Accession: S04855
A;Molecule type: mRNA

A;Residues: 1-76 <FUK>
A;Cross-references: UNIPROT:P12023; EMBL:X15210; NID:g49965; PIDN:CAA33280.1; PID:g93013
A;Note: the authors translated the codon GAT for residue 74 as Val
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F;3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
Pred. No.: 1,68e-06 Length: 76
Score: 149.00 Matches: 24
Percent Similarity: 56.60% Conservative: 26
Best Local Similarity: 45.28% Mismatches: 23
Query Match: 19.50% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x S04855 (1-76)

QY 223 GATATGAGTATGCCAGAGGCTGGCCCTGCTGCCTCCATACCACACTGGTG 282
Db 1 GluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetileSerArgTrpTyr 20
QY 283 TACNATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGAACAT 342
Db 21 PheAspValThrGluGlyLysCysValProPheTyrGlyGlyCysGlyGlyAsnArg 40

QY 343 AACAACTTCCAACTGAAGCTATCTGCTGGTCACCTGC 381
Db 41 AsnAsnPheAspThrGluGluTyrCysMetAlaValCys 53

RESULT 38

A29652

inter-alpha-trypsin inhibitor (BPI type) - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29652
R;Rasp, G.; Hochstrasser, K.; Wächter, E.; Reisinger, P.W.M.
Biol. Chem. Hoppe-Seyler 369, 727-731, 1987
A;Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha
sin inhibitor, XI.)
A;Reference number: A29652; MUID:87299012; PMID:2441725
A;Accession: A29652
A;Molecule type: protein
A;Residues: 1-123 <RAS>
A;Cross-references: UNIPROT:P13371
C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C;Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Alignment Scores:
Pred. No.: 1,63e-06 Length: 123
Score: 149.00 Matches: 24
Percent Similarity: 57.14% Conservative: 8
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 19.50% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x A29652 (1-123)

QY 217 AGAAGGATATATGCAGTATGCCAGAGGCTGGCCCTGCTGCCTCCATACCACAC 276
Db 1 LysGluAspSerCysGlnLeuGlyTyrSerGlnGlyProCysAluGlyMetPhylsArg 20
QY 277 TGGTGGTACAATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheTyrTyrGlyGlyCysMetGly 40
QY 337 AACATACAACTTCCAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheProSerGluLysGluCysLeuGlnThrCysArg 56

RESULT 39

S01803
chymotrypsin inhibitor II - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01803
R;Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A;Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A;Reference number: S01802; MUID:89228538; PMID:3072972
A;Accession: S01803
A;Molecule type: protein
A;Residues: 1-62 <SAS>
A;Cross-references: UNIPROT:P10832
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
Pred. No.: 1,91e-06 Length: 62
Score: 148.50 Matches: 30
Percent Similarity: 61.40% Conservative: 5
Best Local Similarity: 52.63% Mismatches: 21
Query Match: 19.44% Indels: 1
DB: 2 Gaps: 1

US-10-807-204-11 (1-396) x S01803 (1-62)

QY 220 AAGGATATATGCAGTATGCCA---CAGGAGGCTGGCCCTGCTGCCTCCATACCACAC 276
Db 6 LysProIleCysGluGlnAlaPheGlyAsnSerGlyProCysPheAlaTyrIleLysLeu 25
QY 277 TGGTGGTACAATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336

Db 26 TyrSerTyrAenGlnLysThrLysLysCysGluGluPheLeuTyrGlyGlyCysLysGly 45
Qy 337 AACAAATACAACTTCCAAACTGAAGCTATCTGTCTGTGTCACCTGCAAAAAA 387
Db 46 AenAspAenArgPheAspThrLeuAlaGluCysGluGlnLysCysIleLys 62
RESULT 40
T32060
hypothetical protein R12A1.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T32060
R/Pauley, A.; Andrews, S.
A/Submitted to the EMBL Data Library, July 1997
A/Description: The sequence of C. elegans cosmid R12A1.
A/Reference number: Z21118
A/Accession: T32060
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-249 <PAU>
A/Cross-references: UNIPROT:O16701; EMBL:AF016680; PIDN:AAB66164.1; GSPDB:GN000023; CESP:
A/Experimental source: strain Bristol N2; clone R12A1
C/Genetics:
A/Gene: CESP:R12A1.3
A/Map position: 5
A/Introns: 75/1; 139/1
Alignment Scores:
Pred. No.: 1,75e-06 Length: 249
Score: 148.50 Matches: 33
Percent Similarity: 46.23% Conservative: 16
Best Local Similarity: 31.13% Mismatches: 46
Query Match: 19.44% Indels: 11
DB: 2 Gaps: 3
US-10-807-204-11 (1-396) x T32060 (1-249)
Qy 97 TGTCCAAA---ATCAAGTGTGATGCGAAGTGAAGAAATAGACCAGTGTACCAARCCC 153
Db 88 CysProArgProLeuGlyIleSerValPheGlnAspAenThrIleGlyCysTrpMetAsp 107
Qy 154 AGAGATTGCCAGAAACATCAAGTGTTC-----CCGTCAGCGT 195
Db 108 SerAsnCysProGlyIleGlnLysCysValGluProAsnProValThrAsnSerAla 127
Qy 196 GGAAGAAATGTTTAGAC-----TTCAAGAAAGGATATATGTCAGTATGCCACAG 243
Db 128 ThrArgIleCysArgAspProValGlyIleAlaSerThrSerIleCysSerLeuProLeu 147
Qy 244 GAGCTGGCCCTCGCTGGCTCCATACCACACTGGTGGTACATATAAAAACTAAGATC 303
Db 148 AlaValGlySerCysThrAlaProAlaValArgPheTyrTyrAspAlaSerSerGlyArg 167
Qy 304 TGCTCCGAATCATCTATGGGGTTCAGGGGGAACATAACACTTCCAACTGAAAGCT 363
Db 168 CysAsnGlnPheMetTyrSerGlyCysGlyGlyAsnAlaAsnAsnPheGlnSerLeuSer 187
Qy 364 ATCTGTCTGGTCACCTGC 381
Db 188 SerCysGlnGlyThrCys 193
RESULT 41
S21089
alpha-1-microglobulin/inter-alpha-trypsin inhibitor light chain precursor - rat
N/Alternate names: acid-stable proteinase inhibitor; bikunin; trypstatin
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S21089; A53056; A53935; A31890; A61633
R/Lindqvist, A.; Bratt, T.; Altieri, M.; Kastern, W.; Akerstrom, B.
Biochim. Biophys. Acta 1130, 63-67, 1992
A/Title: Rat alpha(1)-microglobulin: co-expression in liver with the light chain of inte
A/Reference number: S21089; MUID:92182014; PMID:1371936

A/Accession: S21089
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-349 <LIN>
A/Cross-references: UNIPROT:Q64240; GB:S87544; NID:g247162; PIDN:AAB21782.1; PID:g247163
R/Itoh, H.; Ide, H.; Ishikawa, N.; Nawa, Y.
J. Biol. Chem. 269, 3818-3822, 1994
A/Title: Mast cell protease inhibitor, trypstatin, is a fragment of inter-alpha-trypsin
A/Reference number: A53056; MUID:94148892; PMID:7508921
A/Accession: A53056
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 285-341 <ITO>
R/Kastern, W.; Bjorck, L.; Akerstrom, B.
J. Biol. Chem. 261, 15070-15074, 1986
A/Title: Developmental and tissue-specific expression of alpha-1-microglobulin mRNA in t
A/Reference number: A25935; MUID:87033744; PMID:2429963
A/Accession: A25935
A/Molecule type: protein
A/Residues: 141,'A',143-195 <KAS>
R/Kido, H.; Yokogoshi, Y.; Katunuma, N.
J. Biol. Chem. 263, 18104-18107, 1988
A/Title: Kunitz-type protease inhibitor found in rat mast cells. Purification, properties
A/Reference number: A31890; MUID:89053978; PMID:3263966
A/Accession: A31890
A/Molecule type: protein
A/Residues: 283-301,'L',303-322,'N',324-329,'PK',332-333,'W',335-343 <KID>
R/Sugiki, M.; Maruyama, M.; Yoshida, E.; Sumi, H.; Mihara, H.
Inflammation 15, 281-289, 1991
A/Title: Acid-stable protease inhibitor in chronic phase of carrageenin-induced inflamma
A/Reference number: A61633; MUID:92120777; PMID:1769732
A/Accession: A61633
A/Molecule type: protein
A/Residues: 205-213,'X',215-229,'N',231-232,'K',234-238 <SUG>
C/Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C/Keywords: chondroitin sulfate proteoglycan; chromoprotein; glycoprotein; plasma; serine
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-202/Product: alpha-1-microglobulin #status predicted <ALM>
F:34-187/Domain: lipocalin homology <LIP>
F:205-349/Product: inter-alpha-trypsin inhibitor #status experimental <IAI>
F:230-280/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:286-336/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:24/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:52/Cross-link: alpha-1-microglobulin-Ig alpha complex chromophore (Cys) (interchain to
F:114,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:214/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
F:296/Inhibitory site: Arg (trypsin) #status predicted
Alignment Scores:
Pred. No.: 2,15e-06 Length: 349
Score: 147.50 Matches: 42
Percent Similarity: 34.66% Conservative: 19
Best Local Similarity: 23.86% Mismatches: 56
Query Match: 19.31% Indels: 59
DB: 2 Gaps: 3
US-10-807-204-11 (1-396) x S21089 (1-349)
Qy 32 TACCATTCATCCTTTTGGGGGACATCC----- 58
Db 108 TyrHisLysSerLysTrpAsnAlaThrLeuGluSerTyrValValHisThrAsnTyrAsp 127
Qy 59 -----AGGAACCTGGCAGCGTGAAGCA 82
Db 128 GluTyrAlaIlePheLeuThrLysLysPheSerHisArgHisGlyProThrIleThrAla 147
Qy 83 TCCTTGGCAAGCCGTGCCAAAATCAAAGTGAATGCGAAGTGAAGAAATACACAGT 142
Db 148 LysLeuTyrGlyArgGluProGlnLeuArg--AspSerLeuLeuGlnGluPheArgGluV 167
Qy 143 GTACCAAAACCAGAGATTGCCAGAAAACATG-----AAGT 178
Db 167 alAlaLeuSerValGlyIleProGluAsnSerIleValPheMetAlaAspArgGlyGluC 187

A;Contents: annotation; disulfide bonds

A;Accession: A90736
A;Molecule type: protein
A;Residues: 36-93 <CHA>
R;Diouha, V.; Pospisilova, D.; Meloun, B.; Sorm, F.
Collect. Czech. Chem. Commun. 33, 1363-1365, 1968
A;Title: Sequence of residues 18-20 in pancreatic trypsin inhibitor.
A;Reference number: A90927
A;Accession: A90927
A;Molecule type: protein
A;Residues: 36-93 <DLO>
R;Huber, R.; Kukla, D.; Ruhlmann, A.; Epp, O.; Formanek, H.
Naturwissenschaften 57, 389-392, 1970
A;Title: The basic trypsin inhibitor of bovine pancreas. I. Structure analysis and conformation of the basic trypsin inhibitor of bovine pancreas.
A;Reference number: A93410; MUID:70255230; PMID:5447861
A;Contents: annotation; X-ray crystallography of basic protease inhibitor, 2.5 angstrom resolution
A;Lewis, R.V.; Ray, P.; Coghill, R.; Kruggel, W.
Biochem. Biophys. Res. Commun. 167, 543-547, 1990
A;Title: Presence of pancreatic trypsin inhibitor in adrenal medullary chromaffin cells.
A;Reference number: A34658; MUID:90211226; PMID:2322242
A;Accession: A34658

A;Molecule type: protein
A;Residues: 36-53,55-81 <LEW>
R;Anderson, S.; Kingston, I.B.
Proc. Natl. Acad. Sci. U.S.A. 80, 6838-6842, 1983
A;Title: Isolation of a genomic clone for bovine pancreatic trypsin inhibitor by using a cDNA library.
A;Reference number: A93977; MUID:84070725; PMID:6580617
A;Accession: A93977

A;Molecule type: DNA
A;Residues: 'PSLFNRDPPIPA', 34-97, 'GKTGARGEGKG' <AND>
A;Cross-references: GB:X03365; GB:X00966; NID:g142; PIDN:CAA27062.1; PID:g1364183
R;Stiekmann, J.; Menzel, H.R.; Schroeder, W.; Teschesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A;Title: Characterization and sequence determination of six aprotinin homologues from bovine aorta.
A;Reference number: S00371; MUID:88221840; PMID:2453200
A;Accession: S10062

A;Molecule type: protein
A;Residues: 36-66, 'P', 68-82, 'S', 84-93 <SIE>
A;Experimental source: lung
A;Note: the authors designated this protein as isoprotinin 2
C;Comment: Basic proteinase inhibitor is an intracellular polypeptide found in many tissues.
C;Genetics:

A;Introns: 34/1; 98/1
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-35/Domain: signal sequence #status predicted <PRO>
F;36-100/Product: basic proteinase inhibitor #status experimental <MAT>
F;40-90/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;40-90,49-73,65-86/Disulfide bonds: #status experimental
F;50/Inhibitory site: Lys (trypsin, chymotrypsin, kallikrein, plasmin) #status experimental

Alignment Scores:
Pred. No.: 3.27e-06 Length: 100
Score: 146.00 Matches: 24
Percent Similarity: 58.18% Conservative: 8
Best Local Similarity: 43.64% Mismatches: 23
Query Match: 19.11% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x TIBO (1-100)

Qy 217 AGAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTCGCTCCATACCACAC 276

Db 36 ArgProaspPheCysLeuGluProProtyrThrGlyProCysLysAlaAraileArg 55

Qy 277 TGGTGGTACATAAACTAAAGTCTGCTCCGAATTCATCTATGGCGGTGGCCAGGG 336

Db 56 TyrPheTyraaaAlaLysAlaGlyLeuCysGlnThrPheValTyrglyGlyCysArgAla 75

Qy 337 AACAAATCAACTCCCAACTGAAGCTATCTGTCTGTGTCACCTGC 381

Db 76 LysArgaenAanPheLysSerAlaGluAspCysMetArgThrCys 90

RESULT 44

C89114

protein C37C3.6a [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: C89114

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Reference number: A75000; MUID:9069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999

A;Accession: C89114

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1558 <STO>

A;Cross-references: UNIPROT:Q8I710; GB:chr_V; PIDN:AAC25867.1; GSPDB:GN00023

C;Genetics:

A;Gene: C37C3.6a

A;Map position: 5

Alignment Scores:

Pred. No.: 2.76e-06 Length: 1558

Score: 146.00 Matches: 22

Percent Similarity: 54.55% Conservative: 8

Best Local Similarity: 40.00% Mismatches: 25

Query Match: 19.11% Indels: 0

DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x C89114 (1-1558)

Qy 226 ATATGCAGTATGCCACAGGAGCTGGCCCTCGCTCCATACCACACTGGTGTAC 285

Db 1446 ValCysaspGluAlaLysAspThrGlyProCysThrAsnPheValThrLysTrpTyr 1465

Qy 286 AATAAAAAAACTAAGATCTGCTCGAATTTCATCTATGCGGTTCACAGGGGAAACAATAAC 345

Db 1466 AsnLysAlaaspGlyThrCysAsnArgPheHisTyrglyGlyCysGlnGlyThrAsnAsn 1485

Qy 346 AACTTCCAACTGAAGTATCTGTCTGTGTCACCTGCAAAAATAAC 390

Db 1486 ArgPheaspAenGluGlnGlnCysLysAlaAlaCysGlnAenHis 1500

RESULT 45

T34395

hypothetical protein C37C3.6b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T34395; T34394

R;Gisels, C.; Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A;Description: The sequence of C. elegans cosmid C37C3.

A;Reference number: Z21518

A;Accession: T34395

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2167 <GEI>

A;Cross-references: UNIPROT:O76840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C37C3

A;Experimental source: strain Bristol N2; clone C37C3

A;Accession: T34394

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1555, 'SKF' <GE2>

A;Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a

A;Experimental source: strain Bristol N2; clone C37C3

C;Genetics:

A;Gene: CESP:C37C3.6b; CESP:C37C3.6a

A;Map position: 5

A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/1

Alignment Scores:

Pred. No.: 2.7e-06 Length: 2167

Score: 146.00 Matches: 22
Percent Similarity: 54.55% Conservative: 8
Best Local Similarity: 40.00% Mismatches: 25
Query Match: 19.11% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x T34395 (1-2167)

QY 226 ATATGAGTATGCCACAGGAGCTGCCCTGCTGCCTCCATACACACTGGGTGATC 285
Db 1446 ValCysAspGluAlaLysAspThrGlyProCysThrAsnPheValThrLysTrpTyr 1465
QY 286 AATAAAAACTAAGATCTGCCGAATTCATCTATGGCGTTGCCAGGGAGCAATAC 345
Db 1466 AsnLysAlaAspGlyThrCysAsnArgPheHisTyrGlyGlyCysGlnGlyThrAsnAsn 1485

QY 346 AACITCCAACTGAGCTATCTGCTGGTCCACCTCCAAAATATAC 390
Db 1486 ArgPheAspAsnGluGlnCysLysAlaAlaCysGlnAsnHis 1500

RESULT 46
A:Status: preliminary
A:Cross-references: UNIPROT:Q29100; GB:U14282; NID:G682652; PIDN:AAA62425.1; PID:G682653
A:Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Arg
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:38-88/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
Pred. No.: 4.05e-06 Length: 122
Score: 145.00 Matches: 24
Percent Similarity: 56.86% Conservative: 5
Best Local Similarity: 47.06% Mismatches: 22
Query Match: 18.98% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x A55115 (1-122)

QY 229 TGCAGTATGCCACAGGAGCTGCCCTGCTGCCTCCATACACACTGGGTGATCAAT 288
Db 38 CysArgGluProGlyProTyrThrGlyProCysSerAlaHisPheValArgTyrPheTyrAsn 57
QY 289 AAAAAAACTAAGATCTGCCGAATTCATCTATGGCGTTGCCAGGGAGCAATACAC 348
Db 58 AlaThrThrGlyLeuCysGlnSerPheValTyrGlyCysArgGlyLysGlnAsnAsn 77

QY 349 TTCCAACTGAAGCTATCTGCTGGTCCACTGC 381
Db 78 PheMetAspGluLysGluCysLeuHisThrCys 88

RESULT 47
T34212
hypotheical protein F10E7.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34212

R:Pauley, A.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F10E7.
A:Reference number: 221489
A:Accession: T34212

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-805 <PAU>
A:Cross-references: UNIPROT:Q19305; EMBL:U41264; PIDN:AAA82427.1; CESP:F10E7.4
C:Genetics:
A:Gene: CESP:F10E7.4
A:Introns: 9/1; 34/3; 57/1; 90/3; 128/3; 162/1; 205/1; 285/2; 417/1; 475/1; 606/1; 745/1

Alignment Scores:
Pred. No.: 3.6e-06 Length: 805
Score: 145.00 Matches: 27
Percent Similarity: 50.57% Conservative: 17
Best Local Similarity: 31.03% Mismatches: 29
Query Match: 18.98% Indels: 14
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x T34212 (1-805)

QY 124 GTGGAGNAATAGACCAGTGTACCAAAACCAGAGATTGCCCGAGAAAACATGAAGTGTTC 183
Db 585 LeuGlnGluLysAspThrCysVal-----MetGlnSerCys 596

QY 184 CGGTTCCGCCCTGGAGAAAGAAATGTTAGACTTCAGA---AAGGATATATGTCAGTATGCCA 240
Db 597 -----ArgArgPheIleGluIleAsnSerGluGluIleCysGlnGluAsp 611

QY 241 CAGGAGCTGGCCCTGCTGCCTCCATACACACTGGTGTACATAATAAAAACTAAG 300
Db 612 LysGlnAlaGlyGlnCysAlaGlyAsnPheProArgTyrTrpTyrAsnHisGluLysThr 631

QY 301 ATCTGCTCCGAATTCATCTATGGCGTTGCCAGGGAGCAATACAACTTCCAACTGAA 360
Db 632 GlnCysGluArgPheIlePheThrGlyCysGlyAsnArgAsnGlnPheGluThrGlu 651

QY 361 GCTATCTGCTGGTCCACTGC 381
Db 652 GluGluCysLysGlnIleCys 658

RESULT 48

B59399
short epsilon-dendrotoxin His55, subunit - Dendroaspis angusticeps

C:Species: Dendroaspis angusticeps
C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004
C:Accession: B59399
R:Sigle, R.; Hackett, M.; Aird, S.D.
Toxinon 40, 297-308, 2002
A:Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis
A:Reference number: A59399
A:Accession: B59399

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-57 <AIR>
A:Cross-references: UNIPROT:Q7L2E3
A:Note: trypsin inhibitor; K+ channel antagonist
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor
F:5-55/Disulfide bonds: #status experimental
F:14-38/Disulfide bonds: #status experimental
F:30-51/Disulfide bonds: #status experimental

Alignment Scores:
Pred. No.: 5.32e-06 Length: 57
Score: 144.00 Matches: 26
Percent Similarity: 57.41% Conservative: 5
Best Local Similarity: 48.15% Mismatches: 23
Query Match: 18.85% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x B59399 (1-57)

QY 220 AGGATATATGAGTATGCCAGAGGCTGCCCTGCTGCCTCCATACACACTGG 279
Db 2 ArgThrPheCysLysLeuProAlaGluProGlyProCysLysAlaSerIleProAlaPhe 21

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2005, 16:50:21 ; Search time 87 Seconds

(without alignments)

4661.686 Million cell updates/sec

Title: US-10-807-204-11

Perfect score: 764

Sequence: 1 atgggactctcaggacttct.....cctgcacaaaataaccattaa 396

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Command line parameters:

-MODE=frame_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10807204/runat_20092005_162900_29226/app_query.fasta_1.583
-DB=UniProt_03 -QFMT=fastan -SUFFIX=std.rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=50
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10807204 @CGN 1 1 101 @runat 20092005 162900 29226 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	693	90.7	131	1 WFD6 HUMAN	Q9by66 homo sapien
2	514	67.3	137	2 Q9BDL0	Q9bd10 oryctolagus
3	455	59.6	133	1 EPPI HUMAN	Q95925 homo sapien
4	455	59.6	143	2 Q86TF9	Q86tp9 homo sapien
5	450	58.9	182	2 Q8IE19	Q6ie19 rattus norv
6	449	58.8	133	2 Q8H245	Q8hz45 papio papio
7	441	57.7	133	1 EPPI MACMU	Q9bd11 macaca mula
8	386	50.5	134	1 EPPI MOUSE	Q9da01 mus musculus
9	219	28.7	77	2 Q8H244	Q8hz44 papio hamad
10	205	26.8	241	1 WFD8 HUMAN	Q8iuu0 homo sapien
11	189.5	24.8	759	2 Q8IT91	Q8it91 ancylostoma
12	186	24.3	110	1 IBP CARCR	P00993 caretta car
13	185.5	24.3	988	2 Q22865	Q22865 caenorhabdi
14	182	23.8	2419	2 Q7PXZ1	Q7pxz1 anopheles g
15	181	23.7	2772	2 Q9AV4	Q9av4 drosophila
16	181	23.7	2776	2 Q869A0	Q869a0 drosophila

17	181	23.7	2894	2 Q7KRX2	Q7krx2 drosophila
18	181	23.7	2898	2 Q868Z9	Q868z9 drosophila
19	180.5	23.6	571	2 Q7TQN3	Q7tqn3 mus musculus
20	174.5	22.8	342	2 Q6P2V8	Q6p2v8 xenopus tro
21	174.5	22.8	342	2 Q7S246	Q7sz46 xenopus lae
22	174	22.8	515	2 Q6DRJ1	Q6drj1 brachydanio
23	173.5	22.7	1599	2 Q99983	Q99983 caenorhabdi
24	173	22.6	587	2 Q6AX20	Q6ax20 xenopus lae
25	173	22.6	751	2 Q708Z0	Q708z0 xenopus lae
26	172.5	22.6	750	2 Q6DJB6	Q6djbe xenopus tro
27	172	22.5	67	1 IBPC BOVIN	P00976 bos taurus
28	171.5	22.4	576	2 Q8TEU8	Q8teu8 homo sapien
29	171.5	22.4	576	2 Q6UXZ9	Q6uxz9 homo sapien
30	171	22.4	1416	1 YN81 CABEL	Q03610 caenorhabdi
31	170	22.3	83	2 Q6ITB9	Q6itb9 pseudochis
32	170	22.3	516	2 Q7T363	Q7t363 brachydanio
33	169	22.1	83	2 Q6ITB5	Q6itb5 oxyuranus m
34	169	22.1	169	2 Q9N0X7	Q9n0x7 bos taurus
35	169	22.1	1297	2 Q9N343	Q9n343 caenorhabdi
36	168.5	22.1	750	2 Q708Y9	Q708y9 xenopus lae
37	168	22.0	86	2 Q9GP15	Q9gp15 ixodes ric
38	168	22.0	1743	2 Q9XW5	Q9xwx5 caenorhabdi
39	168	22.0	3198	2 Q9U8G8	Q9u8g8 manduca sex
40	167.5	21.9	342	2 P70004	P70004 xenopus lae
41	167.5	21.9	922	2 Q21418	Q21418 caenorhabdi
42	167.5	21.9	1474	2 Q62504	Q62504 caenorhabdi
43	167	21.9	80	2 Q8T3S7	Q8t3s7 araneus ven
44	167	21.9	83	2 Q6ITB4	Q6itb4 oxyuranus m
45	167	21.9	83	2 Q6ITB6	Q6itb6 oxyuranus s
46	167	21.9	90	2 Q6T6S5	Q6t6s5 bitis gabon
47	166	21.7	83	2 Q90WAL	Q90wal pseudonaja
48	166	21.7	122	1 BTIA BOOMI	P83609 boophilus m
49	166	21.7	507	2 Q6I750	Q6i750 rattus norv
50	165.5	21.7	337	1 AMBP_PIG	P04366 sus scrofa

ALIGNMENTS

RESULT 1

WFD6 HUMAN STANDARD; PRT; 131 AA.
ID Q9BY66; Q8NFV6;
AC Q9BY66; Q8NFV6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WAP four-disulfide core domain protein 6 precursor (Putative protease inhibitor WAP6).
DE inhibitor WAP6).
GN Name=WAP6; Synonyms=C20orf171, WAP6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RA Claus A., Lilja H., Lundwall A.;
RT "A locus on human chromosome 20 contains several genes expressing protease inhibitor domains with homology to whey acidic protein."; Biochem. J. 368:233-242(2002).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,


```

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Mareh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RT Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BQV6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9BQV6-2; Sequence=VSP_007550; VSP_007551;
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels
CC are found in epididymis, testis and trachea.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF411861; AA030684.1; -.
DR EMBL; AL031663; CAC36264.1; -.
DR HSSP; P02760; 1B1K.
DR Genew; HGNC:16164; WFDG6.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; FALSE_NEG.
DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Alternative splicing: Serine protease inhibitor; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 131 WAP four-disulfide core domain protein 6.
FT DOMAIN 31 69 WAP.
FT DOMAIN 70 128 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT VARSPLIC 75 86 IYVCHRRRLAFA -> VSLTYLHKEELE (in isoform
FT 2).
FT FTId=VSP_007550.
FT VARSPPLIC 87 131 Missing (in isoform 2).
FT FTId=VSP_007551.
SQ SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;

```

Alignment Scores:

```

Pred. No.: 1.28e-61 Length: 131
Score: 693.00 Matches: 129
Percent Similarity: 97.73% Conservative: 0
Best Local Similarity: 97.73% Mismatches: 2
Query Match: 90.71% Indels: 2
DB: 1 Gaps: 0

```

```

US-10-807-204-11 (1-396) x WFD6_HUMAN (1-131)
QY 1 ATGGAGCTCTCAGGACTCTGCGCAATCTGGTACCATTCCTCTTTGGGGGACATCCAG 60
Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuGlyAspIleGln 20
QY 61 GAACCTGGGACGCTGAAGGCGATCCTTGGCAAGCGGTGTCCCAAAATCAAAGTGGAAATGC 120
Db 21 GluProGlyHisAlaGluGlyIleLeuGlySerProIleLeuValGluCys 40
QY 121 GAAGTGAAGAAATAGACCACTGTACCAACCCAGAGATTGCCAGAAACATCAAGTGT 180
Db 41 GluValGluIleAspGlnCysThrLysProArgAspCysProGluAenMetLysCys 60
QY 181 TGGCCGTTTACCGCTGGAAGAAATGTTAGACTTTCAGAAAGGATATATGCAAGTATGCCA 240
Db 61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLys-IleTyrAlaValCysHi 80
QY 241 CAGGAGGCTGGCCCTCGCTGGCTCCATACCACTGGTGGTACCAAT-AAAAAACTAA 299
Db 80 sArgArgLeuAlaProAlaIleProProTyrHisThrGlyGlyThrIleLysLysThrLy 100
QY 300 GATCTGCTCCGAATTCATCTATCGCGTTGCCAGGGGAAACAATAACAACTTCCAAACTGA 359
Db 100 sIleCysSerGluPheIleTyrGlyGlySerGlnGlyAsnAsnAenPheGlnThrGl 120
QY 360 AGCTATCTGTCTGCTGCTGCAACCAAAATACCAT 393
Db 120 uAlaIleCysLeuValThrCysLysLysTyrHis 131
RESULT 2
Q9BDL0 PRELIMINARY; PRT; 137 AA.
AC Q9BDL0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Silvasammugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of mouse Eppin and a gene cluster of similar
RL Gene 312:125-134(2003).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF346415; AA31337.1; -.
DR HSSP; Q16019; 1AAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;

```

Alignment Scores:

```

Pred. No.: 2.09e-43 Length: 137
Score: 514.00 Matches: 90
Percent Similarity: 81.25% Conservative: 14

```



```
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PFam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02779; BPTI_KUNITZ_2; 1.
KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 21
FT CHAIN 22 133
FT DOMAIN 29 73
FT DOMAIN 77 127
FT DISULFID 33 61
FT DISULFID 40 65
FT DISULFID 48 60
FT DISULFID 54 69
FT DISULFID 77 127
FT DISULFID 86 110
FT DISULFID 102 123
FT VARSPLIC 1 31
SQ SEQUENCE 133 AA; 15284 MW; F7831B20336D9DC CRC64;

Alignment Scores:
Pred. No.: 2.09e-37 Length: 133
Score: 455.00 Matches: 77
Percent Similarity: 74.22% Conservative: 18
Best Local Similarity: 60.16% Mismatches: 33
Query Match: 59.55% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x EPPI_HUMAN (1-133)
Qy 1 ATGGGACTCTCAGGACTTCTGCCAATCTGTGACCATTCATCTTTTGGGGGACATCCAG 60
Db 1 MetGlySerGlyLeuThrPheLeuValLeuPheValLeuLeuAlaAsnValGln 20
Qy 61 GAACCTGGGACGCTGAAGGATCTCTGGCAAGCGTGTCCCAAAATCAAAAGTGAATGC 120
Db 21 GlyProGlyLeuThrPheLeuPheProArgCysProLysIleArgGluGluCys 40
Qy 121 GAAGTGGAGAAATAGACCATGTACCAACCCAGAGATTGCCCGAAGAAACATGAAGTGT 180
Db 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60
Qy 181 TGCCGCTTCAGCCGCGGAGAAAGAAATGTTTAGACTTCAGAAAGGATATATGAGTATGCCA 240
Db 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
Qy 241 CAGGAGGCTGCCCTGCTGCTGCCCTCCATATACACACTGGTGGTACAAATAAAAACTAAG 300
Db 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpTyrAspLysLysAspAsn 100
Qy 301 ATCTGCTCCGAATTCATCTATGCGGCTGGCAGGGGAAACAATAACAATCTTCCAACTGAA 360
Db 101 ThrCysSerMetPheValTyrGlyCysGlnGlyAsnAsnAsnAsnAsnAsnAsn 120
Qy 361 GCTATCTGCTGGTCACTGCAAA 384
Db 121 AlaAsnCysLeuAsnThrCysLys 128

RESULT 4
ID Q86TP9 PRELIMINARY; PRT; 143 AA.
AC Q86TP9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SPINLW1 protein (Fragment).

GN Name=SPINLW1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins L., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH44829.1; -.
DR HSSP; P00974; 1UUA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02779; BPTI_KUNITZ_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;

Alignment Scores:
Pred. No.: 2.1e-37 Length: 143
Score: 455.00 Matches: 77
Percent Similarity: 74.22% Conservative: 18
Best Local Similarity: 60.16% Mismatches: 33
Query Match: 59.55% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q86TP9 (1-143)
Qy 1 ATGGGACTCTCAGGACTTCTGCCAATCTGTGACCATTCATCTTTTGGGGGACATCCAG 60
Db 11 MetGlySerGlyLeuLeuSerLeuValLeuPheValLeuAlaAsnValGln 30
Qy 61 GAACCTGGGACGCTGAAGGATCTCTGGCAAGCGTGTCCCAAAATCAAAAGTGAATGC 120
Db 31 GlyProGlyLeuThrAspTrpLeuPheProArgCysProLysIleArgGluGluCys 50
Qy 121 GAAGTGGAGAAATAGACCATGTACCAACCCAGAGATTGCCCGAAGAAACATGAAGTGT 180
Db 121 GAAGTGGAGAAATAGACCATGTACCAACCCAGAGATTGCCCGAAGAAACATGAAGTGT 180
```


Db	51	GlupheGlnGluArgAspValCysThrIysAsnArgGlnCysGlnAspAsnIysLysCys	70
Qy	181	TGCCCGTTTCAGCCGTGGAAAGAAATGTTTACAGTTCAGAAAGAGTATATGACGATATGCCA	240
Db	71	CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro	90
Qy	241	CAGGAGGCTGGCCCTGGCTCCATACCACTGGTGGTACAAATAAAAAAACAATGAA	300
Db	91	LysGluThrGlyProCysLeuAlaIatyrPheLeuHisItrpItyrAspLysIysAspAsn	110
Qy	301	ATCTGCTCCGAATTCATCTATGGGGGTTTGCAGCGGGAACAATAACAACTTCACAACTGAA	360
Db	111	ThrCysSerMetPheValtyrGlyGlyCysGlnGlyAsnAsnAsnAsnAsnAsnAsnAsn	130
Qy	361	GCTATCTGTCTGGTCACCTGCAGAA	384
Db	131	AlaAsnCysLeuAsnThrCysLys	138
RESULT 5			
Q6IE19 PRELIMINARY; PRT; 182 AA.			
ID	Q6IE19	PRELIMINARY; PRT; 182 AA.	
AC	Q6IE19;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	WAP four-disulfide core 6-like 1.		
GN	Name=wfdc61;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley;		
RX	PubMed=15060002; DOI=10.1101/gr.1946304;		
RA	Puente X.S., Lopez-Otin C.;		
RL	"A genomic analysis of rat proteases and protease inhibitors.";		
RT	Genome Res. 14:609-622(2004)		
CC	-1- SIMILARITY: Contains 1 BPT/Kunitz inhibitor domain.		
CC	-1- MISCELLANEOUS: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBJ third party annotation (TPA) entry.		
DR	EMBL; BN000374; CAE51900.1; -.		
DR	HSP; P00974; 1K6U		
DR	GO; GO:0004867; F.serine-type endopeptidase inhibitor activity; IEA.		
DR	InterPro; IPR002293; Prot_Inh_Kunz-m.		
DR	InterPro; IPR008197; WAP.		
DR	Pfam; PF00014; Kunitz BPTI; 1.		
DR	Pfam; PF00095; WAP; 1.		
DR	PRINTS; PR00003; 4DISULPHCORE.		
DR	PRINTS; PR00759; BASICPTASE.		
DR	ProDom; PD000222; Prot_Inh_Kunz-m; 1.		
DR	SMART; SM00131; KU; 1.		
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.		
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 1.		
SO	SEQUENCE 182 AA; 21018 MW; -EB12D7BFF756707E CRC64;		

Alignment Scores:		
Pred. No.:	6.91e-37	182
Score:	450.00	73
Percent Similarity:	73.23%	Conservative: 20
Best Local Similarity:	57.48%	Mismatches: 34
Query Match:	58.90%	Indels: 0
DB:	2	Gaps: 0
US-10-807-204-11	(1-396) x 061E19	(1-182)

QY	13	GGACTCTGCCAATCCTGGTACCATTCATCCTTTTGGGGGACATCCAGAGAACTCTGGGCAC	72
Db	5	GlyLeuLeuProPheLeuValProLeuIlePheLeuTrpSerIleGlnLysProGlnLeu	24
QY	73	GCTGAAGGCATCCTTTGGCAAGCCGTGTCCCAAAATCAAAGTGGATGCCAAGTGGAAAGAA	132
Db	25	ThrGluGlyLeuPhePheLysThrCysProLysTyrLysIleLysCysAspPheGluGlu	44

Qy	133	ATAGACCAAGTGTACCAAAACCACGAGATGTCGCCAGAAAACATGAAGTGTGTCGCCGCTTCAGC	192
Db	45	ArgSerGlnCysSerArgHisGlnCysProGluLysGlnCysProGluLysArgCysMetPheAla	64
Qy	193	CGTGAAGAAGAAATGTTTAGACTTCAGAAAAGATATATGCAAGTATGCCACAGAGAGCGTGGC	252
Db	65	CysGlyLysLysCysLeuAsnGluAspIleCysSerLeuProGlnAspAlaGly	84
Qy	253	CCCTCGCTGGCTGCATACCAACACTGGTGTGTACATATAAAAACTAAGATCTGCTCCGAA	312
Db	85	ProCysLeuAlaItyrLeuProArgTrpTrpTyrAsnLysLysThrAsnLeuCysThrGln	104
Qy	313	TTTCATCTATGCGGTTCGACGGGAAACAATAACAACCTTCGAAAGCTATCTCTCTCTG	372
Db	105	PheIleItyrGlyGlyCysGlnGlyAsnThrAsnAsnPheLeuSerLysAspIleCysThr	124
Qy	373	GTCACTGCATAAAATATCCAT	393
Db	125	SerIleCysThrArgLysHis	131

RESULT 6

ID	Q8HZ45	PRELIMINARY;	PRT; 133 AA.
AC	Q8HZ45;		
DT	01-MAR-2003	(TREMBLrel. 23, Created)	
DT	01-WAR-2003	(TREMBLrel. 23, Last sequence update)	
DT	01-WAR-2004	(TREMBLrel. 26, Last annotation update)	
DE	Epididymal protease inhibitor 1.		
GN	Name:Eppin;		
OS	Papio papio (Guinea baboon).		
OC	Eukaryota; Metazoa; Chordata;		
OC	Mammalia; Eutheria; Primates;		
OC	Cercopitheciinae; Papio.		
OX	NCBI_TaxID=100937;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	TISSUE=Testis;		
RC	Sivaathanugam P., O'Rand M.G., Richardson R.T.;		
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.		
CC	- - SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.		
EMBL:	AV141973; AAN08507.1; -.		
DR	HSP; P00974; LUUA.		
DR	GO; CO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.		
DR	InterPro; IPR002223; Prot_Inh_Kunzm-m.		
DR	InterPro; IPR008197; WAP-		
DR	Pfam; PF00014; Kunitz_BPTI.		
DR	Pfam; PF00095; WAP; 1.		
DR	PRINTS; PR00759; BASICPTASE.		
DR	PRODom; PD000222; Prot_Inh_Kunzm-m; 1.		
DR	SMART; SM00131; KU; 1.		
DR	SMART; SM00217; WAP; 1.		
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.		
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 1.		
KW	Protease.		
SV	SEQUENCE 133 AA; 15277 MW; B33ABE57ECBBB84 CRC64;		

Alignment Scores:	
Pred. NO.:	8.54e-37
Score:	449.00
Percent Similarity:	71.88%
Best Local Similarity:	60.16%
Query Match:	58.77%
DB:	2
Gaps:	0
Indels:	0
Mismatches:	36
Conservative:	15
Matches:	77
Length:	133

US-10-807-204-11 (1-396) X O8HZ45 (1-133)

[illegible]


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Db      21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProThrIleArgGluCys 40
      |||||      : : :      : : :      |||||      ||| : : |||||
Qy      121 GAAGTGGAGAAATAGACAGGTGTACCAAAACCCAGAGATTGCCAGAAAACATGAAGTGT 180
      |||      |||      ||| : : : |||      ||| : : |||||
Db      41 GluPheArgGluArgAspValCysThrArgHisArgGlnCysProAspAsnLysLysCys 60
      |||      |||      ||| : : : |||      ||| : : |||||
Qy      181 TGCCCGTTCCAGCGTGGGAAGAAATGTTAGACTTCAGAAAGGATATATGAGTATGCCA 240
      |||      |||      ||| : : : |||      ||| : : |||||
Db      61 CysValPheSerCysGlyLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
      |||      |||      ||| : : : |||      ||| : : |||||
Qy      241 CAGGAGGCTGCCCTCGCTGCCCTCCATACCACACTGGTGTACCAATAAAAAAACTAAG 300
      |||      |||      ||| : : : |||      ||| : : |||||
Db      81 AsnGluThrGlyProCysLeuAlaPhePheIleArgTrpTrpTrpAspLysLysAsnAsn 100
      |||      |||      ||| : : : |||      ||| : : |||||
Qy      301 ATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAAACAATAACAATCTCCAACTGAA 360
      |||      |||      ||| : : : |||      ||| : : |||||
Db      101 ThrCysSerThrPheValTyrGlyGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerGlu 120
      |||      |||      ||| : : : |||      ||| : : |||||
Qy      361 GCTATCTGCTGCTGGTGCCTGCAAA 384
      |||      |||      ||| : : : |||      ||| : : |||||
Db      121 AlaAsnCysLeuAsnThrCysLys 128
      |||      |||      ||| : : : |||      ||| : : |||||

RESULT 7
EPPI_MACMU
ID EPPI_MACMU STANDARD; PRT; 133 AA.
AC Q9BDL1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=SPINLW1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF346414; AAK31336.1; -.
DR HSSP; P00974; 1BPTI.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.

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FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 133 AA; 15279 MW; 433AB946E39A35B9 CRC64;

Alignment Scores:
Pred. No.: 5.56e-36 Length: 133
Score: 441.00 Matches: 76
Percent Similarity: 71.88% Conservative: 16
Best Local Similarity: 59.38% Mismatches: 36
Query Match: 57.72% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x EPPI_MACMU (1-133)
Qy 1 ATGGGACTCTCAGGACTTCTGCCAATCTCGTACCATCTCTTTGGGGACATCCAG 60
      |||||      |||||      |||||      |||||      |||||      |||||
Db 1 MetGlySerSerGlyLeuLeuSerLeuValLeuPheIleLeuValAsnValGln 20
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 61 GAACCTGGGCAGCTGAAGCATCTTGGCAAGCCGTGTCGCAAAATCAAAGTGAATGC 120
      |||||      |||||      |||||      |||||      |||||      |||||
Db 21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProThrIleArgGluCys 40
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 121 GAAGTGGAGAAATAGACAGGTGTACCAAAACCCAGAGATTGCCAGAAAACATGAAGTGT 180
      |||||      |||||      |||||      |||||      |||||      |||||
Db 41 GluPheArgGluArgAspValCysThrArgHisArgGlnCysProAspAsnLysLysCys 60
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 181 TGCCCGTTCCAGCGTGGGAAGAAATGTTAGACTTCAGAAAGGATATATGAGTATGCCA 240
      |||||      |||||      |||||      |||||      |||||      |||||
Db 61 CysValPheSerCysGlyLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 241 CAGGAGGCTGCCCTCGCTGCCCTCCATACCACACTGGTGTACCAATAAAAAAACTAAG 300
      |||||      |||||      |||||      |||||      |||||      |||||
Db 81 AsnGluThrGlyProCysLeuAlaPhePheIleArgTrpTrpTrpAspLysLysAsnAsn 100
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 301 ATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAAACAATAACAATCTCCAACTGAA 360
      |||||      |||||      |||||      |||||      |||||      |||||
Db 101 ThrCysSerThrPheValHisGlyGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerGlu 120
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 361 GCTATCTGCTGCTGCCTGCAAA 384
      |||||      |||||      |||||      |||||      |||||      |||||
Db 121 AlaAsnCysLeuAsnThrCysLys 128
      |||||      |||||      |||||      |||||      |||||      |||||

RESULT 8
EPPI_MOUSE
ID EPPI_MOUSE STANDARD; PRT; 134 AA.
AC Q9DA01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=Spinlwi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]

```


RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nitaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Bataulda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -|- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -|- TISSUE SPECIFICITY: Expressed in epididymis and testis.
 CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -|- SIMILARITY: Contains 1 WAP-type domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AF346413; AK31335.1; -
 CC EMBL; AK006296; BAB24514.1; -
 CC EMBL; BC048637; AAF48637.1; -
 CC HSP; P31713; 1SHP.

DR MGD; MGI:1922776; Spinlwl.
 DR GO; GO:0001689; C:cytosol; IDA.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR InterPro; IPR008197; WAP.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF00095; WAP; 1.
 DR PRINTS; PR00003; 4DISULPHORE.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRODom; PD00222; Prot_Inh_Kunz-m; 1.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 134 Eppin.
 FT DOMAIN 29 73 WAP.
 FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
 FT DISULFID 33 61 By similarity.
 FT DISULFID 40 65 By similarity.
 FT DISULFID 48 60 By similarity.
 FT DISULFID 54 69 By similarity.
 FT DISULFID 77 127 By similarity.
 FT DISULFID 86 110 By similarity.
 FT DISULFID 102 123 By similarity.
 SQ SEQUENCE 134 AA; 15470 MW; DFE63D4D4C427F CRC64;
 Alignment Scores:
 Pred. No.: 2,19e-30 Length: 134
 Score: 386.00 Matches: 66
 Percent Similarity: 70.54% Conservative: 25
 Best Local Similarity: 51.16% Mismatches: 38
 Query Match: 50.52% Indels: 0
 DB: 1 Gaps: 0
 US-10-807-204-11 (1-396) x BPPI_MOUSE (1-134)
 QY 1 ATGGGACTCTCAGGACTTCTGCGCAATCTGTCATCTTCTGCGGACATCCAG 60
 DB 1 MetLysLeuSerGlyPheValSerLeuValLeuPheGlyLeuLeuAlaArgValGln 20
 QY 61 GAACCTGGCGCAGCTGAAGGATCTCTGCGAAGCGCTGCCAATCAAGTGAATGC 120
 DB 21 GlyProSerLeuAlaAspLeuLeuPheProArgCysPheArgGluGluCys 40
 QY 121 GAAGTGGAGAAATAGACAGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
 DB 41 GluHisGlnGluArgAspLeuCysThrArgAspArgAspCysProLysLysGluLysCys 60
 QY 181 TGCCCGTTTCAGCCGTGGAAAGAAATGTTTAGACTTCAGAAAGGATATATGCAATGCCA 240
 DB 61 CysValPheAsnGlyLysLysCysLeuAsnProGlnGlnAspIleCysSerLeuPro 80
 QY 241 CAGGAGGCTGCCCTGCTGCCCTCCATACCACTGGTGTACATAAATAAAACTAAG 300
 DB 81 LysAspSerGlyTyrCysMetAlaTyrPheArgArgTrpPheAsnLysGluAsnSer 100
 QY 301 ATCTGCTCCGAATTCATCTATGCGCGTGGCCAGGGAACAATAACAACCTTCCAACTGAA 360
 DB 101 ThrCysGlnValPheIleTyrGlyCysGlnGlyAsnAsnAsnAsnAsnPheGlnSerGln 120
 QY 361 GCTATCTGTGTGTCACCTGCAAAATA 387
 DB 121 SerIleCysGlnAsnAlaCysGluLys 129
 RESULT 9
 Q8H244 PRELIMINARY; PRT; 77 AA.
 AC Q8H244;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Epididymal protease inhibitor 2.

GN Name=Eppin;
OS Papi hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis; O'Rand M.G., Richardson R.T.;
RA Sivashanmugam P., to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY141975; AAN08509.1; -
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
KW Protease.
SQ SEQUENCE 77 AA; 8787 MW; B86E5868C57CEBD0 CRC64;

Alignment Scores:
Pred. No.: 2.05e-13 Length: 77
Score: 219.00 Matches: 40
Percent Similarity: 68.92% Conservative: 11
Best Local Similarity: 54.05% Mismatches: 23
Query Match: 28.66% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q8HZ44 (1-77)
Qy 1 ATGGACTCTCAGGACTTCTGCAATCTGCTGATTCATCTCTTTGGGGACATCCAG 60
Db 1 MetGlySerSerGlyLeuLeuSerLeuValLeuPheLeuLeuAlaAsnValGln 20
Qy 61 GAACCTGGGACGCTGAGGACATCTCTGGCAAGCGGTGCTCCAAATCAAAAGTGAATGC 120
Db 21 GlyProGlyLeuThrArgPheProArgCysProThrIleArgGluGluCys 40
Qy 121 GAATGGAGAAATAGACCATGCTACCAACCCAGAGTTCGCCAGAAAACATGAAGTGT 180
Db 41 GluPheArgGluArgPheValCysThrArgHisArgGlnCysProAspAsnLysLysCys 60
Qy 181 TGCCCGTTCAGCGCTGGAAAGAAATGTTTAGACTTCAGAAAG 222
Db 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGln 74

RESULT 10
WFD8 HUMAN
ID WFD8 HUMAN STANDARD; PRT; 241 AA.
AC O8TUÅO; O96A34;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WAP four-disulfide core domain protein 8 precursor (Putative protease inhibitor WAP8).
GN Name=WFD8; Synonyms=C20orf170, WAP8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RX Claus A., Lilja H., Lundwall A.;
RT "A locus on human chromosome 20 contains several genes expressing protease inhibitor domains with homology to whey acidic protein.";
RL Biochem. J. 368:233-242(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Coley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dharm P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulten J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Expressed ubiquitously, the highest levels are found in the epididymis followed by testis and trachea.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 3 WAP-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AF492015; AAN70997.1; -
CC EMBL; AF492016; AAN70998.1; -
CC EMBL; AL031663; CAB37634.2; -
CC EMBL; AL591715; CAB39449.1; -
CC HSP; P31713; 1SHF.
CC Genew; HGNC:16163; WFDC8.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 3.
CC PRINTS; PR00003; 4DISULPHCORE.
CC PRINTS; PR00759; BASICTPASE.
CC ProDom; PD000222; Prot_Inh_Kunz-m; 1.
CC SMART; SM00131; KU; 1.
CC SMART; SM00317; WAP; 3.
CC PROSITE; PS00317; 4 DISULFIDE CORE; 3.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE; PS0279; BPTI_KUNITZ_2; 1.
CC Repeat; Serine protease inhibitor; Signal.
KW SIGNAL 1 38 Potential.
FT CHAIN 39 241 WAP four-disulfide core domain protein 8.
FT DOMAIN 47 90 WAP 1.
FT DOMAIN 95 145 BPTI/Kunitz inhibitor.
FT DOMAIN 150 193 WAP 2.
FT DOMAIN 197 239 WAP 3.
FT DISULFID 51 79 By similarity.
FT DISULFID 58 83 By similarity.
FT DISULFID 66 78 By similarity.
FT DISULFID 95 145 By similarity.
FT DISULFID 104 128 By similarity.
FT DISULFID 120 141 By similarity.
FT DISULFID 72 87 By similarity.
FT DISULFID 154 182 By similarity.
FT DISULFID 165 186 By similarity.
FT DISULFID 169 181 By similarity.


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FT DISULFID 175 190 By similarity.
FT DISULFID 201 229 By similarity.
FT DISULFID 208 232 By similarity.
FT DISULFID 216 228 By similarity.
FT DISULFID 222 236 By similarity.
SQ SEQUENCE 241 AA; 27797 MW; 2566B54AF4BDC57B CRC64;

Alignment Scores:
Pred. No.: 5,91e-12 Length: 241
Score: 205.00 Matches: 39
Percent Similarity: 50.00% Conservative: 13
Best Local Similarity: 27.50% Mismatches: 48
Query Match: 26.83% Indels: 4
DB: 1 Gaps: 1

US-10-807-204-11 (1-396) x WFD8_HUMAN (1-241)
QY 70 CAGCGTGAAGGATCTTGGCAGCGGTGCCAAATCAAGTGAATGCGAAGTGGAA 129
Db 46 HSLysProGlyLeu-----CysProLysGluArgLeuThrCysThrThrGlu 61
QY 130 GAAATAGACCACTGTACCAACCCAGAGATTCGCCAGAAACATGAAGTGTTCGCCCGTTC 189
Db 62 LeuProAspSerCysAsnThrAspPheAspCysLysGluTyrGlnLysCysCysPhePhe 81
QY 190 AGCCGTGGAAGAAATGTTTAGACTTCAGAAAGGATATATGAGTATGCCACAGGAGGCT 249
Db 82 AlaCysGlnLysCysMetAspProPheGlnGluProCysMetLeuProValArgHis 101
QY 250 GGCCTCGCTGCTCCATACACACACACACACACACACACACACACACACACACACAC 309
Db 102 GlyAsnCysAsnHisGluAlaGlnArgTrpHisPheAspPheLysAsnTyrArgCysThr 121
QY 310 GAATTCATCTATGGGTGGTGGCAGGGGACAAATACAACTTCCAACTGAAGCTATCTGT 369
Db 122 ProPheLysTyrArgGlyCysGluGlyAsnAlaAsnAsnPheLeuSerGluAspAlaCys 141
QY 370 CTGGTCACCTCT 381
Db 142 ArgThrAlaCys 145

RESULT 11
Q8IT91 PRELIMINARY; PRT; 759 AA.
AC Q8IT91:
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kunitz-like protease inhibitor precursor.
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Baltimore;
RX MEDLINE=22645137; PubMed=12760667;
RA Hawdon J.M., Datu B., Crowell M.;
RT Inhibitor from the hookworm Ancylostoma caninum.;
RL J. Parasitol. 89:402-407(2003).
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF533590; AAN10061.1; -.
DR HSSP; P31713; ISHP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot Inh Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 12.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00131; KU; 12.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 12.
DR Protease; signal.
KW

FT SIGNAL 1 16 Potential.
SQ SEQUENCE 759 AA; 84886 MW; C431A3C3F418F40A CRC64;

Alignment Scores:
Pred. No.: 2,42e-10 Length: 759
Score: 189.50 Matches: 42
Percent Similarity: 40.71% Conservative: 15
Best Local Similarity: 30.00% Mismatches: 30
Query Match: 24.80% Indels: 53
DB: 2 Gaps: 4

US-10-807-204-11 (1-396) x Q8IT91 (1-759)
QY 127 GAAGAATAGACCACTGTACCAA-----CCAGAGATTGCCAGAA 168
Db 496 GluSerMetGluGluCysThrArgThrCysLysLysAlaValProGluProGluProGlu 515
QY 169 AACATGAAGTCTTGC---CCGTTTCAGCGCTGGA----- 198
Db 516 LysGluThrCysSerGlnProIleGluAlaGlyProCysLysAlaMetValArgArgPhe 535
QY 199 -----AAGAAATGTTTAGACTTC----- 216
Db 536 AlaTyrAspAsnAlaLysGluLysCysValGluPhePheTyrGlyGlyCysLysGlyAsn 555
QY 216 ----- 216
Db 556 LysAsnAsnPheGluThrMetGluAspCysThrPheThrCysGluGlnArgLeuAlaLys 575
QY 217 -----AGAAAGGATATATGCAATGATGCACAGGAGGTGGCCCTGCTGCCCTCC 267
Db 576 ProGluLeuGluLysAspValCysSerGlnProIleThrAlaGlyProCysArgAlaSer 595
QY 268 ATACCACACTGGTGTACATAAATAAACTAAGATCTGCTCCGAATTCATCTATGCCGT 327
Db 596 IleProArgTyrGlyTyrAspSerLysLysArgLysCysValLysPheThrTyrGlyGly 615
QY 328 TGCCAGGGGAACAATAACAACCTTCCAACTGAAGCTATCTGCTGGTCACCTGCCAAAAA 387
Db 616 CysLysGlyAsnGlyAsnArgPheProThrLysAsnGluCysGluLysThrCysLysArg 635

RESULT 12
IBP_CARCR STANDARD; PRT; 110 AA.
AC P00993;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chelonianin (Basic protease inhibitor) (RTPI).
OS Carretta caretta (loggerhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Chelonioidae; Chelonidae; Carretta.
OX NCBI_TaxID=8467;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg white;
RA Kato I., Tominaga N.;
RT "Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of
RT two tandem domains -- one Kunitz -- one of a new family.";
RL Fed. Proc. 38:832-832(1979).
CC -1- FUNCTION: The first domain inhibits trypsin; the second one
CC inhibits subtilisin.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -1- CAUTION: As the paper only indicates the species as "red sea
CC turtle", the species indicated here is therefore an inference.
DR PIR; A01224; TITTOR.
DR HSSP; P00974; 1K09.
DR InterPro; IPR002223; Prot Inh Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.

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NCBI_TaxID=180454;
[1]
RN
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008987; EAA01339.1; -.
DR HSP; F10646; IIRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00900; PLAC; 1.
DR PROSITE; PS00902; TSP1; 5.
FT NON_TER
SQ SEQUENCE 2419 AA; 260249 MW; 58078660983C946 CRC64;

Alignment Scores:
Pident. No.: 1 52e-09 Length: 2419
Score: 182.00 Matches: 39
Percent Similarity: 44.35% Conservatives: 12
Best Local Similarity: 33.91% Mismatches: 32
Query Match: 23.82% Indels: 32
DB: Gaps: 4

US-10-807-204-11 (1-396) x Q7PXZ1 (1-2419)
QY 136 GACCAAGTGTACCAACCCAGA----- 156
Db 1515 AspValCysHisLeuProLysIleSerGlyProCysThrGlyHisIleTyrAsnMetTrpTyr 1534
QY 157 ----GATTGCCCGAAGAACATGAAGTGTTCGCCGTTCCAGCCGTGGA----- 198
Db 1535 TyrAspAlaGluArgAsnMet---CysAlaGlnPheThrTyrGlyCysLeuGlyAsn 1553
QY 199 -----AAGAAATGCT-----TTAGACTTCAGAAAG 222
Db 1554 AlaAsnArgPheGluSerGlnGluCysLysAlaLeuCysSerValAspSerLys 1573
QY 223 GATATATGCAAGTATGCCACAGGAGGTGGCCCTGCCTGCCTCCATACACACTGGTGG 282
Db 1574 ProProCysGluGlnProMetGluAlaGlyProCysAsnGlyThrPheGluArgTrpTyr 1593
QY 283 TACAATAAATAAATAAGATCTCTCGAATTCATCTATGGCGGTGCCAGGGACACAT 342
Db 1594 TyrAspLysGluThrAspAlaCysHisProPheGlyGlyCysLysGlyAsnLys 1613
QY 343 AACAACTTCCAACTGAAGTATCTCTGTGGTCCACCTGCACAAATAA 387
Db 1614 AsnAsnTyrProThrGluAlaSerCysGlyTyrHisCysLysLys 1628

RESULT 15
Q9VAV4
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ID AC Q9VAV4 PRELIMINARY; PRT; 2772 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG33103-PB.
OS Name=fpn; ORFNames=CG33103;
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.B.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
RA Flossler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mirkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusakern D.J., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodagef, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2242065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
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DR PROSITE; PS50092; TSP1; 5.
KW Matrix protein.
SQ SEQUENCE 2776 AA; 299741 MW; 92D38A17360D2D42 CRC64;

Alignment Scores:
Pred. No.: 1.95e-09 Length: 2776
Score: 181.00 Matches: 36
Percent Similarity: 42.98% Conservativity: 13
Best Local Similarity: 21.58% Mismatches: 35
Query Match: 33.65% Indels: 30
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x Q869A0 (1-2776)
QY 136 GACCACTGTACCAAAACCAGG-----GATTGCCCCAGAAAACATGAAGTGTGCCCGC 186
Db 1788 AspArgCysAlaLeuProGlySerGlnThrGlyAspCysSerGluGlyLeuAlaLysTrpHis 1807
QY 187 TTCACCGCTGGA---AAGAAATGTTTACACTTC----- 216
Db 1808 PheSerGluSerGluGlyArgCysValProPheTyrTyrSerGlyCysGlyGlyAsnLys 1827
QY 217 -----AGAAAGCANT 225
Db 1828 AsnAsnPheProThrLeuGluSerCysGluAspHisCysProArgGlnValAlaLysAsp 1847
QY 226 ATATGCAGTATCCACAGAGAGCGTCCGCCCTCGCTCCATCCACACACTGGTGGTAC 285
Db 1848 IleCysGluIleProAlaGluValGlyGluCysAlaAsnTyrValThrSerTrpTyrTyr 1867
QY 286 AATAAANAACCTAAGATCTCCGAAATTCATCTATGGCGGTGGCCAGGGGAACAAATAAC 345
Db 1868 AspThrGlnAspGlnAlaCysArgGlnPheTyrTyrGlyGlyCysGlyGlyAsnGluAen 1887
QY 346 AACTTCCAAACTGAGACTATCTGTCTGTACCTGCACCAAAAAA 387
Db 1888 ArgPheProThrGluGluSerCysAlaLeuAlaArgCysAspArg 1901

RESULT 17
Q7KRX2 PRELIMINARY; PRT; 2894 AA.
AC Q7KRX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG33103-PA.
GN Name=Ppn; ORFNames=CG33103;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA LaRo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence."
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
CC EMBL: AE003765; AAF56795.3; -
DR HSP; P10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM_Spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR003599; Ig_Like.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
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DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODom; PR000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS09092; TSP1; 5.
DR PROSITE; PS00092; TSP1; 5.
SQ SEQUENCE 2894 AA; 312663 MW; A1BFE1BAD9B214BC CRC64;

Alignment Scores:
Pred. No.: 1.95e-09 Length: 2894
Score: 181.00 Matches: 36
Percent Similarity: 42.98% Conservative: 13
Best Local Similarity: 31.58% Mismatches: 35
Query Match: 23.69% Indels: 30
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x Q7KRX2 (1-2894)
Qy 136 GACCAGTGTACCAACCCAGA-----GATTGCCAGAAAACATGAAGTTGTGCCCG 186
Db 1788 AspArgCysAlaLeuProGlyGlnThrGlyAspCysSerGluLysLeuAlaLysTrpHis 1807
Qy 187 TTCAGCCGTGGA---AAGAAATGTTAGACTTC----- 216
Db 1808 PheSerGluSerGluLysArgCysValProPheTyrTyrSerGlyGlyAsnLys 1827
Qy 217 -----AGAAAGGAT 225
Db 1828 AsnAsnPheProThrLeuGluSerCysGluAspHisCysProArgGlnValAlaLysAsp 1847
Qy 226 ATATGCAGTATGCCACAGGAGGTGGCCCTCGCTCCATACACACTGGTGTGATC 285
Db 1848 IleCysGluIleProAlaGluValGlyGluCysAlaAsnTyrValThrSerTrpTyrTyr 1867
Qy 286 AATAAAAAAACTAAGATCTGCTCGAATTTCATCTATGTCGGTTCGACGGGGAACAATAAC 345
Db 1868 AspThrGlnAspGlnAlaCysArgGlnPheTyrTyrGlyGlyCysGlyGlyAsnGluAsn 1887
Qy 346 AACTTCCAAACTGAAGCTATCTGTCTGCTACCTGCACCAAAAAA 387
Db 1888 ArgPheProThrGluGluSerCysLeuAlaArgCysAspArg 1901

RESULT 18
Q86829 ID Q86829 PRELIMINARY; PRT; 2898 AA.
AC Q86829
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin 3.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=22552133; PubMed=12666201; DOI=10.1002/advdy.10265;
RA Kramerova I.A.; Kramerov A.A.; Fessler J.H.;
RT "Alternative splicing of papilin and the diversity of Drosophila
RL extracellular matrix during embryonic morphogenesis.";
RN Dev. Dyn. 226:634-642(2003).
[2]

RP SEQUENCE FROM N.A.
RA Kramerova I.; Fessler J.H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF529180; AAO84908.1; -.
DR HSSP; P12111; 1KTH.
DR FlyBase; FBgn0003137; Ppn.
DR GO; GO:0005604; C-basement membrane; IDA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODom; PD000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS09092; TSP1; 5.
DR PROSITE; PS00092; TSP1; 5.
KW Matrix protein.
SQ SEQUENCE 2898 AA; 313250 MW; 2F992742F2D64A00 CRC64;

Alignment Scores:
Pred. No.: 1.95e-09 Length: 2898
Score: 181.00 Matches: 36
Percent Similarity: 42.98% Conservative: 13
Best Local Similarity: 31.58% Mismatches: 35
Query Match: 23.69% Indels: 30
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x Q86829 (1-2898)
Qy 136 GACCAGTGTACCAACCCAGA-----GATTGCCAGAAAACATGAAGTTGTGCCCG 186
Db 1788 AspArgCysAlaLeuProGlyGlnThrGlyAspCysSerGluLysLeuAlaLysTrpHis 1807
Qy 187 TTCAGCCGTGGA---AAGAAATGTTAGACTTC----- 216
Db 1808 PheSerGluSerGluLysArgCysValProPheTyrTyrSerGlyGlyAsnLys 1827
Qy 217 -----AGAAAGGAT 225
Db 1828 AsnAsnPheProThrLeuGluSerCysGluAspHisCysProArgGlnValAlaLysAsp 1847
Qy 226 ATATGCAGTATGCCACAGGAGGTGGCCCTCGCTCCATACACACTGGTGTGATC 285
Db 1848 IleCysGluIleProAlaGluValGlyGluCysAlaAsnTyrValThrSerTrpTyrTyr 1867
Qy 286 AATAAAAAAACTAAGATCTGCTCGAATTTCATCTATGTCGGTTCGACGGGGAACAATAAC 345
Db 1868 AspThrGlnAspGlnAlaCysArgGlnPheTyrTyrGlyGlyCysGlyGlyAsnGluAsn 1887
Qy 346 AACTTCCAAACTGAAGCTATCTGTCTGCTACCTGCACCAAAAAA 387
Db 1888 ArgPheProThrGluGluSerCysLeuAlaArgCysAspArg 1901
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Db 1868 AspThrGlnAspGlnAlaCysArgGlnPheTyrtYrGlyGlyCysGlyGlyAsnGluAsn 1887
QY 346 AACTTCCAACTGAAGCTATCTGTCTGTGTACCTGCAAAAAA 387
Db 1888 ArgPheProThrGluGluSerCysLeuAlaArgCysAspArg 1901
RESULT 19
Q7QN3
ID Q7QN3 PRELIMINARY; PRT; 571 AA.
AC Q7QN3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth and differentiation factor-associated serum protein 1.
GN Name=Gasp1;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=22656519; PubMed=12595574; DOI=10.1210/me.2002-0366;
RA Hill J.J., Qiu Y., Hewick R.M., Wolfman N.M.;
RT "Regulation of myostatin in vivo by growth and differentiation factor-
associated serum protein-1: a novel protein with protease inhibitor
and follistatin domains";
RL Mol. Endocrinol. 17:1144-1154(2003).
CC -|- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY308804; AAP72503.1; -.
DR HSP; P00974; 1K09.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007179; P:transforming growth factor beta receptor si. . .; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot inh Kazal.
DR InterPro; IPR011497; Prot inh Kazal 2.
DR InterPro; IPR002223; Prot inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR ProDom; PD000222; Prot inh_Kunz-m; 2.
DR SMART; SM00408; ICG2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG-LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 571 AA; 63321 MW; B28B676B3DC71256 CRC64;

Alignment Scores:
Pred. No.: 1.95e-09 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 3 Gaps: 3

US-10-807-204-11 (1-396) x Q7QN3 (1-571)
QY 139 CAGTGATACCAACCC-----AGAGATTGCCAGAAAAACATG----- 174
Db 322 GluCysLeuYsProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
QY 175 -----AAGTGTCCCGTTTCAGCCGTGGGAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheHisCysHisAsnLeuAsn 361
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QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
Db 362 HisPheGluThrTyrtYrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGGAGGCTGCCCTGCTCCATACCACACTGTGTGTACAAATAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrtValProArgTrpAlaTyrtAsnSer 401
QY 292 AAAAATAAGATCTCTCCGAATTCATCTATGCGCGTGTGCCAGGGGAAACAATAACAATTC 351
Db 402 GlnThrGlyLeuCysGlnSerPheValtyrGlyGlyCysGluGlyAsnGlyAsnAsnBhe 421
QY 352 CAAACTGAAGCTATCTGTCTGTGTACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431
RESULT 20
Q6P2V8
ID Q6P2V8 PRELIMINARY; PRT; 342 AA.
AC Q6P2V8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC76314.
GN Name=MGC76314;
OS Xenopus tropicalis (western clawed frog) (Silurana tropicalis).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: Belongs to the lipocalin family.
CC -|- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; BC064278; AAH64278.1; -.
DR HSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002968; A1-microglobin.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR InterPro; IPR002223; Prot inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
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Db 182 AenAenGlyGluCysSerProGlyGluLeuGlu-----ValArgProArgArgThrGln 199
QY 160 -----TGCCACAGAA-----AACATGAAGTGTTCGCCGTTGAGCCGCT 195
Db 200 ArgAlaValLeuProGluGluGluCysSerGlyMetGluAenSerProPheSerIys 219
QY 196 GGAAGAATAATGTTAGATTCTCAGAAAGATATATGACATGATGCCACAGAGGCTGCCCC 255
Db 220 AenIys-----ValGluSerCysArgLeuAlaProAlaSerGlyPro 233
QY 256 TGCTGGCTCCATACACACATGCTGGTGTACATAAATAAAGCTAAGATGCTGCCGAATTC 315
Db 234 CysLeuGlyAenHisAenArgTyrPheTyrAenSerSerThrMetAlaCysGluThrPhe 253
QY 316 ATCTATGCGGCTGTCAGGGGAACTAATCAACTTCCAACTTGAAGTATCTGTCTGCTGTC 375
Db 254 GlnTyrGlyGlyCysLeuGlyAenAenAenAenPheHisSerGluIysLeuGln 273
QY 376 ACCTGCAAA 384
Db 274 ThrCysArg 276

RESULT 22
Q6DRJ1 PRELIMINARY; PRT; 515 AA.
AC Q6DRJ1;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Serine protease inhibitor HGFAI.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15256591; DOI=10.1073/pnas.0403929101;
RA Amsterdam A., Nissen R.M., Sun Z., Swindell B.C., Farrington S.,
RA Hopkins N.
RT "Identification of 315 genes essential for early zebrafish
development."
RL Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY648768; AAT68086.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002172; LDL receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR00601; PKD.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MANSC; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; Ldla; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00088; LDLRA_2; 1.
DR PROSITE; PS50093; PKD; 1.
KW Protease.
SQ SEQUENCE 515 AA; 57579 MW; AF948A7B0EB46DB4 CRC64;

Alignment Scores:
Pred. No.: 8.89e-09 Length: 515
Score: 174.00 Matches: 43
Percent Similarity: 38.51% Conservative: 19

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Best Local Similarity: 26.71% Mismatches: 57
Query Match: 22.77% Indels: 42
DB: 2 Gaps: 5

US-10-807-204-11 (1-396) x Q6DRJ1 (1-515)

QY 13 GGACTTCGCAATCCTGGTACCATTCATCTTTGGGGACATCCAGAA----- 63
Db 271 GlyCysValProAenArgAenAsnTyrLeuAlaLeuAenGluCysGlnSerAlaCysAen 290
QY 64 -----CCTGGCACGCTGAGAGGCATCTCTGGC--- 90
Db 291 LysValSerValSerAenIleGlySerProProProHisProSerGlyArgIleGlyPro 310
QY 91 -----AAGCCGTGTCCTCCAAAATCAAAAGTGAAGTCCGAATGCGAAGTG 126
Db 311 IleAspAlaValGluGlnCysAspArgProCysSerProGluHisPheThrCysAsp--- 329
QY 127 GNAGNAATAGACCACTGTACCAACCCAGAGAT-----TGCCAGAAAAACATGAAGTGT 180
Db 330 -----AenIysCysCysIleGlyLysAspLeuValCysAspLysGluIysGlnCys 346
QY 181 TGCCGCTTCAGCCGTGGAAAGAAATGT----- 207
Db 347 SerAspGlySerAspGluLysGluCysAspLysTyrAspLysLeuLeuLysLeuArg 366
QY 208 -----TTAGACTTCAGAAAGATATATGCGATATGCCACAGAGGCTGCCCCCTGC 258
Db 367 GlyIleSerProAspValSerLysAlaArgCysValLysProProValThrGlyThrCys 386
QY 259 CTGGCTTCATACCACTGTGTGTACATAAAAAAATCAAGATCTGCTCGAATTCATC 318
Db 387 ProGlySerGlnThrLysTyrTyrAsnProAenLysArgLeuCysTyrArgPheAen 406
QY 319 TATGCGGTTCGAGGGGAAACAATAACAATTCCTCAAGTATCTGTCTGCTGCACC 378
Db 407 TyrGlyGlyCysGluGlyAsnGlnAsnArgPheGluThrGluAlaGlyCysMetThrPhe 426
QY 379 TGC 381
Db 427 Cys 427

RESULT 23
Q09983 PRELIMINARY; PRT; 1599 AA.
AC Q09983;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein F30H5.3.
GN Name=F30H5.3; ORFNames=F30H5.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA -Pauley A., Stellyes L.;
RT "The sequence of C. elegans cosmid F30H5."
RL Submitted (JUN-1995) to the EMBL/GenBank/DDAJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;

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RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR EMBL; U29096; AAA68408.1; -.
DR PIR; T16210; T16210.
DR HSSP; P10646; 1ADZ.
DR IntAct; Q09983; -.
DR WormBase; WBGene0017937; F30H5.3.
DR WormPep; F30H5.3; C501927.
DR CO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 3.
DR Pfam; PF00014; Kunitz_BPTI; 5.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WRI; 15.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 5.
DR KW Hypothetical protein.
SQ SEQUENCE 1599 AA; 171658 MW; AB5B6A1D86E9880D CRC64;

Alignment Scores:
Pred. No.: 1.08e-08 Length: 1599
Score: 173.50 Matches: 35
Percent Similarity: 48.48% Conservative: 13
Best Local Similarity: 35.35% Mismatches: 42
Query Match: 22.71% Indels: 9
DB: 2 Gaps: 2

US-10-807-204-11 (1-396) x Q09983 (1-1599)

Qy 109 AAGTGGAAATCGAAGTGTG-----GAAGAAATAGACGAGTGAC 147
Db 118 LysLeuGlnCysLysTyGlyThrProLeuLysIleGlySerSerAsnGlnArgCysSer 537
Qy 148 AAACCCAGAGATGCCAGAAACATGAAGTGTGCGCGTTCAGCCGTGGAAGAAATGT 207
Db 158 AlaSerAlaAspCysProSerThrHisGluCys-----GlnSerAspHisAsnValCys 555
Qy 208 TTAGACTTCAGAAAGGATATGCGATATGCGACAGAGGCTGGCCCTGCTGCCTCC 267
Db 218 CysProArgProGlnAlaIleCysSerGlnProLeuArgLeuGlyAspCysLysGlnSer 575
Qy 268 ATACACACTGGTGTGACATAAATAAACTAAGATCTGCTCGAATTCATCTATGGCGGT 327
Db 278 ValargargTyTrpTyAsnAlaValThrArgAlaCysGluIlePheAspTyThrGly 595
Qy 328 TGCCAGGGGAACAATAACAATTCGAACTGCAAGCTATCTCTGCTGGTCACTGCAAA 384
Db 338 CysGlnGlyAsnAspAsnAsnPhelGluThrLeuLeuGluCysGlnAsnThrCysGlu 614

RESULT 24
Q6AX20 PRELIMINARY; PRT; 587 AA.
ID Q6AX20
AC Q6AX20;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Aip2 A protein.
GN Name=aip2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;

Xenopodinae: Xenopus.
NCBI_TaxID=8355;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.,
"Genetic and genomic tools for Xenopus research: The NIH Xenopus
Dev. Dyn. 225:384-391(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC079801; AAH79801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 587 AA; 66870 MW; 7DF224C2138B94BF CRC64;

Alignment Scores:
Pred. No.: 1.13e-08 Length: 587
Score: 173.00 Matches: 29
Percent Similarity: 58.73% Conservative: 8
Best Local Similarity: 46.03% Mismatches: 26
Query Match: 22.64% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q6AX20 (1-587)

Qy 196 GGAAGAAATGTTTACGATTCAGAAAGGATATGCGATATGCCACAGGAGGTGGCCCC 255
Db 273 GlyLysAspIleThrAspValLysSerValCysSerGlnGluAlaIleThrGlyPro 292
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QY 256 TGCCTGGCTCCATACACACTGGTGTGATCAATATAAATAAATAAAGTCTGCTCGAATTC 315
DB 293 CysArgAlaMetMetProArgTrpTrpPheAsnLeuGlyGlnLysCysPheArgPhe 312
QY 316 ATCTATGGCGGTGGCAGGGAGCAATACAACTTCCAACTGAGAGCTATCTGCTGTC 375
DB 313 IleTyrGlyGlyCysGlyGlyAsnArgAsnPheGluSerGluAspTyrCysMetAla 332
QY 376 ACCTGCAAA 384
DB 333 ValCysLys 335

RESULT 25
Q70820 PRELIMINARY; PRT; 751 AA.
ID Q70820;
AC Q70820;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Amyloid-beta-like protein A precursor.
GN Name=alp2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Collins R.W.J., van Strien D., Leunissen J.A., Martens G.J.M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ608932; CAA75662.1; -.
DR HSSP; Q16019; IAPP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR002043; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 751 amyloid-beta-like protein A.
SQ SEQUENCE 751 AA; 85200 MW; C5E8FE7302C36B58 CRC64;

Alignment Scores:
Pred. No.: 1.15e-08 Length: 751
Score: 173.00 Matches: 29
Percent Similarity: 58.73% Conservative: 8
Best Local Similarity: 46.03% Mismatches: 26
Query Match: 22.64% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q70820 (1-751)
QY 196 GGAAGAAATGTTAGACTTCAGAAAGGATATATGCAAGTATGCCACAGAGGCTGCCGCC 255
DB 281 GlyLysAspIleIleThrAspValLysSerValCysSerGlnGluAlaIleThrGlyPro 300
QY 256 TGCCTGGCTCCATACACACTGGTGTGATCAATATAAATAAATAAAGTCTGCTCGAATTC 315
DB 301 CysArgAlaMetMetProArgTrpTrpPheAsnLeuGlyGlnLysCysPheArgPhe 320
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QY 316 ATCTATGGCGGTGGCAGGGAGCAATACAACTTCCAACTGAGAGCTATCTGCTGTC 375
DB 321 IleTyrGlyGlyCysGlyGlyAsnArgAsnPheGluSerGluAspTyrCysMetAla 340
QY 376 ACCTGCAAA 384
DB 341 ValCysLys 343

RESULT 26
Q6DJB6 PRELIMINARY; PRT; 750 AA.
ID Q6DJB6;
AC Q6DJB6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE APP-prov protein.
GN Name=app-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC075266; AAH5266.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR002043; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 750 AA; 84927 MW; -4222350843147CAF CRC64;

Alignment Scores:
Pred. No.: 1.3e-08 Length: 750
Score: 172.50 Matches: 35
Percent Similarity: 45.71% Conservative: 13
Best Local Similarity: 33.33% Mismatches: 42
Query Match: 22.58% Indels: 15
DB: 2 Gaps: 1

US-10-807-204-11 (1-396) x Q6DJB6 (1-750)
QY 112 GTGAATCGAAGTGGAGAAATAGACAGCTGTACCAACCAGAGATTGCCAGAAAC 171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
235 ValGluValGluGluGluGluGluAlaAspAspGluAspGlyAspGluAlaGlu 254
QY 172 ATGAAGTGTGCCCTTCAGCCGTGGA----- 198
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
255 GluProGluGluProTyThrGluGluAlaThrGluArgThrThrSerIleAlaThrThr 274
QY 199 -----AGAAATGTTAGACTTCAGAAAGGATATATGACGATGCCACAGAG 246
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
275 ThrThrThrThrGluSerValGluGluValValArgGluValCysSerGluGluAlaGlu 294
QY 247 GCTGCCCCCTGCTGCTCCATCCACACCTGGTGGTACATAAATAAATAAAGATCTGC 306
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
295 ThrGlyProCysArgAlaMetIleProArgTrpTyThrAspValThrGluArgLysCys 314
QY 307 TCCGAATTCATCTATGCGCGTTGTCAGGGGGAACATAACAATTCACAACTGAAAGCTATC 366
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
315 AlaGlnPheIleTyThrGlyGlyCysGlyGlyAsnArgAsnAsnPheAspSerGluAspTyr 334
QY 367 TGCTGTGTCACCTGC 381
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
335 CysMetalValCys 339

RESULT 27
IBPC_BOVIN
ID IBPC_BOVIN STANDARD; PRT; 67 AA.
AC P00976;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Colostrum trypsin inhibitor (Colostrum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Cechova D., Jonakova V., Sorm F.;
RT "Primary structure of trypsin inhibitor from cow colostrum (component B2).";
RL Collect. Czech. Chem. Commun. 36:3342-3357 (1971).
RN [2]
RP DISULFIDE BONDS.
RA Cechova D., Ber E.;
RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
RL Collect. Czech. Chem. Commun. 39:680-688 (1974).
RN [3]
RP CHARACTERIZATION.
RX PubMed=11947537;
RA Cechova D., Muszynska G.;
RT "Role of lysine 18 in active center of cow colostrum trypsin inhibitor.";
RL FEBS Lett. 8:84-86 (1970).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01207; TIBOC.
DR HSSP; P02760; 1BIK.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.

DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Glycoprotein; Serine protease inhibitor.
FT SITE 18 19 Reactive bond for trypsin.
FT DISULFID 8 58
FT DISULFID 17 41
FT DISULFID 33 54
FT CARBOHYD 27 27 N-linked (GlcNAc...).
SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;

Alignment Scores:
Pred. No.: 1.23e-08 Length: 67
Score: 172.00 Matches: 26
Percent Similarity: 68.52% Conservative: 11
Best Local Similarity: 48.15% Mismatches: 17
Query Match: 22.51% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x IBPC_BOVIN (1-67)
QY 223 GATATATGCTAGTATGCCACAGAGGCTGCGCCCTGCTGCCTCATACACACTGGTGG 282
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6 AspLeuCysGlnLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 25
QY 283 TACAATAAAAACTAAGATCTGCTCCGAATTCACTATATGCGGTGCCAGGGGAAACAAT 342
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
26 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 45
QY 343 AACAACTTCCAACTGAAGCTATCTGCTGCTGCTACCTGCACAA 384
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
46 ***AsnPheGluThrThrGluMetCysLeuArgIleCysGlu 59

RESULT 28
Q8TEU8
ID Q8TEU8 PRELIMINARY; PRT; 576 AA.
AC Q8TEU8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WF1KXNP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyai L., Patthy L.;
RT "A human protein containing multiple types of protease-inhibitory modules.";
RL proc. Natl. Acad. Sci. U.S.A. 98:3705-3709 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Trexler M., Banyai L., Patthy L.;
RT "Distinct expression pattern of two related human proteins containing multiple types of protease-inhibitory modules.";
RL Biol. Chem. 383:0-0 (2002).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AF468657; AAL77058.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
```


DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG_LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Alignment Scores:
Pred. No.: 1,61e-08 Length: 576
Score: 171.50 Matches: 35
Percent Similarity: 40.91% Conservative: 10
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 22.45% Indels: 29
DB: 3 Gaps: 3

US-10-807-204-11 (1-396) x Q8TEU8 (1-576)
QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 327 GluCysLeuLysProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 346
QY 175 -----AAGTGTGCCCGTTCAGCCGTGGAAG----- 201
Db 347 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisArgAsnLeuAen 366
QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
Db 367 HisPheGluThrTyrrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaAlaCys 386
QY 232 AGTATGCCACAGAGGCTGGCCCTCGCTCCATACACACTGGTGGTACAAATAA 291
Db 387 SerLeuProAlaLeuGlnGlyProCysAlaTyrrAlaProArgTrpAlaTyrrAsnSer 406
QY 292 AAAACTAAGATCTGCTCCGAATTCATATGCGGTTCACGGGGAACAATAACAATTC 351
Db 407 GlnThrGlyGlnCysGlnSerPheValTyrrGlyGlyCysGluGlyAsnGlyAsnAsnPhe 426
QY 352 CAAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 427 GluSerArgGluAlaCysGluGluSerCys 436

RESULT 29
Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bikunin hlg.
GN ORFNames=UNQ9235;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.B., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Wadlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
CC -I- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAQ88509.1; -.
DR HSRF; P00974; IK09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG_LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Alignment Scores:
Pred. No.: 1,61e-08 Length: 576
Score: 171.50 Matches: 35
Percent Similarity: 40.91% Conservative: 10
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 22.45% Indels: 29
DB: 3 Gaps: 3

US-10-807-204-11 (1-396) x Q6UXZ9 (1-576)
QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 327 GluCysLeuLysProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 346
QY 175 -----AAGTGTGCCCGTTCAGCCGTGGAAG----- 201
Db 347 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisArgAsnLeuAen 366
QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
Db 367 HisPheGluThrTyrrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaAlaCys 386
QY 232 AGTATGCCACAGAGGCTGGCCCTCGCTCCATACACACTGGTGGTACAAATAA 291
Db 387 SerLeuProAlaLeuGlnGlyProCysAlaTyrrAlaProArgTrpAlaTyrrAsnSer 406
QY 292 AAAACTAAGATCTGCTCCGAATTCATATGCGGTTCACGGGGAACAATAACAATTC 351
Db 407 GlnThrGlyGlnCysGlnSerPheValTyrrGlyGlyCysGluGlyAsnGlyAsnAsnPhe 426
QY 352 CAAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 427 GluSerArgGluAlaCysGluGluSerCys 436

RESULT 30
YN81_CABEL

ID YN81_CAEEEL STANDARD; PRT; 1416 AA.
AC Q03610;
AT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
GN Hypothetical protein ZC84.1 in chromosome III.
OS ORFNames=ZC84.1;
GN Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OK NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398; DOI=10.1038/368032a0;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kerhaw J., Kirsten J., Laisster N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=93069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
RN [3]
RP REVISIONS.
RA Jones S.J.M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z19157; CAA79569.1; -.
DR PIR; S88550; E88550.
DR PIR; S28291; S28291.
DR HSSP; P00981; 1DTK.
DR WormBase; WBGene00013846; ZC84.1.
DR WormPep; ZC84.1; CE15020.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 3.
DR Pfam; PF00014; Kunitz BPTI; 5.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 5.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WRI; 13.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 5.
KW Hypothetical protein; Repeat; Serine protease inhibitor.
FT DOMAIN 212 266 BPTI/Kunitz inhibitor 1.
FT DOMAIN 337 387 BPTI/Kunitz inhibitor 2.
FT DOMAIN 434 484 BPTI/Kunitz inhibitor 3.
FT DOMAIN 538 590 BPTI/Kunitz inhibitor 4.

FT DOMAIN 646 698 BPTI/Kunitz inhibitor 5.
SQ SEQUENCE 1416 AA; 152986 MW; 531CACE1CB22F70D CRC64;

Alignment Scores:
Pred. No.: 1.99e-08 Length: 1416
Score: 171.00 Matches: 35
Percent Similarity: 46.30% Conservative: 15
Best Local Similarity: 32.41% Mismatches: 40
Query Match: 22.38% Indels: 18
DB: 1 Gaps: 3

US-10-807-204-11 (1-396) x YN81_CAEEEL (1-1416)

QY 109 AAGTGAATGCGAAGTG----- 126
DB 380 LyHisGluCysGluMetTyrCysAlaArgLeuGlnCysGluArgGlySerProLeuArg 399
QY 127 -----GAAGAAATAGACACAGTGTACCAACCAGAGATTGCCAGAAAACATGAAGTGT 180
DB 400 IleGlyGluGluAlaGlnArgCysGlnAsnAlaGlnCysProSerSerHisGlu--- 418
QY 181 TGCCCGTTCAGCCGTGGAAGAATGTTAGACTTCAGAAAGGATATATCGAGTATGCCA 240
DB 419 CysLysAlaAspGlnGly---ValCysCysProArgLysGlnThrIleCysAlaGlnPro 437
QY 241 CAGGAGGCTGCGCCCTGCCTGCCTCCATACACACTGGTGTACATAATAAATAAATAAAGTAA 300
DB 438 LeuArgIleGlyAspCysThrGluAsnValIleArgTyrTrpTyrAsnAlaArgThrArg 457
QY 301 ATCTGCTCGAATTCATCTATGCGGTTCAGGGGAACAATAACAACATCTTCCAAACTGAA 360
DB 458 GlnCysGlnMetPheGluTyrThrGlyCysGlnGlyAsnAspAsnAenPheAspSerIle 477
QY 361 GCTATCTGCTGCTGCCTGCCTGCAAA 384
DB 478 MetAspCysGlnAsnPheCysLys 485

RESULT 31
Q6ITB9 PRELIMINARY; PRT; 83 AA.
ID Q6ITB9
AC Q6ITB9, 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mulgin-3.
OS Pseudechis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudechis.
OK NCBI_TaxID=8670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filipovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626926; AAT45402.1; -.
DR HSSP; Q16019; IAAp.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9103 MW; 315C361D8EC99221 CRC64;

Alignment Scores:
Pred. No.: 1.99e-08 Length: 83
Score: 170.00 Matches: 29
Percent Similarity: 61.82% Conservative: 5
Best Local Similarity: 52.73% Mismatches: 21


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Query Match: 22.25% Indels: 0
DB: 2 Gaps: 0
US-10-807-204-11 (1-396) x Q6ITB9 (1-83)
QY 217 AGAAGGATATATGACAGTATGCCAGAGGCTGCGCTGCTCCATACCACAC 276
Db 27 ArzProAspPheCysGluLeuProAlaAspThrGlyProCysArgValGlyPheProSer 46
QY 277 TGGTGTACAAATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGGCCAGGG 336
Db 47 PheTyTyAsnProAspGluLysCysLeuGluPheLeuTyGlyGlyCysGlyGly 66
QY 337 AACAAATCAACTTCCAACTGAAGTATCTCTGTCGTCACTGC 381
Db 67 AsnAlaAsnAsnPhelleThrLysGluGluCysGluSerThrCys 81
RESULT 32
QY 7T363 PRELIMINARY; PRT; 516 AA.
AC QY7363;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Zgc:64075.
GN ORFNames=zgc:64075;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; BC053239; AAH53329.1; -.
DR HSSP; P10646; 1ADZ.
DR ZFIN; ZDB-GENE-040426-2169; zgc:64075.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002172; LDL receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR000601; PKD.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR Pfam; PF00057; Ldl recept_a; 1.
DR Pfam; PF07502; MANSC; 1.
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DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SMO0131; KU; 2.
DR SMART; SMO0192; LDLa; 1.
DR SMART; SMO0089; PKD; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02379; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS01209; LDLa_1; 1.
DR PROSITE; PS00068; LDLa_2; 1.
SQ SEQUENCE 516 AA; 57695 MW; 2080A4C5B270DE16 CRC64;
Alignment Scores:
Pred. No.: 2,27e-08 Length: 516
Score: 170.00 Matches: 40
Percent Similarity: 41.43% Conservative: 18
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 22.25% Indels: 30
DB: 2 Gaps: 5
US-10-807-204-11 (1-396) x Q7T363 (1-516)
QY 40 ATCTTTTGGGGGACATCCAGAACCTGGG---CACGCTGAAGCATCTCTGGC----- 90
Db 292 ValSerValSerAsnIleGlySerProAlaProHisProSerGlyArgIleGlyProIle 311
QY 91 -----AAGCGTGTCCCAAAATCAAAGTGGAAATCGAAGTGGAA 129
Db 312 AspAlaValGluGlnCysAspArgProCysSerProGluHisPheThrCysAsp----- 329
QY 130 GAATAGACCACTGTATACCAACCCAGACAT-----TGCCAGAAACATGAAGTGTTC 183
Db 330 -----AsnLysCysCysIleGlyLysAspLeuValCysAspLysGluLysGlnCysSer 347
QY 184 CGGTTCAGCGCTGGAAAGAAATGT----- 207
Db 348 AspGlySerAspGluLysGluCysAspLysTrpAspTyrAspLeuValLysLeuArgGly 367
QY 208 -----TTAGACTTCAGAAAGATATATGCGATGATGCCACAGGAGGCTGGCCCTGCCTG 261
Db 368 IleSerProAspValSerLysAlaArgCysValLysProProValThrGlyThrCysPro 387
QY 262 GCCTCCATACCACTGTGTGTACATAAATAAATAAAGTATGCTCGCAATTCATCTAT 321
Db 388 GlySerGlnThrLysLysTrpTyrTrpAsnProAsnLysArgLysCysTyrArgPheAsnTyr 407
QY 322 GCGCGTTCAGGGGGAACAATAACAACTTCCAACTGAAGCTATCTGTCTGCTCACTGC 381
Db 408 GlyGlyCysGluGlyAsnGlnAsnArgPheGluThrGluAlaGlyCysMetThrPheCys 427
RESULT 33
QY 6ITB5 PRELIMINARY; PRT; 83 AA.
AC Q6ITB5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-1.
OS Oxururus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxururus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626930; AAT45406.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
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QY 163 -----CCAGAAACATGAAGTGTGCCCGTTACGCCGT-----GGAAAG 201
Db 262 GluAspTyrAsnAspGluAsnProThrGluProGluAsnGluArgGlnLeuSerGlyLys 281
QY 202 AAATGTTTACAGCTTCAGAAAGCATATATGACAGTATGCCACAGGAGGCTGGCCCTGCCTG 261
Db 282 AspilelleThrAspValLysSerValCysSerGlnGluAlaValThrGlyProCysArg 301
QY 262 GCCTCCATACACACTGTGTGGTACAAATAAAAACTAAGATGTGTCGGAATTCATCTAT 321
Db 302 AlaMetMetProArgTrpTyrPheAspLeuGlyGlnLysCysValArgPheIleTyr 321
QY 322 GCGCGTTCAGGAGGAACAATAACAACTCCAACTGAAGCTATCTGTCTGGTACCTGC 381
Db 322 GlyGlyCysGlyGlyAsnArgAsnPheGluSerAlaAspTyrCysMetAlaValCys 341
QY 382 AAA 384
Db 342 Lys 342

RESULT 37
Q9GP15 PRELIMINARY; PRT; 86 AA.
AC Q9GP15;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Ixodes ricinus (Sheep tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
OX NCBI_TaxID=34613;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary glands;
RX MEDLINE=12139212; PubMed=12139212;
RA Lebouille G., Rochez C., Louahed J., Rutti B., Brossard M., Bollen A.,
RA Godfroid E.;
RT "Isolation of Ixodes ricinus salivary gland mRNA encoding factors
RT induced during the blood feeding process.";
RL Am. J. Trop. Med. Hyg. 66:225-233(2002).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ269641; CAB55816.1; -.
DR HSSP; P12111; 1KNT.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 86 AA; 9727 MW; 9473B17974A055F0 CRC64;

Alignment Scores:
Pred. No.: 3.19e-08 Length: 86
Score: 168.00 Matches: 25
Percent Similarity: 69.23% Conservative: 11
Best Local Similarity: 48.08% Mismatches: 16
Query Match: 21.99% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q9GP15 (1-86)
QY 229 TGCAGTATGCCAGGAGGCTGGCCCTGCCTGCCTCATACACACTGGTGGTACAAAT 288
Db 31 CysLysLeuProProAspAspGlyProCysArgAlaArgIleProSerTyrTyrPheAsp 50
QY 289 AAAAAAATAAGATCTGTCCGAATTCATCTATGCGGTTCGCCAGGGGAAACAATAACAC 348
Db 51 ArgLysThrLysThrCysLysGluPheMetTyrGlyGlyCysGluGlyAsnGluAsn 70

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QY 349 TTCCAAACTGAAGCTATCTGTCTGGTCACTGCCTGCAAA 384
Db 71 PheGluAsnIleThrThrCysGlnGluGluCysArg 82

RESULT 38
Q9XWX5 PRELIMINARY; PRT; 1743 AA.
AC Q9XWX5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Y43F8B.3.
GN ORFNames=Y43F8B.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Ainscough R.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 15 BPTI/Kunitz inhibitor domains.
DR EMBL; AL032623; CAA21511.1; -.
DR PIR; T26859; T26859.
DR HSSP; Q16019; 1AAP.
DR WormBase; WBGene00012814; Y43F8B.3.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 15.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00131; KU; 15.
DR SMART; SM00289; WR1; 10.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 15.
KW Hypothetical protein.
SQ SEQUENCE 1743 AA; 191111 MW; B93C163556433C2A CRC64;

Alignment Scores:
Pred. No.: 3.96e-08 Length: 1743
Score: 168.00 Matches: 37
Percent Similarity: 39.32% Conservative: 9
Best Local Similarity: 31.62% Mismatches: 49
Query Match: 21.99% Indels: 22
DB: 2 Gaps: 2

US-10-807-204-11 (1-396) x Q9XWX5 (1-1743)
QY 97 TGTCCCAAAATCAAAGTGGAAATCGAAGTGAAGAAATAGACCAGTGTACCAAAACCAGA 156
Db 1621 CysProHisGlyLysProAspValThrAspHisSerLeuThrThrCysGlyIleAspThr 1640
QY 157 GATTGCCCAAAAACATGAAGTGTGCCCGCTTCAGCGTGGAAAGAAA-----TGTTTA 210
Db 1641 GlyCysProArgAspHisValCysHisValSerLysArgGlySerLysThrValCysCys 1660
QY 211 GACTTCAGAAAGGATATATCGAGTATGCCACAGAGGCTGCCCTGGCCTCCATA 270
Db 1661 ProAspProAlaSerPheCysLeuValArgAlaAspProGlyProCysAsnArgGluIle 1680
QY 271 CCACACTGGTGTACATAAAAAAATAAGATCTGTCTCCGAATTCATCTATGCGGTTC 330
Db 271 CCACACTGGTGTACATAAAAAAATAAGATCTGTCTCCGAATTCATCTATGCGGTTC 330

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Db 1681 ProArgTrrpAlaTyAspLysAlaSerGlySerCysLysLysPheIlePheGlyCys 1700
QY 331 CAGGGGAACAATAACAACACTTCCAAACTGAA----- 360
Db 1701 GlnGlyAsnLeuAsnAsnAsnPheAspThrAsnGlnCysValAlaPheGluTyThrGlyCys 1720
QY 361 -----GCTATCTGTCGTGCTCACTGC 381
Db 1721 GlyGlyAsnLeuAsnAsnPheValSerIleAlaAspCysGlnAlaThrCys 1737
RESULT 39
Q9UG8 PRELIMINARY; PRT; 3198 AA.
AC Q9UG8;
DT 01-WAY-2000 (TRENBLrel. 13, Created)
DT 01-WAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE Lacunin precursor.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99457716; PubMed=10528409; DOI=10.1016/S0965-1748(99)00064-8;
RA Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
RT "Expression of lacunin, a large multidomain extracellular matrix
protein, accompanies morphogenesis of epithelial monolayers in Manduca
sexta.";
RL Insect Biochem. Mol. Biol. 29:883-897(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Nardi J., Martos R., Walden K., Lampe D., Robertson H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.
DR EMBL; AF078161; AAF04457.1; -.
DR HSSP; P12111; 1KTH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR004094; Prot inh antiatn.
DR InterPro; IPR002223; Prot inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF02822; Antistatin; 4.
DR Pfam; PF00014; Kunitz_BPTI; 10.
DR Pfam; PF00090; TSP_1-5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00131; KU; 10.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS0900; PLAC; 1.
DR PROSITE; PS0092; TSP1; 5.
KW Signal.
FT SIGNAL
SQ SEQUENCE 3198 AA; 349366 MW; AB4ACD459CD9134 CRC64;
Alignment Scores:
Pred. No.: 4.13e-08 Length: 3198
Score: 168.00 Matches: 39
Percent Similarity: 43.88% Conservative: 22
Best Local Similarity: 28.06% Mismatches: 51

Query Match: 21.99% Indels: 27
DB: Gaps: 4
US-10-807-204-11 (1-396) x Q9UG8 (1-3198)
QY 9 CTCAGGAGCTCTGCCAATCTCTGGTACCATTCATCTTTTGGGGACATC----- 57
Db 2190 ILeThrThrValArgProThrGluAlaHisPro-LeuThrGluMetCysPheMetG1 2209
QY 58 -CAGGAACCTGGGCACGCTGAAGGCATCTTTGGCAAGCCGTGTCCCAAAATCAAAGTG-- 114
Db 2209 uLysaspProgly-----ProCysThrAspThrGluThrAr 2221
QY 115 -----GAATGGAAGTGGAGAAATAGACACAGTGTACCAA 149
Db 2221 gTrrpValTyrrAspTyrrLysLeuGlyLysCysValThrPheGluTyrrGlyGlyG1 2241
QY 150 ACCCAGAGATTGCCCAGAGAAACATGAAGTGTTCGCCGTTCAGCCGTGAAGAAATGTTT 209
Db 2241 yAsnArgAsnAsnPheProThrGluGluTyrrCysGlnTyrrTyrrCysGlyThr----- 2258
QY 210 AGACTTCAGAAAGATATATATGAGTATATGCCACAGGAGGCTGGCCCTCCCTGGCCTCCAT 269
Db 2259 -----AlaGlnAspIleCysGlnLeuProMetArgSerGlyProCysThrGluSerLe 2276
QY 270 ACCACACTGGTGTACAAATAAAATAAGATCTGTCGAATTCATCTATGGCGGTG 329
Db 2276 uMetArgtrpPheTyrrAspProSerSerAspSerCysSerGlnPheThrTyrrGlyGlyCy 2296
QY 330 CCAGGGGAACATACAACTTCCAAACTGGAAGTCTCTGTCGTGCACCTGCAAA 384
Db 2296 sAspGlyAsnAspAsnArgPheGluThrArgAspAspCysGluSerArgCysArg 2314
RESULT 40
P70004
ID P70004 PRELIMINARY; PRT; 342 AA.
AC P70004;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Alpha1-microglobulin/bikunin precursor (AMBP).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Kawahara A., Hikosaka A., Sasado T., Hirota K.;
RT "Thyroid hormone-dependent repression of alpha1-microglobulin/bikunin
RT (AMBP) gene expression during amphibian metamorphosis.";
RL Dev. Genes Evol. 206:355-362(1997).
CC -!- SIMILARITY: Belongs to the lipocalin family.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; D87752; BAA13453.1; -.
DR HSSP; P02760; 1BIK.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0008810; F:transport; IEA.
DR InterPro; IPR002968; A1-microgloblin.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR002223; Prot inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR01215; ALMCGLOBULIN.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00179; LIPOCALIN.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.

QY 196 GGAAAGAAATGTTTAGACTTCAGAAAGGATATATGCAGTATGCCACAGGAGCTGGCCCC 255


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RESULT 48
BTIA_BOOMI
ID_BTIA_BOOMI STANDARD; PRT; 122 AA.
AC P83609;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kuniz-type serine protease inhibitor Bmt1-A (Fragments) .
OS Boophilus microplus (cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
NCBI_TaxID=6941;
[1]
RN
RP SEQUENCE, AND FUNCTION.

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RX PubMed=10615008; DOI=10.1016/S0162-3109(99)00074-0;
 RA Tanaka A.S., Andreotti R., Gomes A., Torquato R.J.S., Sampaio M.U.,
 RA Sampaio C.A.M.;
 RT "A double headed serine proteinase inhibitor-human plasma kallikrein
 RT and elastase inhibitor-from boophilus microplus larvae.";
 RL Immunopharmacology 45:171-177(1999).
 CC -1- FUNCTION: Inhibits bovine trypsin, bovine chymotrypsin, human
 CC plasmin, human plasma kallikrein and human neutrophil elastase,
 CC but not bovine thrombin, human factor Xa or porcine pancreatic
 CC kallikrein. May play a role in blocking blood coagulation during
 CC the larvae fixation on cattle.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 CC Interpro: IPR002223; Kunitz_BPTI.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRODOM; FD000222; Prot_inh_Kunz-m; 2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.

Alignment Scores:	5.23e-08	Length:	122
Pred. NO.:			
DK	PROS1B; P50029; BPTI_Kunitz_2; 2.		
KW	Direct protein sequencing; Repeat; Serine protease inhibitor.		
FT	BPTI/Kunitz inhibitor 1.		
FT	DOMAIN 10 60		
FT	FT DOMAIN 62 112		
FT	FT DOMAIN 60 60		
FT	FT DISULFID 10 60		
FT	FT DISULFID 35 56		
FT	FT DISULFID 35 56		
FT	FT NON CONS 69 70		
FT	FT DISULFID 71 121		
FT	FT DISULFID 80 104		
FT	FT DISULFID 96 117		
FT	FT SITE 19 20		
FT	FT SITE 71 72		
FT	FT NON TER 122 122		
FT	SQ SEQUENCE 122 AA; 13736 MW; 8F5B1F48E10C566F CRC64;		

Percent Similarity:	52.94%	Conservative:	9
Best Local Similarity:	42.35%	Mismatches:	22
Query Match:	21.73%	Indels:	18
DB:	1	Gaps:	4
US-10-807-204-11 (1-396) x BTIA_BOOMI (1-122)			

QY ---CGTGGAAAGAAATGTTTAGACTTCAGAAAGGATATATGCAGCTATGTCCACAGAGCGCT 249
Db TyrGluAlaLysLysCysLeu-----AlaaArgpro---GlusGr 77
QY GGCCTGCTGCTGGCGCTCCATACCACACTGGTGGAACAATAAAAAAAGTAATCTGCTCTCC 309

DB 78 GlyProCysuLeuAlaIyMetProMetIlePoiIyAspSerIleuGluGlyAsnGlySerVal
310 GAATTCATCTATGGCGGTTGCCAGGGGAACAATAACAACTTCCAACTGAAGCTATCTGT

56 *Giur. it.*, 1994, 4, 1, 109.


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QY 370 CTGGTCACCTGCAGAA 384
D 118 LeuylsSerCysLys 122
RESULT 49
Q6I750 PRELIMINARY; PRT; 507 AA.
AC Q6I750;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hepatocyte growth factor activator inhibitor-1.
GN Name=HAI-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tezuka S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AB154834; BAD23971.1; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002172; LDL receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MANSC; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS0068; LDLRA_2; 1.
SQ SEQUENCE 507 AA; 56465 MW; 810043AE28C47AF3 CRC64;

Alignment Scores:
Pred. No.: 5,79e-08 Length: 507
Score: 166.00 Matches: 33
Percent Similarity: 51.55% Conservative: 17
Best Local Similarity: 34.02% Mismatches: 39
Query Match: 21.73% Indels: 8
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x Q6I750 (1-507)
QY 118 TGCAGATGGAAGAAATAGACAGTGTAACCAACCCAGAGATTGCCCA-----GAA 168
D 324 CysCysIleAspGlyPheLeuGluCysAspThrProAspCysProAspGlySerAsp 343
QY 169 AACATGAAGTCTGCCCGTTCAGCCGTGGA-----AGAAATGTTTAGACTTCAGA 219
D 344 GluAlaThrCysGluLysTyrSerSerGlyPheAspGluLeuGlnSerIleHisPheLeu 363
QY 220 AAGGAT-----ATATGAGTATGATGCACAGAGGCTGCCCTGCTGCCCTCCATACCA 273
D 364 SerAspLysGlyTyrCysAlaGluLeuProAspThrGlyPheCysLysGluAsnIlePro 383
QY 274 CACTGGTGGTACATAAAAAAATAAGATCTGCTCCGGAATTCATCTATGGGGGTGCCAG 333
D 384 ArgTrpTyrAsnProPheSerGluArgCysAlaArgPheThrTyrGlyGlyCysTyr 403
QY 334 GGGAACAATACAACTCCAACTGAAGCTATCTGCTGCTGCTGCACCTGCAGAA 384
D 404 GlyAsnLysAsnAsnPheGluLysGluGlnGlnCysLeuGluSerCysArg 420
RESULT 50
ANBP_PIG
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ID AC P04356; P34954; STANDARD; PRT; 337 AA.
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ANBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-
DE trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (EI-14)]
DE (Fragment).
DE Name=ANBP; Synonyms=ITIL;
GN Sub scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90353595; PubMed=1696914; DOI=10.1016/0014-5793(90)91112-2;
RA Gebhard W., Schreimüller T., Vetr H., Wachter E., Hochstrasser K.;
RT "Complementary DNA and deduced amino acid sequences of porcine alpha
RT 1-microglobulin and bikunin.";
RL FEBS Lett. 269:32-36(1990).
RN [2]
RP SEQUENCE OF 2-337 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91113729; PubMed=1703444; DOI=10.1016/0167-4781(91)90152-C;
RA Tavakkol A.;
RT "Molecular cloning of porcine alpha 1-microglobulin/HI-30 reveals
RT developmental and tissue-specific expression of two variant messenger
RT ribonucleic acids.";
RL Biochim. Biophys. Acta 1088:47-56(1991).
RN [3]
RP SEQUENCE OF 212-334.
RX MEDLINE=85225967; PubMed=2408637;
RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of the
RT inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
RT trypsin-released inhibitors from horse and pig inter-alpha-trypsin
RT inhibitors.";
RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological
CC fluids including plasma, urine, and cerebrospinal fluid. It
CC appears not only as a free monomer but also in complexes with IgA
CC and albumin.
CC -1- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
CC elastase.
CC -1- SUBUNIT: I-alpha-I plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-alpha-LI) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- PTM: The precursor is proteolytically processed into two
CC separately functioning proteins.
CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
CC chromophores (By similarity).
CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ebi.ac.uk/ebis/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; X53685; CAA37725.1; -.
CC EMBL; X52087; CAA36306.1; -.
CC PIR; S11066; TIFGBI.
CC HSSP; P02760; 1BIK.
CC -----
DR
DR
DR
```


DR GO; GO:0005576; C:extracellular; ISS.
 DR GO; GO:0005886; C:plasma membrane; ISS.
 DR GO; GO:0019855; F:calcium channel inhibitor activity; ISS.
 DR GO; GO:0046904; F:calcium oxalate binding; ISS.
 DR GO; GO:0020037; F:heme binding; ISS.
 DR GO; GO:0019862; F:IGA binding; ISS.
 DR GO; GO:0030568; F:plasmin inhibitor activity; ISS.
 DR GO; GO:0042803; F:protein homodimerization activity; ISS.
 DR GO; GO:0030304; F:trypsin inhibitor activity; ISS.
 DR GO; GO:0030236; P:anti-inflammatory response; ISS.
 DR GO; GO:0007155; P:cell adhesion; ISS.
 DR GO; GO:0042167; P:heme catabolism; ISS.
 DR GO; GO:0050777; P:negative regulation of immune response; ISS.
 DR GO; GO:0046329; P:negative regulation of JNK cascade; ISS.
 DR GO; GO:0007565; P:pregnancy; ISS.
 DR InterPro; IPR002968; A1-microglobulin.
 DR InterPro; IPR01038; Calycin.
 DR InterPro; IPR002345; Lipocalin.
 DR InterPro; IPR000566; Lipocalin_cytFABP.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz BPTI; 2.
 DR Pfam; PF00061; Lipocalin; 1.
 DR PRINTS; PRO0759; BASICPTASE.
 DR PRINTS; PRO0179; LIPOCALIN.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
 DR PROSITE; PS00213; LIPOCALIN; 1.
 DR Direct protein sequencing; Glycoprotein; Lipocalin; Plasma; Repeat;
 KW Serine protease inhibitor; Signal.
 FT NON_TER 1 4
 FT SIGNAL <1 4
 FT CHAIN 5 198
 FT CHAIN 191 337
 FT DOMAIN 216 266
 FT DOMAIN 272 322
 FT BINDING 38 32
 FT BINDING 96 96
 FT BINDING 122 122
 FT BINDING 134 134
 FT DISULFID 76 173
 FT DISULFID 216 266
 FT DISULFID 225 249
 FT DISULFID 241 262
 FT DISULFID 272 322
 FT DISULFID 281 305
 FT DISULFID 297 318
 FT CARBOHYD 100 100
 FT CARBOHYD 235 235
 FT SITE 226 282
 FT SITE 282 283
 FT CONFLICT 49 49
 FT CONFLICT 259 259
 FT CONFLICT 270 270
 FT CONFLICT 278 278
 FT CONFLICT 283 283
 FT CONFLICT 285 286
 FT CONFLICT 293 293
 FT CONFLICT 311 311
 FT CONFLICT 315 315
 FT CONFLICT 337 AA; 37690 MW; 1F630FF98E3CD70F CRC64;
 SQ SEQUENCE 337 AA; 37690 MW; 1F630FF98E3CD70F CRC64;
 Alignment Scores:
 Pred. No.: 6.32e-08 Length: 337
 Score: 165.50 Matches: 51
 Percent Similarity: 37.50% Conservative: 15
 Best Local Similarity: 28.98% Mismatches: 51
 Query Match: 21.66% Indels: 59
 DB: 1 Gaps: 7

QY 32 TACCATTCACTCTTTTGGGGACA----- 55
 Db 94 TyrHisLysSerLysTyrPheHisGlyProThrLeuValHisThrAsnTyrAsp 113
 QY 56 -----TCCAGGAACCTGGGC-----ACGCTGAAGGCA 82
 Db 114 GluTyrAlaLeuPheLeuThrLysPheSerArgHisGlyProThrLeuThrAla 133
 QY 83 TCCTTGGCAAGCCGTGTCCCAAAATCAAGTGGAAATGCGAAGTGAAGAAATAGACCAAGT 142
 Db 134 LysLeuTyrGlyArgGluProGlnLeuArg--GluSerLeuLeuGluGluPheArgGluV 153
 QY 143 GTACAAA-----CCCAGAGAT-----TGCCCAAAAACATGAAGT 178
 Db 153 alAlaLeuGlyValGlyIleProGluAspSerIlePheThrMetProAspArgGlyGluC 173
 QY 179 GTTGGCG-----TTCCAGCCGTGGAAAGAAATGTTTA- 210
 Db 173 ysValProGlyGluGlnGluProGluProThrLeuLeuSerArgAlaArgAlaValL 193
 QY 211 -----GACTTCAGAAAG----- 222
 Db 193 euProGlnGluGluGlySerGlyAlaGlyGlnProValAlaAspPheSerLysLysG 213
 QY 223 --GATATATGCAAGTATGCCACAGAGGCTGCCCTGCTGCTGCCCTCCATACCACTGGT 280
 Db 213 luAspSerCysGlnLeuGlyTyrSerGlnGlyProCysLeuGlyMetIleLysArgTyrP 233
 QY 281 GGTACATAAAAAAATAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAACA 340
 Db 233 heTyrAsnGlySerSerMetAlaCysGluThrPheHisTyrGlyGlyCysMetGlyAsnG 253
 QY 341 ATAACAACCTCCAAACCTGAAGCTATCTCTGTCACCTGCAAA 384
 Db 253 lyAsnAsnPheValSerGluLysGluCysLeuGlnThrCysArg 267

Search completed: September 21, 2005, 16:59:28
 Job time : 110 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:37:09 ; Search time 107 Seconds
(without alignments)
473.510 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 131
Sequence: 1 MGLSGLPILVFFILLSDIQ.....GNNNFQTEAICLVTCCKYH 131

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	131	100.0	131	7	ADAI19800
2	131	100.0	131	7	ADAI19811
3	106	80.9	106	7	ADAI19801
4	64	48.9	86	5	ABP69809
5	64	48.9	86	6	ABJ26667
6	64	48.9	98	7	ADAI19808
7	64	48.9	101	4	ABB12236
8	64	48.9	131	7	ADAI19814
9	33	25.2	43	7	ADAI19804
10	33	25.2	179	8	ABM85103
11	30	22.9	30	7	ADAI19803
12	24	18.3	24	7	ADAI19805
13	21	16.0	33	7	ADAI19806
14	21	16.0	33	7	ADAI19809
15	14	10.7	134	7	ADAI19813
16	12	9.2	43	4	AAE13096
17	12	9.2	51	2	AAW75257
18	12	9.2	51	5	AAE27025
19	12	9.2	51	5	AAE27163
20	12	9.2	51	8	ADG98845
21	12	9.2	58	4	AAE13084
22	12	9.2	58	4	AAE60630
23	12	9.2	58	7	ADF41997
24	12	9.2	58	8	ADL16838
25	12	9.2	58	8	ADR89980

26	12	9.2	64	4	AAE13093	AAE13093 Human ser
27	12	9.2	102	5	AAE27095	AAE27095 Human sec
28	12	9.2	102	5	AAE28009	AAE28009 Human gen
29	12	9.2	102	6	ABU65039	ABU65039 Human sec
30	12	9.2	102	8	ADG89848	ADG89848 Human sec
31	12	9.2	117	5	AAE27094	AAE27094 Human sec
32	12	9.2	117	5	AAE27165	AAE27165 Human gen
33	12	9.2	117	6	ABU65038	ABU65038 Human sec
34	12	9.2	117	8	ADG89847	ADG89847 Human sec
35	12	9.2	133	2	AAW75219	AAW75219 Human sec
36	12	9.2	133	5	AAE26982	AAE26982 Human gen
37	12	9.2	133	5	AAE27120	AAE27120 Human gen
38	12	9.2	133	6	ABU64993	ABU64993 Human sec
39	12	9.2	133	7	ADA19812	ADA19812 Human sec
40	12	9.2	133	8	ADG89802	ADG89802 Human pro
41	12	9.2	164	3	AAAY70010	AAAY70010 Human pro
42	11	8.4	54	4	AAE13092	AAE13092 Trypsin i
43	10	7.6	136	7	ADA19815	ADA19815 Mouse DJ1
44	9	6.9	58	2	AAE78401	AAE78401 Human LAC
45	8	6.1	126	7	ADG64021	ADG64021 Human pro
46	8	6.1	140	5	AAU79498	AAU79498 Mouse par
47	8	6.1	140	5	AAU80150	AAU80150 Mouse par
48	8	6.1	166	4	AAE18394	AAE18394 Peptide #
49	8	6.1	166	4	ABB37425	ABB37425 Peptide #
50	8	6.1	175	5	AAU79499	AAU79499 Mouse par

ALIGNMENTS

RESULT 1
ADAI19800

ID ADAI19800 standard; protein; 131 AA.

XX AC ADAI19800;

XX AC

DT 20-NOV-2003 (first entry)

XX

DE Engineered human DJ11 protein SEQ ID NO:1.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoaratic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..131 /note= "eppin-like precursor"

FT Peptide 1..25 /label= signal

FT Protein 26..131 /note= "mature DJ11 protein"

FT Disulfide-bond 33..61 /note= predicted disulfide bond

FT Disulfide-bond 40..65 /note= predicted disulfide bond

FT Disulfide-bond 48..60 /note= predicted disulfide bond

FT Disulfide-bond 54..69 /note= predicted disulfide bond

FT Domain 77..127 /note= predicted disulfide bond

FT Disulfide-bond 77..127 /note= Kunitz domain predicted by pfscan

FT Disulfide-bond 86..110 /note= predicted disulfide bond

FT Disulfide-bond 102..123 /note = predicted disulfide bond
 FT Disulfide-bond 102..123 /note = predicted disulfide bond
 XX WO2003070770-A2.
 EN 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 PR (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 PI WPI; 2003-663849/62.
 XX N-ESDB; ADA19810.
 DR New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX Claim 5; Page 69-70; 87pp; English.
 PS The present invention describes an isolated, purified or recombinant DJ11
 XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.
 XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 131; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 8.3e-131;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGLSGLLPILVFFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
 Db 1 MGLSGLLPILVFFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
 Qy 61 CPFSGCKKCLDFRDXDCSMQPEAGPCLASIPHWYNNKTKICSEFFIYGGCGGNNNNFQTE 120
 Db 61 CPFSGCKKCLDFRDXDCSMQPEAGPCLASIPHWYNNKTKICSEFFIYGGCGGNNNNFQTE 120
 Qy 121 AICLVTKKXKH 131
 Db 121 AICLVTKKXKH 131
 RESULT 2
 ADA19811
 ID ADA19811 standard; protein; 131 AA.
 XX

AC ADA19811;
 XX 20-NOV-2003 (first entry)
 DT Engineered human DJ11 protein SEQ ID NO:12.
 XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 XX WO2003070770-A2.
 PN 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 PR (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 PI WPI; 2003-663849/62.
 DR New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX Disclosure; Page 84; 87pp; English.
 PS The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.
 XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 131; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 8.3e-131;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGLSGLLPILVFFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
 Db 1 MGLSGLLPILVFFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

QY 61 CPFCGKKCLDFRKDICSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFOTE 120
DB 61 CPFCGKKCLDFRKDICSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFOTE 120

QY 121 AICLVTCCKYH 131
DB 121 AICLVTCCKYH 131

RESULT 3
ID ADA19801 standard; protein; 106 AA.
AC ADA19801;
DT 20-NOV-2003 (first entry)
DE Mature form of engineered human DJ11 protein SEQ ID NO:2.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antiporiatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.
OS Homo sapiens.
XX

XX Key Location/Qualifiers
FH Disulfide-bond 8..36 /note = predicted disulfide bond
FT Disulfide-bond 15..40 /note = predicted disulfide bond
FT Disulfide-bond 23..35 /note = predicted disulfide bond
FT Disulfide-bond 29..44 /note = predicted disulfide bond
FT Disulfide-bond 52..102 /note = predicted disulfide bond
FT Domain 52..102 /note = Kunitz domain predicted by pfscan
FT Disulfide-bond 52..102 /note = predicted disulfide bond
FT Disulfide-bond 61..85 /note = predicted disulfide bond
FT Disulfide-bond 77..98 /note = predicted disulfide bond
XX WO2003070770-A2.
XX 28-AUG-2003.
XX 18-FEB-2003; 2003WO-EP001629.
XX 21-FEB-2002; 2002US-0358683P.
XX (GENE-) GENEPROT INC.
XX Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX hemorrhage.
XX Claim 5; Page 71; 87pp; English.
XX The present invention describes an isolated, purified or recombinant DJ11

CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (SI, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents the mature form of an engineered human
CC DJ11 protein from the present invention.
XX
SQ Sequence 106 AA;
Query Match 80.9%; Score 106; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.6e-104;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EGIIGKCPKTKVCEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKDICSMPEAGP 85
DB 1 EGIIGKCPKTKVCEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKDICSMPEAGP 60
QY 86 CLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTCCKYH 131
DB 61 CLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTCCKYH 106

RESULT 4
ABP69809
ID ABP69809 standard; protein; 86 AA.
XX
AC ABP69809;
XX
DT 20-JAN-2003 (first entry)
XX Human polypeptide SEQ ID NO 1856.
XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
XX WO200270539-A2.
XX
PD 12-SEP-2002.
XX
XX 05-MAR-2002; 2002WO-US005095.
XX
XX 05-MAR-2001; 2001US-00799451.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX


```

DR WPI; 2002-759812/82.
DR N-PSDB; ABZ12026.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
XX Claim 9; SEQ ID NO 1856; 1012pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (ABZ11119-
XX ABZ12066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX platelet or coagulation disorders, wound, burns, incision, ulcers, liver
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX arthritis, etc. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 86 AA;
XX
XX Query Match 48.9%; Score 64; DB 5; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 9.4e-60;
XX Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTPRDCPENMKC 60
Dy |||||
Dy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTPRDCPENMKC 60
Qy 61 CPFS 64
Dy |||||
Dy 61 CPFS 64
XX
RESULT 5
ABJ26667
ID ABJ26667 standard; protein; 86 AA.
XX
AC ABJ26667;
XX
XX 01-MAY-2003 (first entry)
XX
XX Human protein modification + maintenance molecule protein SEQ ID No 21.
XX
XX Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
XX cerebroprotective; antiparkinsonian; nootropic; antiinflammatory;
XX antitumor; hepatotropic; gynaecological; antibacterial; virucide;
XX protozoacide; antiparasitic; cell proliferative disease; PMOD;
XX protein modification and maintenance molecule; immunogenic fragment;
XX cancer; autoimmune; inflammatory disease; neurological disorder;
XX gastrointestinal; developmental; vesicle trafficking disorder; infection;
XX protein-protein interaction; drug-target interaction;
XX gene expression profile; human.
XX
XX Homo sapiens.
XX
XX WO200300844-A2.
XX
XX 03-JAN-2003.
XX
XX 18-JUN-2002; 2002WO-US019360.
XX
XX 22-JUN-2001; 2001US-0300508P.
XX
XX 06-JUL-2001; 2001US-0303445P.
XX
XX 13-JUL-2001; 2001US-0305405P.
XX

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PR 09-AUG-2001; 2001US-0311442P.
PR 24-AUG-2001; 2001US-0314821P.
PR 29-AUG-2001; 2001US-0315992P.
PR 03-MAY-2002; 2002US-0378205P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Gandhi AR, Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggan BM,
XX Warren BA, Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Yue H;
XX Forsythe IJ, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang J;
XX Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG;
XX Wallia NK, Mason PM, Gururajan R, Lee S, Becha SD, Lee SY, Tran UK;
XX Elliott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zebbarjadian Y;
XX WPI; 2003-184039/18.
XX N-PSDB; ABT23220.
XX
XX New isolated human PMOD polypeptide and polynucleotide, useful for
XX diagnosing, treating and preventing diseases or conditions associated
XX with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis and
XX infections.
XX
XX Claim 76; Page 196; 225pp; English.
XX
XX The invention relates to an isolated polypeptide comprising: any of 28
XX sequences of 48-1256 amino acids; a natural amino acid sequence at least
XX 90% identical to the 28 amino acid sequences, 94% identical to a sequence
XX of 703 or 267 amino acids, 98% identical to a sequence of 414 amino
XX acids, or 97% identical to a sequence of 242 amino acids, all given in
XX the specification; or a biologically active or immunogenic fragment of
XX the isolated polypeptide. The polypeptides and polynucleotides are useful
XX in diagnosing, treating and preventing diseases or conditions associated
XX with the decreased expression of protein modification and maintenance
XX molecules (PMOD), such as cell proliferative diseases (e.g. cancer,
XX atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS,
XX allergies), gastrointestinal disorders (e.g. stroke, Parkinson's disease,
XX epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g.
XX endometriosis), developmental, vesicle trafficking disorders, and
XX infections (e.g. bacterial, viral, parasitic, protozoal). These are also
XX useful in assessing the effects of exogenous compounds on the expression
XX of nucleic acid and amino acid sequences of PMOD. The PMOD or its
XX fragments are useful in screening compounds for effectiveness as agonist
XX or antagonist of the polypeptides, or in altering the expression of the
XX target polynucleotide and compounds that specifically bind to or modulate
XX the activity of the polypeptide. The microarray is useful in monitoring
XX or measuring protein-protein interactions, drug-target interactions, and
XX gene expression profiles. This sequence represents a human PMOD protein
XX of the invention
XX
XX Sequence 86 AA;
XX
XX Query Match 48.9%; Score 64; DB 6; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 9.4e-60;
XX Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTPRDCPENMKC 60
Dy |||||
Dy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTPRDCPENMKC 60
Qy 61 CPFS 64
Dy |||||
Dy 61 CPFS 64
XX
RESULT 6
ADA19808
ID ADA19808 standard; protein; 98 AA.
XX
XX ADA19808;
XX
XX 20-NOV-2003 (first entry)
XX
XX Engineered human DU11 partial amino acid sequence SEQ ID NO:9.
XX

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XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipruritic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX Disclosure; Page 82; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipruritic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a partial engineered human DJ11 protein
 CC amino acid sequence from the present invention.
 XX Sequence 98 AA;
 SQ
 Query Match 48.9%; Score 64; DB 7; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1e-59;
 Matches 64; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 MGLSGLLPILVFLIGDIOBPGHAEILGKPCPKIKVCEVEEIDQCTKPRDCPENMKC 60
 DB 1 MGLSGLLPILVFLIGDIOBPGHAEILGKPCPKIKVCEVEEIDQCTKPRDCPENMKC 60
 QY 61 CPFS 64
 DB 61 CPFS 64

RESULT 7
 ABB12236
 ID ABB12236 standard; peptide; 101 AA.
 XX
 AC ABB12236;
 DT 11-JAN-2002 (first entry)
 DE Human eppin-1 homologue, SEQ ID NO:2606.
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnary; antiulcer.
 XX Homo sapiens.
 OS
 XX WO200157188-A2.
 XX 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US003800.
 XX 03-FEB-2000; 2000US-00496914.
 XX 27-APR-2000; 2000US-00560875.
 XX (HVSE-) HVSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 WPI; 2001-457740/49.
 N-PSDB; ABA09480.
 Human proteins and DNA encoding sequences useful for preventing, treating
 and ameliorating a medical condition in a mammalian subject e.g. arthritis
 and cancer.
 Claim 20; Page 318; 1963pp; English.
 Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 invention also relates to vectors and recombinant host cells comprising a
 nucleotide of the invention, methods of producing the novel polypeptides,
 antibodies against the polypeptides, methods of detecting the nucleotides
 or polypeptides in a sample, and methods of identifying compounds which
 bind to polypeptides of the invention. Although novel, many of the
 polypeptides of the invention have homology to known proteins, thereby
 giving an insight into their probable biological activities, and hence
 potential therapeutic applications. The polypeptides of the invention may
 have various activities, including cytokine, cell proliferation or cell
 differentiation activities; stem cell growth factor activity;
 haematopoiesis regulatory activity; tissue growth activity;
 immunomodulatory activity; activin- or inhibin-related activities;
 chemotactic or chemokinetic activities; haemostatic, thrombotic or
 thrombolytic activities; receptor or ligand activities; or may be
 involved in oncogenesis, cancer cell proliferation or metastasis.
 Depending on their biological activities, polypeptides and nucleotides of
 the invention are useful for preventing, treating or ameliorating medical
 conditions, e.g., by protein or gene therapy. Such conditions include
 cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 proliferative retinopathy, atherosclerosis, coronary heart disease,
 arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (of nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention

XX Sequence 101 AA;

Query Match 48.9%; Score 64; DB 4; Length 101;
 Best Local Similarity 100.0%; Pred. No. 1.1e-59;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Db 16 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 75

Qy 61 CPFS 64
 Db 76 CPFS 79

RESULT 8
 ADA19814

ID ADA19814 standard; protein; 131 AA.

XX ADA19814;

XX 20-NOV-2003 (first entry)

XX Human DJ11 protein SEQ ID NO:15.

XX DJ11; Kunitz-type protease inhibitor domain; antinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Homo sapiens.

XX W02003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI, 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11

CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a human DJ11 protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.

XX Sequence 131 AA;

Query Match 48.9%; Score 64; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.3e-59;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Qy 61 CPFS 64

Db 61 CPFS 64

RESULT 9
 ADA19804

ID ADA19804 standard; protein; 43 AA.

XX ADA19804;

XX 20-NOV-2003 (first entry)

XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:5.

XX DJ11; Kunitz-type protease inhibitor domain; antinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.

XX Homo sapiens.

XX W02003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

DR WPI; 2003-663849/62.
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Disclosure; Page 79; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX polypeptidally active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, anti-allergic, thrombolytic,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antipariatic and vulnerary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents a partial engineered human DJ11 protein
XX amino acid sequence from the present invention.
XX
XX Sequence 43 AA;
XX
XX Query Match 25.2%; Score 33; DB 7; Length 43;
XX Best Local Similarity 100.0%; Pred. No. 4.6e-27;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 32 PCPKIKVEVEEIDQCTKPRDCPENMKCCPFS 64
XX |||||
XX DB 1 PCPKIKVEVEEIDQCTKPRDCPENMKCCPFS 33
XX
XX RESULT 10
XX ABM85103
XX ID ABM85103 standard; protein; 179 AA.
XX
XX AC ABM85103;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5352.
XX
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
XX OS Homo sapiens.
XX
XX PN WO2004023973-A2.
XX
XX PD 25-MAR-2004.
XX
XX PF 12-SEP-2003; 2003WO-05028227.
XX
XX PR 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX
XX PA (INCY-) INCYTE CORP.
XX
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Eider LV;
XX Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Legace RE, Spiro FA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
XX N-PSDB; ACN43755.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dithp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a dithp protein of the
XX invention. Note: The present sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
XX Sequence 179 AA;
XX
XX Query Match 25.2%; Score 33; DB 8; Length 179;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-26;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 32 PCPKIKVEVEEIDQCTKPRDCPENMKCCPFS 64
XX |||||
XX DB 132 PCPKIKVEVEEIDQCTKPRDCPENMKCCPFS 164
XX
XX RESULT 11
XX ADA19803
XX ID ADA19803 standard; peptide; 30 AA.
XX
XX AC ADA19803;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:4.
XX
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
XX antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX nephrotropic; antipariatic; vulnerary; protease inhibitor; gene therapy;
XX acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX deep vein thrombosis; myocardial infarction; shock; septic shock;
XX hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX chronic inflammatory bowel disease; psoriasis.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX PN WO2003070770-A2.
XX
XX PD 28-AUG-2003.
XX
XX PF 18-FEB-2003; 2003WO-EP001629.
XX
XX PR 21-FEB-2002; 2002US-0358683P.


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XX PA (GENE-) GENEPROT INC.
XX PI Bougueleret L, Bairoch A, Niknejad A;
XX DR WPI; 2003-663849/62.
XX XX
XX PT New engineered human Kunitz-type protease inhibitor for diagnosing,
XX PT preventing or treating conditions associated with excessive proteinase
XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX PT hemorrhage.
XX PS Disclosure; Page 79; 87pp; English.
XX CC The present invention describes an isolated, purified or recombinant DJ11
XX CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX CC biologically active portion. The polypeptide comprises at least 98 %
XX CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
XX CC activities, and can be used as a protease inhibitor and in gene therapy.
XX CC Composition and methods for the present invention can be used in
XX CC diagnosing, preventing or treating conditions associated with excessive
XX CC proteinase activity, such as acute pancreatitis, pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, myocardial
XX CC infarction, shock (including septic shock), hyperfibrinolytic
XX CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX CC be used in preserving platelet function, organ preservation or in wound
XX CC healing. The polynucleotide sequence encoding DJ11 may be used as
XX CC hybridisation probes, in chromosome and gene mapping, in the generation
XX CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX CC The present sequence represents a partial engineered human DJ11 protein
XX CC amino acid sequence from the present invention.
XX SQ Sequence 30 AA;
XX Query Match 22.9%; Score 30; DB 7; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 5.2e-24;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGLSGLLPILVPFILLGDIQPGHAEGLG 30
Db 1 MGLSGLLPILVPFILLGDIQPGHAEGLG 30
RESULT 12
ADAL9805
ID ADAL9805 standard; peptide; 24 AA.
XX AC ADA19805;
XX XX
XX DT 20-NOV-2003 (first entry)
XX DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:6.
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
XX KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
XX KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX KW deep vein thrombosis; myocardial infarction; shock; septic shock;
XX KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX KW chronic inflammatory bowel disease; psoriasis.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO2003070770-A2.

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XX PD 28-AUG-2003.
XX PF 18-FEB-2003; 2003WO-EP001629.
XX XX
XX PR 21-FEB-2002; 2002US-0358683P.
XX XX
XX PA (GENE-) GENEPROT INC.
XX PI Bougueleret L, Bairoch A, Niknejad A;
XX XX
XX DR WPI; 2003-663849/62.
XX XX
XX PT New engineered human Kunitz-type protease inhibitor for diagnosing,
XX PT preventing or treating conditions associated with excessive proteinase
XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX PT hemorrhage.
XX PS Disclosure; Page 79-80; 87pp; English.
XX CC The present invention describes an isolated, purified or recombinant DJ11
XX CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX CC biologically active portion. The polypeptide comprises at least 98 %
XX CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
XX CC activities, and can be used as a protease inhibitor and in gene therapy.
XX CC Composition and methods for the present invention can be used in
XX CC diagnosing, preventing or treating conditions associated with excessive
XX CC proteinase activity, such as acute pancreatitis, pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, myocardial
XX CC infarction, shock (including septic shock), hyperfibrinolytic
XX CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX CC be used in preserving platelet function, organ preservation or in wound
XX CC healing. The polynucleotide sequence encoding DJ11 may be used as
XX CC hybridisation probes, in chromosome and gene mapping, in the generation
XX CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX CC The present sequence represents a partial engineered human DJ11 protein
XX CC amino acid sequence from the present invention.
XX SQ Sequence 24 AA;
XX Query Match 18.3%; Score 24; DB 7; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1e-17;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 75 DICSMPOEAGPCLASTPHWYNNK 98
Db 1 DICSMPOEAGPCLASTPHWYNNK 24
RESULT 13
ADAL9806
ID ADAL9806 standard; peptide; 33 AA.
XX AC ADA19806;
XX XX
XX DT 20-NOV-2003 (first entry)
XX DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:7.
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
XX KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
XX KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX KW deep vein thrombosis; myocardial infarction; shock; septic shock;
XX KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;

```


KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX hemorrhage.
 XX Disclosure; Page 80; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
 XX biologically active portion. The polypeptide comprises at least 98 %
 XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
 XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnarary
 XX activities, and can be used as a protease inhibitor and in gene therapy.
 XX Composition and methods from the present invention can be used in
 XX diagnosing, preventing or treating conditions associated with excessive
 XX proteinase activity, such as acute pancreatitis, pulmonary injury,
 XX allergy-induced protease release, deep vein thrombosis, myocardial
 XX infarction, shock (including septic shock), hyperfibrinolytic
 XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 XX be used in preserving platelet function, organ preservation or in wound
 XX healing. The polynucleotide sequence encoding DJ11 may be used as
 XX hybridisation probes, in chromosome and gene mapping, in the generation
 XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 XX The present sequence represents a partial engineered human DJ11 protein
 XX amino acid sequence from the present invention.
 XX Sequence 33 AA;
 XX Query Match 16.0%; Score 21; DB 7; Length 33;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e-14;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 111 QGNNNNFQTEAICLVTCCKYH 131
 DB 13 QGNNNNFQTEAICLVTCCKYH 33
 RESULT 14
 ADA19809
 ID ADA19809 standard; peptide; 33 AA.
 XX ADA19809;
 XX 20-NOV-2003 (first entry)
 XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:10.
 DE DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 XX

KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antiporiatic; vulnarary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX hemorrhage.
 XX Disclosure; Page 82-83; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
 XX biologically active portion. The polypeptide comprises at least 98 %
 XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
 XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnarary
 XX activities, and can be used as a protease inhibitor and in gene therapy.
 XX Composition and methods from the present invention can be used in
 XX diagnosing, preventing or treating conditions associated with excessive
 XX proteinase activity, such as acute pancreatitis, pulmonary injury,
 XX allergy-induced protease release, deep vein thrombosis, myocardial
 XX infarction, shock (including septic shock), hyperfibrinolytic
 XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 XX be used in preserving platelet function, organ preservation or in wound
 XX healing. The polynucleotide sequence encoding DJ11 may be used as
 XX hybridisation probes, in chromosome and gene mapping, in the generation
 XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 XX The present sequence represents a partial engineered human DJ11 protein
 XX amino acid sequence from the present invention.
 XX Sequence 33 AA;
 XX Query Match 16.0%; Score 21; DB 7; Length 33;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e-14;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 111 QGNNNNFQTEAICLVTCCKYH 131
 DB 13 QGNNNNFQTEAICLVTCCKYH 33
 RESULT 15
 ADA19813
 ID ADA19813 standard; protein; 134 AA.
 XX ADA19813;
 XX

DT 20-NOV-2003 (first entry)
 DE Mouse EPPIN protein SEQ ID NO:14.
 XX
 KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antiporiatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis; EPPIN.
 XX
 OS Mus musculus.
 XX
 XX WO2003070770-A2.
 XX
 XX 28-AUG-2003.
 XX
 XX 18-FEB-2003; 2003WO-EP001629.
 XX
 XX 21-FEB-2002; 2002US-0358683P.
 XX
 XX (GENE-) GENEPROT INC.
 XX
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX
 XX WPI; 2003-663849/62.
 XX
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX hemorrhage.
 XX
 XX Disclosure; Fig 1; 87pp; English.
 XX
 XX The present invention describes an isolated, purified or recombinant DJ11
 XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
 XX biologically active portion. The polypeptide comprises at least 98 %
 XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
 XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnary
 XX activities, and can be used as a protease inhibitor and in gene therapy.
 XX Composition and methods from the present invention can be used in
 XX diagnosing, preventing or treating conditions associated with excessive
 XX proteinase activity, such as acute pancreatitis, pulmonary injury,
 XX allergy-induced protease release, deep vein thrombosis, myocardial
 XX infarction, shock (including septic shock) hyperfibrinolytic
 XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 XX be used in preserving platelet function, organ preservation or in wound
 XX healing. The polynucleotide sequence encoding DJ11 may be used as
 XX hybridisation probes, in chromosome and gene mapping, in the generation
 XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 XX The present sequence represents a mouse EPPIN protein given in comparison
 XX with DJ11 proteins in the exemplification of the present invention.
 XX
 XX Sequence 134 AA;

Query Match 10.7%; Score 14; DB 7; Length 134;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FYGGCGGNNNNFQ 118
 Db 105 FYGGCGGNNNNFQ 118
 |||||

RESULT 16

AAE13096
 ID AAE13096 standard; peptide; 43 AA.
 XX
 AC AAE13096;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Human serine proteinase inhibitor BTL.009 peptide fragment #2.
 XX
 KW Human, BTL.009 protein; serine proteinase inhibitor; cytostatic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angiodiastis;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.
 XX
 XX Homo sapiens.
 XX
 XX US6294648-B1.
 XX
 XX 25-SEP-2001.
 XX
 XX 20-JUL-1999; 99US-00358569.
 XX
 XX 20-JUL-1999; 99US-00358569.
 XX
 XX (FARB) BAYER CORP.
 XX
 XX Delaria K, Roczniaak S, Davies C;
 XX
 XX WPI; 2001-662224/76.
 XX
 XX New isolated protein for inhibiting human serine proteinase activity in the
 XX treatment of e.g. emphysema and adult respiratory distress syndrome.
 XX
 XX Disclosure; Col 5-6; 16pp; English.
 XX
 XX The invention relates to human BTL.009 protein, a serine proteinase
 XX inhibitor of the Kunitz family that exhibits greater potency towards
 XX neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
 XX elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
 XX protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 XX adult respiratory distress syndrome, cystic fibrosis, rheumatoid
 XX arthritis, organ failure, glomerulonephritis, other inflammatory diseases
 XX and diseases involving lung and vascular injury. BTL.009 is also useful
 XX for preventing neutrophil and monocyte activation and formation of active
 XX oxygen species during the oxidative burst of stimulated granulocytes.
 XX BTL.009 is useful for reducing platelet activation and blood coagulation
 XX and for the prophylactic or therapeutic treatment of patients undergoing
 XX angioplasty. The present sequence is human serine proteinase inhibitor
 XX BTL.009 peptide fragment related to the invention
 XX
 XX Sequence 43 AA;
 XX
 XX Query Match 9.2%; Score 12; DB 4; Length 43;
 XX Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 107 YGGCGGNNNNFQ 118
 Db 21 YGGCGGNNNNFQ 32
 |||||

RESULT 17
 AAW75257

ID AAW75257 standard; protein; 51 AA.

XX AAW75257;

DT 29-JAN-1999 (first entry)

DE Fragment of human secreted protein encoded by gene 24.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX Homo sapiens.
 XX WO9840483-A2.
 XX 17-SEP-1998.
 XX 12-MAR-1998; 98WO-US004858.
 XX 14-MAR-1997; 97US-0040710P.
 XX 14-MAR-1997; 97US-0040762P.
 XX 30-MAY-1997; 97US-0048100P.
 XX 30-MAY-1997; 97US-0048189P.
 XX 30-MAY-1997; 97US-0048357P.
 XX 30-MAY-1997; 97US-0050934P.
 XX 06-JUN-1997; 97US-0048970P.
 XX 05-SEP-1997; 97US-0057765P.
 XX 19-DEC-1997; 97US-0068368P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX WPI; 1998-520811/44.
 DR N-PSDB; AAV34309.
 XX Isolated human poly:nucleotide(s) encoding secretory peptide(s) - used to
 PT develop products for the diagnosis and treatment of e.g. inflammation,
 PT cancers, CNS disorders or immune system disorders.
 XX Disclosure; Page 24; 201pp; English.
 CC This sequence represents a fragment of a secreted human protein encoded
 CC by the nucleic acid molecule designated Gene 24 (AAV34309). The gene can
 CC be used to generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of
 CC the fused protein as compared to the human protein only. The invention
 CC relates to 28 novel genes and their fragments (nucleic acid sequences:
 CC AAV34286-V34325; amino acid sequences AAV75196-W75235) which are useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. Also, pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 28 polynucleotides, based on
 CC which tissues they are most highly expressed in (see AAV34286 for
 CC described uses)
 XX Sequence 51 AA;
 SQ
 Query Match 9.2%; Score 12; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 107 YGCGCGNNNFQ 118
 DB 31 YGCGCGNNNFQ 42
 RESULT 18
 AAE27025
 ID AAE27025 standard; protein; 51 AA.
 XX

AC AAE27025;
 XX 13-DEC-2002 (first entry)
 DT Human gene 24 encoded secreted protein variant, SEQ ID NO:118.
 DE Human; immunodeficiency; X-linked agammaglobulinemia; septic shock;
 XX autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropic; vulvare; cytostatic; nootropic; cardiac;
 KW anti-HIV; tranquilliser; gout; antiparasitic.
 XX Homo sapiens.
 OS US2002077287-A1.
 PN 20-JUN-2002.
 XX 11-MAY-2001; 2001US-00852659.
 PF 11-SEP-1998; 98US-00152060.
 XX (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX WPI; 2002-598780/64.
 XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 XX Disclosure; Page 16; 209pp; English.
 PS
 XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory

CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
CC sarcoidosis and allogeneic transplant rejection, blood-related disorder
CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
CC lung cancer, allergic disorders, pneumonitis, renal disorders. e.g. acute
CC glomerulonephritis, neurological diseases, liver disorders, endocrine
CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
CC infectious diseases and reproductive system disorders e.g. endometriosis.
CC The present sequence represents a human secreted protein variant of the
CC invention

XX SQ Sequence 51 AA;

Query Match 9.2%; Score 12; DB 5; Length 51;

Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 0;

Qy 107 YGGCQGNNNFQ 118

Db 31 YGGCQGNNNFQ 42

RESULT 19

AAE27163
ID AAE27163 standard; protein; 51 AA.

XX AC AAE27163;

XX DT 13-DEC-2002 (first entry)

XX DE Human gene 24 encoded secreted protein fragment kunitz-type domain.

XX KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnerary.

XX OS Homo sapiens.

XX PN US2002076756-A1.

XX PD 20-JUN-2002.

XX PF 11-MAY-2001; 2001US-00853161.

XX PR 02-FEB-2001; 2001US-0265583P.

XX PA (RUBE/) RUBEN S M.

XX PA (ROSE/) ROSEN C A.

XX PA (LIYY/) LI Y.

XX PA (ZENG/) ZENG Z.

XX PA (KYAW/) KYAW H.

XX PA (FISC/) FISCHER C L.

XX PA (LIHH/) LI H.

XX PA (SOPP/) SOPPET D R.

XX PA (GENT/) GENTZ R L.

XX PA (WEIY/) WEI Y.

XX PA (MOOR/) MOORE P A.

XX PA (YOUN/) YOUNG P E.

XX PA (GREE/) GREENE J M.

XX PA (FERR/) FERRIE A M.

XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;

XX DR WPI; 2002-574454/61.

XX PT New nucleic acid molecules encoding 28 human secreted proteins, useful
XX for diagnosing, preventing, treating or ameliorating medical conditions
XX and as food additives or preservatives.

XX PS Disclosure; Page 16; 209pp; English.

XX CC AAD4854-AAD4984 represent cDNAs corresponding to 28 human secreted
XX protein genes, and AAE27097-AAE27137 represent the proteins they encode.
XX CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
XX and their corresponding secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Secreted protein sequences of the invention are useful for the
XX diagnosis or treatment of disorders such as autoimmune diseases (e.g.
XX rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
XX the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
XX angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
XX system disorders (e.g. Alzheimer's disease), infections caused by fungi,
XX bacteria and viruses and ocular disorders (e.g. corneal infection). The
XX polypeptides can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues and in chemotaxis. They can also be used as food
XX additives or preservative to increase or decrease storage capabilities,
XX fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
XX and other nutritional components. The present sequence represents a human
XX secreted protein fragment kunitz-type domain referred to in the
XX disclosure of the invention

XX SQ Sequence 51 AA;

Query Match 9.2%; Score 12; DB 5; Length 51;

Best Local Similarity 100.0%; Pred. No. 0.00011;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNFQ 118

Db 31 YGGCQGNNNFQ 42

RESULT 20

ADG89845

ID ADG89845 standard; protein; 51 AA.

XX AC ADG89845;

XX DT 11-MAR-2004 (first entry)

XX DE Human secreted protein gene 24 protein #3.

XX KW Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.

XX OS Homo sapiens.

XX PN US2003225009-A1.

XX PD 04-DEC-2003.

XX PF 30-JAN-2002; 2002US-00058993.

XX PR 14-MAR-1997; 97US-0040710P.

XX PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
PR 11-MAY-2001; 2001US-00852659.
PR 11-MAY-2001; 2001US-00852797.
PR 11-MAY-2001; 2001US-00853161.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.
XX
PI Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
DR WPI; 2004-042167/04.
XX
PT New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
PS Disclosure; SEQ ID NO 118; 320pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, a domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative

CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.
XX
XX Sequence 51 AA;
XX
XX Query Match 9.2%; Score 12; DB 8; Length 51;
XX Best Local Similarity 100.0%; Pred. No. 0.00011;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 107 YGGCGGNNNNFQ 118
XX |||||
XX DB 31 YGGCGGNNNNFQ 42
XX
XX RESULT 21
XX AAEL13084
XX ID AAEL13084 standard; peptide; 58 AA.
XX AC AAEL13084;
XX DT 28-JAN-2002 (first entry)
XX DE Human serine proteinase inhibitor BTL.009 peptide.
XX KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
XX KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
XX KW rheumatoid arthritis; adult respiratory distress syndrome; angiotensin;
XX KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
XX KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
XX KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
XX KW therapeutic.
XX OS Homo sapiens.
XX PN US6294648-B1.
XX PD 25-SEP-2001.
XX PF 20-JUL-1999; 99US-00358569.
XX PR 20-JUL-1999; 99US-00358569.
XX (FARB) BAYER CORP.
XX PI Delaria K, Roczniak S, Davies C;
XX WPI; 2001-662224/76.
XX
XX New isolated protein for inhibiting human serine protease activity in the
XX treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
XX Claim 1; Col 15-16; 16pp; English.
XX
XX The invention relates to human BTL.009 protein, a serine proteinase
XX inhibitor of the Kunitz family that exhibits greater potency towards
XX neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
XX elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
XX protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
XX adult respiratory distress syndrome, cystic fibrosis, rheumatoid
XX arthritis, organ failure, glomerulonephritis, other inflammatory diseases
XX and diseases involving lung and vascular injury. BTL.009 is also useful
XX for preventing neutrophil and monocyte activation and formation of active
XX oxygen species during the oxidative burst of stimulated granulocytes.
XX BTL.009 is useful for reducing platelet activation and blood coagulation
XX and for the prophylactic or therapeutic treatment of patients undergoing


```

XX SQ Sequence 58 AA;
Query Match 9.2%; Score 12; DB 7; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNNFQ 118
DB 35 YGGCGGNNNNFQ 46

RESULT 24
ADL16838
ID ADL16838 standard; peptide; 58 AA.
XX AC ADL16838;
XX DT 06-MAY-2004 (first entry)
XX DE Human Kunitz domain (KD) peptide.
XX KW BTL.010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;
XX KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
XX KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
XX KW inflammatory disease; oxidative burst; platelet activation;
XX KW blood coagulation; gene therapy; human; KD.
XX OS Homo sapiens.
XX PN US6689582-B1.
XX PD 10-FEB-2004.
XX PF 12-MAY-2000; 2000US-00569670.
XX PR 05-AUG-1999; 99US-00369494.
XX PA (FARB ) BAYER PHARM CORP.
XX PI Davies C, Chen D, Roczniak S;
XX WPI; 2004-141424/14.
XX New isolated polynucleotide encoding BTL.010 serine proteinase, useful
XX for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
XX respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
XX glomerulonephritis.
XX Disclosure; SEQ ID NO 8; 17pp; English.
XX The invention relates to BTL.010, a human serine proteinase inhibitor of
XX the Kunitz family and its corresponding nucleic acid sequence. The
XX sequences of the invention are useful for treating diseases, e.g.
XX emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
XX syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
XX glomerulonephritis or inflammatory diseases. The BTL.010 protein is also
XX useful for preventing neutrophil and monocyte activation and formation of
XX active oxygen species during the oxidative burst of stimulated
XX granulocytes. It is also useful for reducing platelet activation and
XX blood coagulation. BTL.010 DNA is useful in gene therapy. The present
XX sequence is human Kunitz domain (KD) peptide.
XX SQ Sequence 58 AA;
Query Match 9.2%; Score 12; DB 8; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNNFQ 118
DB 35 YGGCGGNNNNFQ 46

RESULT 25
ADR89980
ID ADR89980 standard; peptide; 58 AA.
XX AC ADR89980;
XX DT 18-NOV-2004 (first entry)
XX DE Human CAB37 protein kunitz domain peptide.
XX KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
XX KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
XX KW cytostatic; haemostatic; CAB37 protein; human.
XX OS Homo sapiens.
XX PN US2004171794-A1.
XX PD 02-SEP-2004.
XX PF 07-FEB-2003; 2003US-00361997.
XX PR 07-FEB-2003; 2003US-00361997.
XX PA (LADN/) LADNER R C.
XX PA (LEVA/) LEY A C.
XX PI Ladner RC, Ley AC;
XX WPI; 2004-625120/60.
XX New Kunitz domain peptide useful as human neutrophil elastase inhibitor
XX for the treatment of e.g. cystic fibrosis and related disease.
XX Disclosure; SEQ ID NO 5; 123pp; English.
XX The invention relates to proteins comprising kunitz domain peptide,
XX designated DPI-14 for inhibiting human neutrophil elastase, fused to
XX albumin. The invention is useful for treating cystic fibrosis and related
XX diseases, hereditary angioedema, cancer and related diseases including
XX chronic obstructive pulmonary disease, asthma, bronchitis, acute
XX respiratory syndrome, pneumonia and bleeding. The invention acts as a
XX cytostatic and haemostatic agent. The present sequence is the human CAB37
XX protein (A4) kunitz domain peptide. This sequence is used in the
XX invention.
XX SQ Sequence 58 AA;
Query Match 9.2%; Score 12; DB 8; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNNFQ 118
DB 35 YGGCGGNNNNFQ 46

RESULT 26
AAE13093
ID AAE13093 standard; peptide; 64 AA.
XX AC AAE13093;
XX DT 28-JAN-2002 (first entry)
XX DE Human serine proteinase inhibitor BTL.009 C-terminal peptide.
XX KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
XX KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
XX KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
XX KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;

```


KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
XX Homo sapiens.
OS
XX US6294648-B1.
PN
XX
XX 25-SEP-2001.
PD
XX
XX 20-JUL-1999; 99US-00358569.
PF
XX
XX 20-JUL-1999; 99US-00358569.
PR
XX
XX (FARB) BAYER CORP.
PA
XX Delaria K, Rocznik S, Davies C;
PI
XX WPI; 2001-662224/76.
DR
XX
XX New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
XX
XX Disclosure; Col 6; 16pp; English.
XX
XX The invention relates to human BTL 009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL 009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL 009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL 009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL 009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL 009 C-terminal peptide containing Kunitz domain which is used in the
CC exemplification of the invention
XX
XX Sequence 64 AA;
SQ
Query Match 9.2%; Score 12; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.00013; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;
Qy 107 YGGCGGNNNFQ 118
Db 37 YGGCGGNNNFQ 48
RESULT 27
AAE27095
ID AAE27095 standard; protein; 102 AA.
XX
XX AAE27095;
AC
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Human secreted protein #2.
DE
XX
XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotrophic; vulnery; cytostatic; nootropic; cardiant;

KW anti-HIV; tranquilliser; gout; antiparasitic.
XX
XX Homo sapiens.
OS
XX US2002077287-A1.
PN
XX
XX 20-JUN-2002.
PD
XX
XX 11-MAY-2001; 2001US-00852659.
PF
XX
XX 11-SEP-1998; 98US-00152060.
PR
XX
XX (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (FYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2002-598780/64.
DR
XX
XX Novel human secreted polypeptides and polynucleotides for diagnosing,
PT preventing, treating immune, hyperproliferative, cardiovascular, of
PT neurological, reproductive disorders and identifying modulators of
PT therapeutic use.
XX
XX Disclosure; Page 16; 209pp; English.
XX
XX AAD4636-ABD44676 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
CC AAE27000-AAE27025 represent human secreted protein fragments or their
CC variants. The secreted proteins and genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Specific uses are described for each of the 28 genes, based on
CC the tissues in which they are most highly expressed and include
CC developing products for the diagnosis or treatment of immunodeficiencies,
CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
CC sarcoidosis and allogeneic transplant rejection, blood-related disorder
CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
CC lung cancer, allergic disorders, pneumonitis, renal disorders. e.g. acute
CC glomerulonephritis, neurological diseases, liver disorders, endocrine
CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
CC infectious diseases and reproductive system disorders e.g. endometriosis.
CC The present sequence represents a human secreted protein of the invention
XX
XX Sequence 102 AA;


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Query Match      9.2%; Score 12; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNFQ 118
DB 76 YGGCGGNNNFQ 87

RESULT 28
AAE28009
ID AAE28009 standard; protein; 102 AA.
XX
AC AAE28009;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human gene 24 encoded secreted protein fragment #2.
XX
KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnary.
XX
OS Homo sapiens.
XX
PN US2002076756-A1.
XX
PD 20-JUN-2002.
XX
PF 11-MAY-2001; 2001US-00853161.
XX
PR 02-FEB-2001; 2001US-0265583P.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIJH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
DR WPI; 2002-574454/61.
XX
PT New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
XX Disclosure; Page 17; 209pp; English.
XX
AAAD4854-AAA44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.

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CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment referred to in the disclosure of the invention
XX
SQ Sequence 102 AA;

Query Match      9.2%; Score 12; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNFQ 118
DB 76 YGGCGGNNNFQ 87

RESULT 29
ABU65039
ID ABU65039 standard; peptide; 102 AA.
XX
AC ABU65039;
XX
DT 15-MAY-2003 (first entry)
XX
DE Human secreted protein gene 24, protein #3.
XX
KW Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
KW body height; hair colour; human.
XX
OS Homo sapiens.
XX
PN US2002172994-A1.
XX
PD 21-NOV-2002.
XX
PF 11-MAY-2001; 2001US-00852797.
XX
PR 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-0015206P.
PR 02-FEB-2001; 2001US-0265583P.
XX
XX (RUBE/) RUBEN S M.
XX (ROSE/) ROSEN C A.

```


PA (LIYY//) LI Y.
PA (ZENG//) ZENG Z.
PA (KYAW//) KYAW H.
PA (FISC//) FISCHER C L.
PA (LIHH//) LI H.
PA (SOPP//) SOPPET D R.
PA (GENT//) GENTZ R L.
PA (WEIY//) WEI Y.
PA (MOOR//) MOORE P A.
PA (YOUN//) YOUNG P E.
PA (GREE//) GREENE J M.
PA (FERR//) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2003-310989/30.
XX
XX New human secreted polypeptides and polynucleotides for diagnosing,
PT prognosing, preventing and treating immune, hyperproliferative, liver,
PT kidney, reproductive disorders and for identifying modulators of
PT therapeutic use.
XX
XX Disclosure; Page 16; 209pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an amino acid
CC sequence at least 95% identical to sequence of 28 human secreted
CC proteins, their fragment, polypeptide domain, epitope, secreted form,
CC variant, allelic variant, or species homologue, or the encoded sequence
CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
CC acids, recombinant vectors, host cells, antibodies, and genes. The
CC proteins and nucleic acids are useful for diagnosing, preventing,
CC treating, prognosing or ameliorating a medical condition e.g.
CC immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell
CC immunodeficiencies, severe combined immunodeficiencies), autoimmune
CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia, multiple
CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
CC injury and/or stroke, traumatic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
CC dementia, and prion disease), cardiovascular disorders (e.g.
CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
CC pancreatitis, sarcoidosis, dermatitis, allogenic transplant rejection),
CC blood-related disorders (thrombosis, arterial thrombosis),
CC hyperproliferative disorders, renal disorders (e.g. acute
CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
CC hyperthyroidism, hyperpituitarism), liver diseases and disorders,
CC reproductive system disorders (e.g. endometriosis), infectious diseases,
CC and pancreatic disorders. Many other diseases and disorders are listed in
CC the specification. They also useful as a vaccine adjuvant. Further they
CC are useful to enhance or inhibit complement mediated cell lysis, for
CC stimulating wound and tissue repair, angiogenesis, and the repair of
CC vascular or lymphatic diseases or disorders. They are also useful to
CC prevent hair loss, to modulate mammalian characteristics such as body
CC height, weight, hair colour, and to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors or other nutritional components. The proteins are
CC also useful for identifying binding partners. The present sequence
CC represents a secreted protein of the invention
XX
SQ Sequence 102 AA;

Query Match 9.2%; Score 12; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGNNNNNFQ 118
Db |||||
76 YGGCGNNNNNFQ 87
RESULT 30
ADG89848
ID ADG89848 standard; protein; 102 AA.
XX
XX AC ADG89848;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human secreted protein gene 24 protein #6.
XX
XX Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.
XX
XX Homo sapiens.
XX
XX US2003225009-A1.
XX
XX 04-DEC-2003.
XX
XX 30-JAN-2002; 2002US-00058993.
XX
XX 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050334P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US0004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
PR 11-MAY-2001; 2001US-0085285P.
PR 11-MAY-2001; 2001US-00852797.
PR 11-MAY-2001; 2001US-00853161.
XX (ROSE//) ROSEN C A.
PA (RUBE//) RUBEN S M.
PA (LIYY//) LI Y.
PA (ZENG//) ZENG Z.
PA (KYAW//) KYAW H.
PA (FISC//) FISCHER C L.
PA (LIHH//) LI H.
PA (SOPP//) SOPPET D R.
PA (GENT//) GENTZ R L.
PA (WEIY//) WEI Y.
PA (MOOR//) MOORE P A.
PA (YOUN//) YOUNG P E.
PA (GREE//) GREENE J M.
PA (FERR//) FERRIE A M.
PA (HAST//) HASTINGS G A.
XX
XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
XX WPI; 2004-042167/04.

New polypeptides and nucleic acid molecules for diagnosing, preventing or
treating diseases associated with aberrant expression or activity of the
polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

XX Disclosure; SEQ ID NO 121; 320pp; English.

PS The invention relates to an isolated nucleic acid molecule encoding a

XX secreted protein that is at least 95% identical to a polynucleotide

CC fragment of any of the nucleotide sequences listed in table 1A of the

CC specification, which is hybridisable to the nucleotide sequences, a

CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain

CC or epitope of any of the amino acid sequences) listed in table 1A of the

CC specification, a polynucleotide which is an (allelic) variant of the

CC nucleotide sequences listed in the specification, a polynucleotide which

CC encodes a species homologue of the above amino acid sequences, a

CC polynucleotide capable of hybridising under stringent conditions to any

CC of the above polynucleotides, where the polynucleotide does not hybridise

CC under stringent conditions to a nucleic acid molecule having a nucleotide

CC sequence of only A or T residues. Also included are a recombinant vector

CC comprising the above nucleic acid molecule, making a recombinant host

CC cell comprising the above nucleic acid molecule, an isolated polypeptide

CC comprising a sequence that is at least 95% identical to the polypeptide

CC (or its fragment, domain, epitope, secreted form, (allelic) variant or

CC homologue) encoded by the above nucleic acid molecule, an isolated

CC antibody that binds specifically to the above polypeptide, a recombinant

CC host cell produced by the above method and that expresses the above

CC polypeptide, making an isolated polypeptide, preventing, treating or

CC ameliorating a medical condition, diagnosing a pathological condition or

CC a susceptibility to a pathological condition in a subject, identifying a

CC binding partner to the above polypeptide, the gene corresponding to the

CC cDNA sequence given in the specification, and identifying an activity in

CC a biological assay. The nucleic acid molecule and polypeptide are useful

CC in diagnosing, preventing, prognosing or treating diseases or disorders

CC associated with aberrant expression and/or activity of the above

CC polypeptide, such as neural disorders, immune system disorders, muscular

CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary

CC disorders, cardiovascular disorders, renal disorders, proliferative

CC disorders and/or cancers. In particular, these diseases are systemic

CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,

CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,

CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,

CC atherosclerosis, myocardial infarction, AIDS and infections. The methods

CC may be used for identifying agonists and antagonists of the

CC polynucleotide and polypeptide. The present sequence is a protein from

CC one of the 28 disclosed secreted protein genes, it is not clear whether

CC this is an alternative expressed protein or a fragment of one of the

CC claimed proteins.

XX Sequence 102 AA;

SQ

Query Match 9.2%; Score 12; DB 8; Length 102;

Best Local Similarity 100.0%; Pred. NO. 0.0002;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNFQ 118

DB 76 YGCGCGNNNFQ 87

|||||||

RESULT 31

AAE27094

ID AAE27094 standard; protein; 117 AA.

XX AC

XX AAE27094;

XX 13-DEC-2002 (first entry)

XX DE Human secreted protein #1.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;

KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;

KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;

KW respiratory disorder; asthma; allergy; gastrointestinal disorder;

KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;

KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;

KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;

KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;

KW respiratory disorder; rhinitis; sinusitis; neurological disease;

KW endocrine disorder; Addison's disease; reproductive system disorder;

KW endometriosis; vasotropic; vulvetry; cytostatic; nootropic; cardiant;

KW anti-HIV; tranquilliser; gout; antiparasitic.

XX Homo sapiens.

OS US2002077287-A1.

PN 20-JUN-2002.

PD

XX 11-MAY-2001; 2001US-00852659.

PF

XX 11-SEP-1998; 98US-00152060.

PR

XX (RUBE//) RUBEN S M.

PA (ROSE//) ROSEN C A.

PA (LIYY//) LI Y.

PA (ZENG//) ZENG Z.

PA (KYAW//) KYAW H.

PA (FISC//) FISCHER C L.

PA (LIHH//) LI H.

PA (SOPP//) SOPPET D R.

PA (GENT//) GENTZ R L.

PA (WEIY//) WEI Y.

PA (MOOR//) MOORE P A.

PA (YOUN//) YOUNG P E.

PA (GREE//) GREENE J M.

PA (FERR//) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX WPI, 2002-598780/64.

DR

XX Novel human secreted polypeptides and polynucleotides for diagnosing,

PT preventing, treating immune, hyperproliferative, cardiovascular,

PT neurological, reproductive disorders and identifying modulators of

PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

PS

XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted

CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.

CC AAE27000-AAE27025 represent human secreted protein fragments or their

CC variants. The secreted proteins and genes are useful for preventing,

CC treating or ameliorating medical conditions, e.g., by protein or gene

CC therapy. Specific uses are described for each of the 28 genes, based on

CC the tissues in which they are most highly expressed and include

CC developing products for the diagnosis or treatment of immunodeficiencies,

CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe

CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus

CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune

CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,

CC Grave's disease, diabetes mellitus, dermatitis, inflammatory bowel

CC including septic shock, sepsis, reperfusion injury, inflammatory disorders

CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders

CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory

CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and

CC breast), central nervous system (CNS) disorders e.g., ischaemic brain

CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's

CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,

CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,

CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,

CC sarcoidosis and allogenic transplant rejection, blood-related disorder

CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative

CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,

CC lung cancer, allergic disorders, pneumonitis, renal disorders e.g. acute

CC glomerulonephritis, neurological diseases, liver disorders, endocrine

CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,

CC infectious diseases and reproductive system disorders e.g. endometriosis.

CC The present sequence represents a human secreted protein of the invention
XX
SQ Sequence 117 AA;

Query Match 9.2%; Score 12; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNFQ 118
Db 91 YGCGCGNNNFQ 102
|||||
RESULT 32
AAE27165
ID AAE27165 standard; protein; 117 AA.
XX
AC AAE27165;
XX
XX
DT 13-DEC-2002 (first entry)
XX
XX Human gene 24 encoded secreted protein fragment #1.
DE
XX
XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW
XX
OS Homo sapiens.
XX
XX
XX US2002076756-A1.
XX
XX 20-JUN-2002.
XX
XX 11-MAY-2001; 2001US-00853161.
XX
XX 02-FEB-2001; 2001US-0265583P.
XX
XX (RUBE/) RUBEN S M.
XX (ROSE/) ROSEN C A.
XX (LIYY/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LTHH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2002-574454/61.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins, useful
XX for diagnosing, preventing, treating or ameliorating medical conditions
XX and as food additives or preservatives.
XX
XX Disclosure; Page 17; 209pp; English.
XX
XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
XX protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes

CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasia of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
XX secreted protein fragment referred to in the disclosure of the invention
XX
SQ Sequence 117 AA;

Query Match 9.2%; Score 12; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNFQ 118
Db 91 YGCGCGNNNFQ 102
|||||
RESULT 33
ABU65038
ID ABU65038 standard; protein; 117 AA.
XX
AC ABU65038;
XX
XX 15-MAY-2003 (first entry)
XX
XX Human secreted protein gene 24, protein #4.
XX
XX Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
KW body height; hair colour; human.
XX
XX Homo sapiens.
XX
XX US2002172994-A1.
XX
XX 21-NOV-2002.
XX
XX 11-MAY-2001; 2001US-00852797.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057765P.
XX 19-DEC-1997; 97US-0068368P.
XX 12-MAR-1998; 98WO-US0004858.
XX 11-SEP-1998; 98US-00152060.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
XX Disclosure; SEQ ID NO 120; 320pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.

XX Sequence 117 AA;

Query Match 9.2%; Score 12; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNFQ 118
| | | | | | | | | |
Db 91 YGCGCGNNNFQ 102

RESULT 35
AAW75219
ID AAW75219 standard; protein; 133 AA.

XX AC AAW75219;

XX 29-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 24 clone HTEBY11.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;

KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX W09840483-A2.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US004858.

XX 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.

PR 30-MAY-1997; 97US-0050934P.

PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.

PR 19-DEC-1997; 97US-0068368P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX WPI: 1998-520811/44.

DR N-PSDB; AAV34309.

XX Isolated human poly:nucleotide(s) encoding secretory peptide(s) - used to

PT develop products for the diagnosis and treatment of e.g. inflammation,

PT cancers, CNS disorders or immune system disorders.

XX Claim 1; Page 167-168; 201pp; English.

XX This sequence represents a secreted human protein encoded by the gene

CC clone detailed in the descriptor line. The gene can be used to generate

CC fusion proteins by linking to the gene to a human immunoglobulin Fc

CC portion (e.g. AAV34277) for increasing the stability of the fused protein

CC as compared to the human protein only. The invention relates to 28 novel

CC genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino

CC acid sequences AAV75196-W75235) which are useful for preventing, treating

CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,

CC pathological conditions can be diagnosed by determining the amount of the

CC new polypeptides in a sample or by determining the presence of mutations

CC in the new polynucleotides. Specific uses are described for each of the

CC 28 polynucleotides, based on which tissues they are most highly expressed

CC in (see AAV34286 for described uses)

XX Sequence 133 AA;

Query Match 9.2%; Score 12; DB 2; Length 133;

Best Local Similarity 100.0%; Pred. No. 0.00025;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNFQ 118
| | | | | | | | | |
Db 107 YGCGCGNNNFQ 118

RESULT 36

AAE26982

ID AAE26982 standard; protein; 133 AA.

XX AC AAE26982;

XX 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:34.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotrophic; vulnery; cyostatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= Signal_peptide
 FT Protein 22..133
 FT /note= "Human mature secreted protein"
 XX
 PN US200207297-A1.
 XX
 XX 20-JUN-2002.
 XX
 XX 11-MAY-2001; 2001US-00852659.
 XX
 XX 11-SEP-1998; 98US-00152060.
 XX
 XX (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYV/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPP D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 XX WPI: 2002-598780/64.
 DR N-PSDB; AAD44659.
 DR
 XX
 XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 XX
 XX Claim 11; Page 185-186; 209pp; English.
 XX
 XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel

CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonia, renal disorders, e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperlipidemia,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention
 XX
 XX Sequence 133 AA;

Query Match 9.2%; Score 12; DB 5; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNFQ 118
 |||||

Db 107 YGCGCGNNNFQ 118
 |||||

RESULT 37

AAE27120

ID AAE27120 standard; protein; 133 AA.

XX

AC AAE27120;

XX

DT 13-DEC-2002 (first entry)

XX

DE Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:75.

XX

KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 KW vulnery.

XX Homo sapiens.

OS

FH Key Location/Qualifiers

FT Peptide 1..21

FT Protein /label= Signal_peptide

FT 22..133

FT /note= "Mature human secreted protein"

XX

PN US2002076756-A1.

XX

PD 20-JUN-2002.

XX

PF 11-MAY-2001; 2001US-00853161.

XX

PR 02-FEB-2001; 2001US-0265583P.

XX

XX (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYV/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIHH/) LI H.

PA (SOPP/) SOPP D R.

PA (GENT/) GENTZ R L.

CC dementia, and prion disease), cardiovascular disorders (e.g.
CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
CC pancreatitis, sarcoidosis, dermatitis, allogenic transplant rejection),
CC blood-related disorders (thrombosis, arterial thrombosis),
CC hyperproliferative disorders, renal disorders (e.g. acute
CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
CC hyperthyroidism, hyperpituitarism), liver diseases and disorders,
CC reproductive system disorders (e.g. endometriosis), infectious diseases,
CC and pancreatic disorders. Many other diseases and disorders are listed in
CC the specification. They also useful as a vaccine adjuvant. Further they
CC are useful to enhance or inhibit complement mediated cell lysis, for
CC stimulating wound and tissue repair, angiogenesis, and the repair of
CC vascular or lymphatic diseases or disorders. They are also useful to
CC prevent hair loss, to modulate mammalian characteristics such as body
CC height, weight, hair colour, and to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors or other nutritional components. The proteins are
CC also useful for identifying binding partners. The present sequence
CC represents a secreted protein of the invention

XX Sequence 133 AA;
SQ
Query Match 9.2%; Score 12; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNFQ 118
DB 107 YGGCGGNNNFQ 118
|||||

RESULT 39
ADAL19812
ID ADA19812 standard; protein; 133 AA.
XX ADA19812;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human EPPIN protein SEQ ID NO:13.
XX
XX

DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis; EPPIN.

XX Homo sapiens.
XX WO2003070770-A2.
XX
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Balroch A, Niknejad A;
XX
XX WPI; 2003-663849/62.
XX

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX PT hemorrhage.
XX

PS Disclosure; Fig 1; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antithrombotic, nephrotropic, antipsoriatic and vulnary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents a human EPPIN protein given in comparison
XX with DJ11 proteins in the exemplification of the present invention.

XX Sequence 133 AA;
SQ

Query Match 9.2%; Score 12; DB 7; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNFQ 118
DB 107 YGGCGGNNNFQ 118
|||||

RESULT 40
ADG89802
ID ADG89802 standard; protein; 133 AA.
XX
XX ADG89802;
XX

XX 11-MAR-2004 (first entry)
XX
XX Human protein from secreted protein gene 24 #1.

XX Secreted protein; gene therapy; neural disorder; immune system disorders;
XX muscular disorder; reproductive disorder; gastrointestinal disorder;
XX pulmonary disorder; cardiovascular disorder; renal disorder;
XX proliferative disorder; cancer; systemic lupus erythematosus;
XX rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
XX Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
XX Parkinson's disease; Alzheimer's disease; atherosclerosis;
XX myocardial infarction; AIDS; infection; human.

XX Homo sapiens.
XX
XX US2003225009-A1.
XX
XX 04-DEC-2003.
XX
XX 30-JAN-2002; 2002US-00058993.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057765P.
XX 19-DEC-1997; 97US-0068368P.

CC disease, adult respiratory distress syndrome, allergies, ankylosing
CC spondylitis and amyloidosis
XX
SQ Sequence 164 AA;

Query Match 9.2%; Score 12; DB 3; Length 164;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNF 118
DB 138 YGCGCGNNNF 149
|||||

RESULT 42
AAE13092
ID AAE13092 standard; peptide; 54 AA.
XX
AC AAE13092;
XX
DT 28-JAN-2002 (first entry)
XX
DE Trypsin inhibitor peptide.
XX
KW BTL.009 protein; serine proteinase inhibitor; cytostatic; therapeutic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW trypsin inhibitor.
XX
OS Unidentified.
XX
PN US6294648-B1.
XX
PD 25-SEP-2001.
XX
PF 20-JUL-1999; 99US-00358569.
XX
PR 20-JUL-1999; 99US-00358569.
XX
PA (FARB) BAYER CORP.
XX
PI Delaria K, Roczniak S, Davies C;
XX
DR WPI; 2001-662224/76.
XX
PT New isolated protein for inhibiting human serine proteinase activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
PS Disclosure; Col 5-6; 16pp; English.
XX
CC The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is trypsin inhibitor peptide related to
CC the invention
XX
SQ Sequence 54 AA;

Query Match 8.4%; Score 11; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNF 117
DB 33 YGCGCGNNNF 43
|||||

RESULT 43
ADA19815
ID ADA19815 standard; protein; 136 AA.
XX
AC ADA19815;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mouse DJ11 protein SEQ ID NO:16.
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
OS Mus musculus.
XX
PN WO2003070770-A2.
XX
PD 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-EP001629.
XX
PR 21-FEB-2002; 2002US-0358683P.
XX
PA (GENE-) GENEPROT INC.
XX
PI Bougueleret L, Bairoch A, Niknejad A;
XX
DR WPI; 2003-663849/62.
XX
PT New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
PS Disclosure; Fig 1; 87pp; English.
XX
CC The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a mouse DJ11 protein given in comparison
CC with DJ11 proteins in the exemplification of the present invention.
XX

SQ Sequence 136 AA;
Query Match 7.6%; Score 10; DB 7; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGCGN 113
| | | | | | | | | |
Db 104 EPIYGGCGN 113

RESULT 44
AAR78401
ID AAR78401 standard; peptide; 58 AA.
XX AAR78401;
XX
DT 27-FEB-1996 (first entry)
XX
DE Human LACI-K1 derivative NS9.
XX
KW Human; lipoprotein-associated coagulation inhibitor; peptide library;
KW inhibitor; plasmin; bovine; pancreatic trypsin inhibitor; Kunitz domain;
KW fibrinolysis; fibrinogenolysis; bleeding; thrombolytic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 17
FT /note= "residue change: Ile to Arg"
FT Misc-difference 18
FT /note= "residue change: Met to Phe"
FT Misc-difference 19
FT /note= "residue change: Lys to Glu"
FT Misc-difference 32
FT /note= "residue change: Glu to Gln"
FT Misc-difference 39
FT /note= "residue change: Glu to Gln"
XX
XX WO9518830-A2.
XX
PD 13-JUL-1995.
XX
PF 11-JAN-1995; 95WO-US000298.
XX
PR 11-JAN-1994; 94US-00179658.
PR 10-MAR-1994; 94US-00208265.
XX
PA (PROT-) PROTEIN ENG CORP.
XX
PI Markland W, Ladner RC;
XX
XX WPI; 1995-255042/33.
XX
PT Novel plasmin inhibiting protein comprising a Kunitz Domain - useful to
PT prevent/treat disorders attributable to excess plasmin activity.
XX
PS Example 2; Page 29; 59pp; English.
XX
XX The peptides AAR78391-R78425 are derivatives of the human lipoprotein-
CC associated coagulation inhibitor (LACI) Kunitz domain 1. The peptides
CC were isolated from a peptide library generated based on the human LACI-K1
CC domain (AAR78390). The peptides are mutants homologous to bovine
CC pancreatic trypsin inhibitor (BPTI) Kunitz domain that inhibit plasmin.
CC The peptides can be used to prevent or treat a clinical condition
CC exacerbated by plasmin e.g. inappropriate fibrinolysis or
CC fibrinogenolysis, excessive bleeding associated with thrombolytics
XX
SQ Sequence 58 AA;
Query Match 6.9%; Score 9; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGCGN 113
| | | | | | | | | |
Db 33 FIYGGCGN 41

RESULT 45
ADE64021
ID ADE64021 standard; protein; 126 AA.
XX ADE64021;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q15332, SEQ ID NO 9967.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
FN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR GENBANK; Q15332.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 126 AA;

Query Match 6.1%; Score 8; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 EAGPCLAS 89
| | | | |
DB 35 EAGPCLAS 42

RESULT 46
AAU79498
ID AAU79498 standard; protein; 140 AA.
XX
AC AAU79498;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse partial ADAMTS protein #1.
XX
KW Mouse; ADAMTS; cytostatic; antidiabetic; antirheumatic; antiarthritic;
KW antiulcer; vulnery; neovascularisation; angioma; diabetic omentopathy;
KW chronic rheumatoid arthritis; gene therapy; refractory skin ulcer;
KW gastric ulcer; post-operative healing failure;
KW repolysin-type 2N-metalloprotease domain; disintegrin-like domain; TSPI;
KW thrombospondin type 1 domain; sexual cycle; tumour; 5P-syndrome deletion;
KW chromosome 5p15.2-15.3; Cri-du-chat syndrome.
XX
OS Mus musculus.
XX
PN WO200231163-A1.
XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP008913.
XX
PR 11-OCT-2000; 2000JP-00311309.
PR 02-APR-2001; 2001JP-00102905.
XX
XX (KAZU-) KAZUSA DNA RES INST FOUND.
PA (MITS-) MITSUBISHI PHARMA CORP.
XX
XX Ohara O, Nagase T, Nomura N, Yano K, Murakami K, Yasuda S;
PI Kanzaki K;
XX
XX WPI; 2002-372277/40.
DR N-PSDB; ABK49823.
XX
PT Human brain-originated ADAMTS family polypeptide and encoded gene,
PT applicable in diagnosis and screening compounds for drug compositions in
PT treating diseases due to e.g. neovascularization.
XX
XX Example 8; Page 151-152; 172pp; Japanese.
PS
XX The invention relates to a polypeptide belonging to the ADAMTS family is
XX selected from sequences appearing as AAU79496, AAU79497 and AAU79499, a
XX protein that contains the polypeptide, a protein having not less than 50%
XX homology with the amino acid sequence of the polypeptides or a
XX polypeptide modified from any of the polypeptides but with some amino
XX acids deleted, substituted, added or inserted. Also included are the
XX polynucleotides encoding the polypeptides (or their complementary strands
XX or variants), a recombinant vector containing any of the polynucleotides,
XX a transformant which is transformed with the recombinant vector,
XX producing the polypeptide, protein or peptide by culturing the
XX transformant, an antibody that can recognize the polypeptide, protein or
XX peptide and screening compounds to promote or inhibit activity of the
XX polypeptide or protein, or to promote or inhibit expression of the
XX polynucleotide by using the polypeptide, protein, peptide, the
XX polynucleotide, vector, transformant or/and antibody, particularly in the
XX presence of a test compound for contact before evaluating the activity by
XX measuring signal changes. The polypeptide and encoded gene are applicable
XX in diagnosis and screening compounds for drug compositions in treating

CC diseases due to neovascularisation, diabetic omentopathy, chronic
CC rheumatoid arthritis, angioma, refractory skin and gastric ulcers and
CC post-operative healing failure, including gene therapy. The gene encoding
CC such polypeptide has conserved repolysin-type 2N- metalloprotease
CC domain, disintegrin-like domain and TSPI (thrombospondin type 1) domain.
CC Its encoded protein is characterised by high expression in ovaries,
CC changes in expression dose depending on the sexual cycle, a decrease in
CC tumour cell and location of the gene on the 5P-syndrome deletion site on
CC chromosome 5p15.2-15.3 (associated with Cri-du-chat syndrome). The
CC present sequence represents a ADAMTS protein of the invention
XX
XX Sequence 140 AA;

Query Match 6.1%; Score 8; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 LDFRKDIC 77
| | | | |
DB 47 LDFRKDIC 54

RESULT 47
AAU80150
ID AAU80150 standard; protein; 140 AA.
XX
AC AAU80150;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse partial ADAMTS protein #3.
XX
KW Mouse; ADAMTS; cytostatic; antidiabetic; antirheumatic; antiarthritic;
KW antiulcer; vulnery; neovascularisation; angioma; diabetic omentopathy;
KW chronic rheumatoid arthritis; gene therapy; refractory skin ulcer;
KW gastric ulcer; post-operative healing failure;
KW repolysin-type 2N-metalloprotease domain; disintegrin-like domain; TSPI;
KW thrombospondin type 1 domain; sexual cycle; tumour; 5P-syndrome deletion;
KW chromosome 5p15.2-15.3; Cri-du-chat syndrome.
XX
OS Mus musculus.
XX
PN WO200231163-A1.
XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP008913.
XX
PR 11-OCT-2000; 2000JP-00311309.
PR 02-APR-2001; 2001JP-00102905.
XX
XX (KAZU-) KAZUSA DNA RES INST FOUND.
PA (MITS-) MITSUBISHI PHARMA CORP.
XX
XX Ohara O, Nagase T, Nomura N, Yano K, Murakami K, Yasuda S;
PI Kanzaki K;
XX
XX WPI; 2002-372277/40.
DR
XX Human brain-originated ADAMTS family polypeptide and encoded gene,
PT applicable in diagnosis and screening compounds for drug compositions in
PT treating diseases due to e.g. neovascularization.
XX
XX Example 8; Fig 8; 172pp; Japanese.
PS
XX The invention relates to a polypeptide belonging to the ADAMTS family is
XX selected from sequences appearing as AAU79496, AAU79497 and AAU79499, a
XX protein that contains the polypeptide, a protein having not less than 50%
XX homology with the amino acid sequence of the polypeptides or a
XX polypeptide modified from any of the polypeptides but with some amino
XX acids deleted, substituted, added or inserted. Also included are the
XX polynucleotides encoding the polypeptides (or their complementary strands
XX or variants), a recombinant vector containing any of the polynucleotides,
XX a transformant which is transformed with the recombinant vector,
XX producing the polypeptide, protein or peptide by culturing the
XX transformant, an antibody that can recognize the polypeptide, protein or
XX peptide and screening compounds to promote or inhibit activity of the
XX polypeptide or protein, or to promote or inhibit expression of the
XX polynucleotide by using the polypeptide, protein, peptide, the
XX polynucleotide, vector, transformant or/and antibody, particularly in the
XX presence of a test compound for contact before evaluating the activity by
XX measuring signal changes. The polypeptide and encoded gene are applicable
XX in diagnosis and screening compounds for drug compositions in treating

CC a transformant which is transformed with the recombinant vector,
 CC producing the polypeptide, protein or peptide by culturing the
 CC transformant, an antibody that can recognize the polypeptide, protein or
 CC peptide and screening compounds to promote or inhibit activity of the
 CC polypeptide or protein, or to promote or inhibit expression of the
 CC polynucleotide by using the polypeptide, protein, peptide, the
 CC polynucleotide, vector, transformant or/and antibody, particularly in the
 CC presence of a test compound for contact before evaluating the activity by
 CC measuring signal changes. The polypeptide and encoded gene are applicable
 CC in diagnosis and screening compounds for drug compositions in treating
 CC diseases due to neovascularisation, diabetic omentopathy, chronic
 CC rheumatoid arthritis, angiora, refractory skin and gastric ulcers and
 CC post-operative healing failure, including gene therapy. The gene encoding
 CC such polypeptide has conserved repressin-type ZN- metalloprotease
 CC domain, disintegrin-like domain and TSR1 (chromobospondin type 1) domain.
 CC Its encoded protein is characterised by high expression in ovaries,
 CC changes in expression dose depending on the sexual cycle, a decrease in
 CC tumour cell and location of the gene on the 5p-syndrome deletion site on
 CC chromosome 5p15.2-15.3 (associated with Cri-du-chat syndrome). The
 CC present sequence represents a ADAMTS protein of the invention
 XX
 SQ Sequence 140 AA;

Query Match 6.1%; Score 8; DB 5; Length 140;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 LDFRKDIC 77
 |||||
 Db 47 LDFRKDIC 54

RESULT 48
 AAM18394
 ID AAM18394 standard; protein; 166 AA.
 AC AAM18394;
 DT 12-OCT-2001 (first entry)
 XX
 XX Peptide #4828 encoded by probe for measuring cervical gene expression.
 DE Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX Homo sapiens.
 OS
 XX WO200157278-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000670.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488901/53.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 PS Claim 27; SEQ ID NO 23220; 487pp; English.
 XX The present invention relates to human single exon nucleic acid probes

CC (SENP: see AAI10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 166 AA;

Query Match 6.1%; Score 8; DB 4; Length 166;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
 |||||
 Db 36 LVPFILLG 43

RESULT 49
 ABB37425
 ID ABB37425 standard; peptide; 166 AA.
 AC ABB37425;
 XX 04-FEB-2002 (first entry)
 DT
 XX Peptide #4931 encoded by human foetal liver single exon probe.
 DE Human; foetal liver; gene expression; single exon nucleic acid probe.
 KW Homo sapiens.
 OS
 XX WO200157277-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000669.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483447/52.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 PS Claim 27; SEQ ID NO 30060; 639pp + Sequence Listing; English.
 XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 166 AA;

Query Match 6.1%; Score 8; DB 4; Length 166;
 Best Local Similarity 100.0%; Pred. No. 5.4;

CC domain, disintegrin-like domain and TSPI (thrombospondin type 1) domain.
CC its encoded protein is characterised by high expression in ovaries,
CC changes in expression dose depending on the sexual cycle, a decrease in
CC tumour cell and location of the gene on the 5p-syndrome deletion site on
CC chromosome 5p15.2-15.3 (associated with Cri-du-chat syndrome). The
CC present sequence represents a ADAMTS protein of the invention
XX
SQ Sequence 175 AA;
Query Match 6.1%; Score 8; DB 5; Length 175;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 LDFRKDIC 77
Db 82 LDFRKDIC 89
Search completed: September 21, 2005, 16:47:47
Job time : 111 secs

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 LVPFILLG 17
Db 36 LVPFILLG 43
RESULT 50
AAU79499
ID AAU79499 standard; protein; 175 AA.
XX
AC AAU79499;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse partial ADAMTS protein #2.
XX
KW Mouse; ADAMTS; cytostatic; antidiabetic; antirheumatic; antiarthritic;
KW antiulcer; vulnery; neovascularisation; angioma; diabetic omentopathy;
KW chronic rheumatoid arthritis; gene therapy; refractory skin ulcer;
KW gastric ulcer; post-operative healing failure;
KW repolysin-type ZN-metalloprotease domain; disintegrin-like domain; TSPI;
KW thrombospondin type 1 domain; sexual cycle; tumour; 5p-syndrome deletion;
KW chromosome 5p15.2-15.3; Cri-du-chat syndrome.
XX
OS Mus musculus.
XX
PN WO200231163-A1.
XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP008913.
XX
PR 11-OCT-2000; 2000JP-00311309.
PR 02-APR-2001; 2001JP-00102905.
XX
PA (KAZU-) KAZUSA DNA RES INST FOUND.
PA (MITS-) MITSUBISHI PHARMA CORP.
XX
PI Ohara O, Nagase T, Nomura N, Yano K, Murakami K, Yasuda S;
PI Kanzaki K;
XX
DR WPI; 2002-372277/40.
DR N-PSDB; ABK49824.
XX
PT Human brain-originated ADAMTS family polypeptide and encoded gene,
PT applicable in diagnosis and screening compounds for drug compositions in
PT treating diseases due to e.g. neovascularization.
XX
PS Claim 1; Page 154-155; 172pp; Japanese.
XX
CC The invention relates to a polypeptide belonging to the ADAMTS family is
CC selected from sequences appearing as AAU79496, AAU79497 and AAU79499, a
CC protein that contains the polypeptide, a protein having not less than 50%
CC homology with the amino acid sequence of the polypeptides or a
CC polypeptide modified from any of the polypeptides but with some amino
CC acids deleted, substituted, added or inserted. Also included are the
CC polynucleotides encoding the polypeptides (or their complementary strands
CC or variants), a recombinant vector containing any of the polynucleotides,
CC a transformant which is transformed with the recombinant vector,
CC producing the polypeptide, protein or peptide by culturing the
CC transformant, an antibody that can recognize the polypeptide, protein or
CC peptide and screening compounds to promote or inhibit activity of the
CC polypeptide or protein, or to promote or inhibit expression of the
CC polynucleotide by using the polypeptide, protein, peptide, the
CC polynucleotide, vector, transformant or/and antibody, particularly in the
CC presence of a test compound for contact before evaluating the activity by
CC measuring signal changes. The polypeptide and encoded gene are applicable
CC in diagnosis and screening compounds for drug compositions in treating
CC diseases due to neovascularisation, diabetic omentopathy, chronic
CC rheumatoid arthritis, angioma, refractory skin and gastric ulcers and
CC post-operative healing failure, including gene therapy. The gene encoding
CC such polypeptide has conserved repolysin-type ZN- metalloprotease

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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:42:25 ; Search time 32 Seconds
(without alignments)
305.595 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 131
Sequence: 1 MGLSGLLPILVPFILLGDIQ.....GNNNFQTEAICLVTCCKYH 131

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 513545 seqs, 74649064 residues

Word size : 0
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	9.2	43	US-09-358-569D-13	Sequence 13, Appl
2	12	9.2	54	US-09-358-569D-8	Sequence 8, Appl
3	12	9.2	55	US-09-358-569D-1	Sequence 1, Appl
4	12	9.2	58	US-09-369-494-8	Sequence 8, Appl
5	12	9.2	58	US-09-569-670-8	Sequence 8, Appl
6	12	9.2	64	US-09-358-569D-10	Sequence 10, Appl
7	12	9.2	133	US-09-152-060-75	Sequence 75, Appl
8	11	8.4	54	US-09-358-569D-9	Sequence 9, Appl
9	11	8.4	67	US-08-358-160-123	Sequence 123, App
10	10	7.6	62	US-08-358-160-155	Sequence 155, App
11	10	7.6	63	US-08-358-160-159	Sequence 159, App
12	9	6.9	58	US-08-676-124-13	Sequence 13, Appl
13	9	6.9	58	US-09-414-878-13	Sequence 13, Appl
14	9	6.9	58	US-09-240-136-13	Sequence 13, Appl
15	9	6.9	58	US-09-638-770A-13	Sequence 13, Appl
16	8	6.1	77	5466783-4	Patent No. 5466783
17	8	6.1	77	5466783-4	Patent No. 5466783
18	8	6.1	767	US-09-949-016-11664	Sequence 11664, A
19	7	5.3	24	US-08-463-155A-29	Sequence 29, Appl
20	7	5.3	24	US-08-463-432B-29	Sequence 29, Appl
21	7	5.3	51	US-07-791-213D-1	Sequence 1, Appl
22	7	5.3	51	US-07-791-213D-2	Sequence 2, Appl
23	7	5.3	51	US-07-791-213D-4	Sequence 4, Appl
24	7	5.3	51	US-07-791-213D-7	Sequence 7, Appl
25	7	5.3	51	US-07-791-213D-17	Sequence 17, Appl
26	7	5.3	51	US-07-791-213D-108	Sequence 108, App
27	7	5.3	51	US-08-055-988-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-358-569D-13
; Sequence 13, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznik, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: sequence derived from EST database
US-09-358-569D-13

Query Match 9.2%; Score 12; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNFQ 118
|||
Db 21 YGGCQGNNNFQ 32

RESULT 2

US-09-358-569D-8
; Sequence 8, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznik, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-8

Query Match          9.2%; Score 12; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      107 YGCGCGNNNNFQ 118
Db      33 YGCGCGNNNNFQ 44
|||||

RESULT 3
US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match          9.2%; Score 12; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      107 YGCGCGNNNNFQ 118
Db      35 YGCGCGNNNNFQ 46
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RESULT 4
US-09-369-494-8
; Sequence 8, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-8

Query Match          9.2%; Score 12; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      107 YGCGCGNNNNFQ 118
Db      37 YGCGCGNNNNFQ 48
|||||

RESULT 5
US-09-569-670-8
; Sequence 8, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8

Query Match          9.2%; Score 12; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      107 YGCGCGNNNNFQ 118
Db      35 YGCGCGNNNNFQ 46
|||||

RESULT 6
US-09-358-569D-10
; Sequence 10, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Extension of
; OTHER INFORMATION: Seq Id 1
US-09-358-569D-10

Query Match          9.2%; Score 12; DB 3; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      107 YGCGCGNNNNFQ 118
Db      37 YGCGCGNNNNFQ 48
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RESULT 7
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003PL.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match 9.2%; Score 12; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.98-05; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNFQ 118
Db 107 YGCGCGNNNFQ 118

RESULT 8
US-09-358-569D-9
; Sequence 9, Application US/09358569D
; Patent No. 6234648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-9

Query Match 8.4%; Score 11; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 107 YGCGCGNNNF 117
Db 33 YGCGCGNNNF 43

RESULT 9
US-08-358-160-123
; Sequence 123, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-123

Query Match 8.4%; Score 11; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNF 117
|||||
Db 38 YGCGCGNNNF 48

RESULT 10
US-08-358-160-155
; Sequence 155, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-155

Query Match 7.6%; Score 10; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 EFTYGGCGN 113
|||||

Db 37 EFTYGGCGN 46
RESULT 11
US-08-358-160-159
; Sequence 159, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-159

Query Match 7.6%; Score 10; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 EFTYGGCGN 113
|||||
Db 38 EFTYGGCGN 47

RESULT 12
US-08-676-124-13
; Sequence 13, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676.124
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,658
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,265
; FILING DATE: 10-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: MARKLAND-3B
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-676-124-13

Query Match 6.9%; Score 9; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FIYGGCQGN 113
Db 33 FIYGGCQGN 41

RESULT 13
US-09-414-878-13
; Sequence 13, Application US/09414878
; Patent No. 6071723
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/414,878
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/240,136
; FILING DATE: 29-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-414-878-13

Query Match 6.9%; Score 9; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FIYGGCQGN 113
Db 33 FIYGGCQGN 41

RESULT 14
US-09-240-136-13
; Sequence 13, Application US/09240136
; Patent No. 6103499
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts


```
;
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-240-136-13

Query Match 6.9%; Score 9; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FYGGCQGN 113
Db 33 FYGGCQGN 41

RESULT 15
US-09-638-770A-13
; Sequence 13, Application US/09638770A
; Patent No. 6423498
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; MARKLAND, William
; LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; From The Kunitz Domains
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,770A
; FILING DATE: 15-AUG-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-638-770A-13

Query Match 6.9%; Score 9; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FYGGCQGN 113
Db 33 FYGGCQGN 41

RESULT 16
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chein.;Kretzmer, Kuniko K.;Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
5466783-4

Query Match 6.1%; Score 8; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGQGN 114
Db 38 YGCGQGN 45

RESULT 17
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chein.;Kretzmer, Kuniko K.;Broze,
```


;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
5466783-4

Query Match 6.1%; Score 8; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGN 114
DB 38 YGGCQGN 45

RESULT 18
US-09-949-016-11664
; Sequence 11664, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11664
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11664

Query Match 6.1%; Score 8; DB 4; Length 767;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LVPPFILLG 17
DB 340 LVPPFILLG 347

RESULT 19
US-08-463-155A-29
; Sequence 29, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco

; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-155A-29

Query Match 5.3%; Score 7; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGN 113
DB 1 YGGCQGN 7

RESULT 20
US-08-463-432B-29
; Sequence 29, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,432B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: Amino Acid


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; TOPOLOGY: Linear
US-08-463-432B-29

Query Match          5.3%; Score 7; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 1 YGGCQGN 7

RESULT 21
US-07-791-213D-1
; Sequence 1, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ
; OTHER INFORMATION: ID NOS:20 to 24, respectively, and 107."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 51
; OTHER INFORMATION: /note= "Xaa-2 is selected from SEQ
; OTHER INFORMATION: ID NOS:25 to 40, respectively."
US-07-791-213D-2

Query Match          5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 31 YGGCQGN 37

RESULT 23
US-07-791-213D-4
; Sequence 4, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
```



```
;
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791.213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: /note= "Xaa-1 is Gln or Lys."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 42
; OTHER INFORMATION: /note= "Xaa-2 is Tyr when Xaa-1 is
; OTHER INFORMATION: Lys; and Xaa-2 is Glu when Xaa-1 is Gln."
;
; US-07-791-213D-4
;
; Query Match 5.3%; Score 7; DB 1; Length 51;
; Best Local Similarity 100.0%; Pred. No. 3.7;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 107 YGGCQGN 113
; DB 31 YGGCQGN 37
;
; RESULT 24
; US-07-791-213D-7
; Sequence 7, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791.213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ
; OTHER INFORMATION: ID NOS:20 to 24, respectively."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 51
; OTHER INFORMATION: /note= "Xaa-2 is selected from SEQ
; OTHER INFORMATION: ID NOS:25-40, respectively."
;
; US-07-791-213D-7
;
; Query Match 5.3%; Score 7; DB 1; Length 51;
; Best Local Similarity 100.0%; Pred. No. 3.7;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 107 YGGCQGN 113
; DB 31 YGGCQGN 37
;
; RESULT 25
; US-07-791-213D-17
; Sequence 17, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791.213D
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; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-17

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 30 YGGCQGN 36

RESULT 26
US-07-791-213D-108
; Sequence 108, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ
; OTHER INFORMATION: ID NO:20 to 24 and 107."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: /note= "Xaa-2 is Gln or Lys."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 42
; OTHER INFORMATION: /note= "Xaa-3 is Glu or Tyr."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 51
; OTHER INFORMATION: /note= "Xaa-4 is selected from SEQ
; OTHER INFORMATION: ID NOS:25 to 40."
US-07-791-213D-108

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 31 YGGCQGN 37

RESULT 27
US-08-055-988-3
; Sequence 3, Application US/08055988
; Patent No. 5427937
; GENERAL INFORMATION:
; APPLICANT: Michael Capello
; APPLICANT: Peter J. Hotez
; APPLICANT: Frank F. Richards
; TITLE OF INVENTION: Hookworm Anticoagulant
; NUMBER OF SEQUENCES: 7;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MacArthur Center for Molecular
; ADDRESSEE: Parasitology
; ADDRESSEE: Yale Parasitology and Tropical Medicine
; ADDRESSEE: Center, 700 Laboratory of Epidemiology
; ADDRESSEE: and Public Health
; STREET: 60 College Street
; CITY: New Haven
; STATE: CT
; COUNTRY: USA
; ZIP: 06510
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25" 360 Kb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/055,988
; FILING DATE: 19930430
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Kinsky, St. Onge Steward Johnston & Reens
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: 1751-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-324-6155
; TELEFAX: 203-327-1096
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: polypeptide
DESCRIPTION: internal fragment
FRAGMENT TYPE: internal fragment
FEATURE:
NAME/KEY: Extrinsic Pathway Inhibitor, Tail I
PUBLICATION INFORMATION:
AUTHORS: Rapoport, S.I.
TITLE: The Extrinsic Pathway
TITLE: Inhibitor
JOURNAL: Thrombosis and Haemostasis
VOLUME: 66
ISSUE: 1
PAGES: 6-15, Figure 5
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: segment corresponding to
RELEVANT RESIDUES IN SEQ ID NO: peptide residues 26 to 76
US-08-055-988-3
Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 EFGYGC 110
Db 28 EFGYGC 34
RESULT 28
US-07-972-387-67
; Sequence 67, Application US/07972387
; Patent No. 5451659
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshinori
; APPLICANT: No. 5451659unara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; TITLE OF INVENTION: Producing the Same
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,387
; FILING DATE: 19921105
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-124P
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TLEX: 248345
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-972-387-67
Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 107 YGCGQN 113
Db 31 YGCGQN 37
RESULT 29
US-08-437-841-1
; Sequence 1, Application US/08437841
; Patent No. 5563123
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; APPLICANT: Creasey, Abia
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,521
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Savereide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-437-841-1
Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 EFGYGC 110
Db 28 EFGYGC 34
RESULT 30
US-08-286-521-1
; Sequence 1, Application US/08286521
; Patent No. 5589359
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; APPLICANT: Creasey, Abia
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville

STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,521
 FILING DATE: 05-AUG-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Savereide, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0990.001
 TELEPHONE: 510-601-2585
 TELEFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 51 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-286-521-1

Query Match 5.3%; Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFYGGC 110
 Db 28 EFYGGC 34

RESULT 31
 US-08-431-412-67
 Sequence 67, Application US/08431412
 Patent No. 5589360
 GENERAL INFORMATION:
 APPLICANT: Morishita, Hideaki
 APPLICANT: Kanamori, Toshinori
 APPLICANT: No. 5589360uhara, Masahiro
 TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
 TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: 301 N. Washington St.
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22046-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/431,412
 FILING DATE: 28-APR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/972,387
 FILING DATE: 05-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1110-124P
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-241-1300
 TELEFAX: 703-241-2848
 TELEX: 248345
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 51 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-431-412-67

Query Match 5.3%; Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
 Db 31 YGGCQGN 37

RESULT 32
 US-08-057-971-67
 Sequence 67, Application US/08057971
 Patent No. 5679770
 GENERAL INFORMATION:
 APPLICANT: Morishita, Hideaki
 APPLICANT: Kanamori, Toshinori
 APPLICANT: No. 5679770uhara, Masahiro
 TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
 TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/057,971
 FILING DATE: 06-MAY-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1110-129P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-205-8000
 TELEFAX: 703-205-8050
 TELEX:

INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 51 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-057-971-67

Query Match 5.3%; Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
 Db 31 YGGCQGN 37

US-08-057-971-67
 Sequence 67, Application US/08057971
 Patent No. 5679770
 GENERAL INFORMATION:
 APPLICANT: Morishita, Hideaki
 APPLICANT: Kanamori, Toshinori
 APPLICANT: No. 5679770uhara, Masahiro
 TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
 TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/057,971
 FILING DATE: 06-MAY-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1110-129P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-205-8000
 TELEFAX: 703-205-8050
 TELEX:

INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 51 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-057-971-67

Query Match	5.3%	Score 7	DB 1	Length 51
Best Local Similarity	100.0%	Pred. No. 3.7		
Matches	7	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	107	YGGCQGN 113		
DB	31	YGGCQGN 37		
<p>US-08-293-150A-2</p> <p>Sequence 1, Application US/08293150A</p> <p>Patent No. 5792629</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: MORISHITA, Hideaki</p> <p>APPLICANT: KANAMORI, Toshinori</p> <p>APPLICANT: NOBUHARA, Masahiro</p> <p>TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE</p> <p>TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME</p> <p>TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF</p> <p>TITLE OF INVENTION: TREATING USING THE SAME</p> <p>NUMBER OF SEQUENCES: 110</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS</p> <p>STREET: P.O. Box 1404</p> <p>CITY: Alexandria</p> <p>STATE: Virginia</p> <p>COUNTRY: United States</p> <p>ZIP: 22313-1404</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>OPERATING SYSTEM: IBM PC compatible</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/293,150A</p> <p>FILING DATE: 19-AUG-1994</p> <p>CLASSIFICATION: 514</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 07/791,213</p> <p>FILING DATE: 13-NOV-1990</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: JP 2-306745</p> <p>FILING DATE: 13-NOV-1990</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Meuth, Donna M.</p> <p>REGISTRATION NUMBER: 36,607</p> <p>REFERENCE/DOCKET NUMBER: 029650-049</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (703) 836-6620</p> <p>TELEFAX: (703) 836-2021</p> <p>INFORMATION FOR SEQ ID NO: 1:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 51 amino acids</p> <p>TYPE: amino acid</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>US-08-293-150A-1</p>				
Query Match	5.3% <td>Score 7 <td>DB 1 <td>Length 51</td> </td></td>	Score 7 <td>DB 1 <td>Length 51</td> </td>	DB 1 <td>Length 51</td>	Length 51
Best Local Similarity	100.0% <td>Pred. No. 3.7</td> <td></td> <td></td>	Pred. No. 3.7		
Matches	7	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	104	EFIYGGC 110		
DB	28	EFIYGGC 34		
<p>US-08-293-150A-1</p> <p>Sequence 1, Application US/08293150A</p> <p>Patent No. 5792629</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: MORISHITA, Hideaki</p> <p>APPLICANT: KANAMORI, Toshinori</p> <p>APPLICANT: NOBUHARA, Masahiro</p> <p>TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE</p> <p>TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME</p> <p>TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF</p> <p>TITLE OF INVENTION: TREATING USING THE SAME</p> <p>NUMBER OF SEQUENCES: 110</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS</p> <p>STREET: P.O. Box 1404</p> <p>CITY: Alexandria</p> <p>STATE: Virginia</p> <p>COUNTRY: United States</p> <p>ZIP: 22313-1404</p>				

; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ
; OTHER INFORMATION: ID NOS:20 to 24, respectively, and 107."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 51
; OTHER INFORMATION: /note= "Xaa-2 is selected from SEQ
; OTHER INFORMATION: ID NOS:25 to 40, respectively."
US-08-293-150A-2

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 31 YGGCQGN 37

RESULT 36
US-08-293-150A-4
; Sequence 4, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: /note= "Xaa-1 is Gln or Lys."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 42
; OTHER INFORMATION: /note= "Xaa-2 is Tyr when Xaa-1 is
; OTHER INFORMATION: Lys; and Xaa-2 is Glu when Xaa-1 is Gln."
US-08-293-150A-4

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 31 YGGCQGN 37

RESULT 37
US-08-293-150A-7
; Sequence 7, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 7:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ ID NOS:20 to 24, respectively."
; OTHER INFORMATION: ID NOS:25-40, respectively."
US-08-293-150A-7

Query Match      5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      107 YGCGCQN 113
Db       31 YGCGCQN 37

RESULT 36
US-08-293-150A-17
; Sequence 17, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 51
; OTHER INFORMATION: /note= "Xaa-4 is selected from SEQ
; OTHER INFORMATION: ID NOS:25 to 40."
; US-08-293-150A-108

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 31 YGGCQGN 37

RESULT 40

US-08-943-682-1

; Sequence 1, Application US/08943682

; Patent No. 6174721

; GENERAL INFORMATION:

; APPLICANT: Innis, Michael

; APPLICANT: Creasey, Abia

; TITLE OF INVENTION: Chimeric Proteins

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton St.

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94608

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943.682

; FILING DATE: 03-OCT-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/438,184

; FILING DATE: 09-MAY-1995

; APPLICATION NUMBER: US 08/286.521

; FILING DATE: 05-AUG-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Saveriede, Paul B.

; REGISTRATION NUMBER: 36,914

; REFERENCE/DOCKET NUMBER: 0990.001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 510-601-2585

; TELEFAX: 510-655-3542

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 51 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-943-682-1

Query Match 5.3%; Score 7; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
Db 28 EFIYGGC 34

RESULT 41

US-09-013-896A-4

; Sequence 4, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENITZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,896A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1290001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-013-896A-4

Query Match 5.3%; Score 7; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
Db 28 EFIYGGC 34

RESULT 42

US-09-101-272G-19

; Sequence 19, Application US/09101272G

; Patent No. 6509445

; GENERAL INFORMATION:

; APPLICANT: Nissin Food Products Co., Ltd.

; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR

; FILE REFERENCE: Q50979

; CURRENT APPLICATION NUMBER: US/09/101,272G

; CURRENT FILING DATE: 1998-07-08

; PRIOR APPLICATION NUMBER: JP 1059/1996

; PRIOR FILING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 51

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: residues 5-55 of HI-8 domain of UTI (formula II)

; US-09-101-272G-19

Query Match 5.3%; Score 7; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-741-106-1

Query Match          5.3%; Score 7; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
Db 28 EFIYGGC 34

RESULT 43
US-09-827-948-4
; Sequence 4, Application US/09827948
; Patent No. 6548262
; GENERAL INFORMATION:
; APPLICANT: Gentz, Reiner, L.
; APPLICANT: Hsu, Tsu-An
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Tissue Factor Pathway Inhibitor-3
; FILE REFERENCE: 1488.1290002
; CURRENT APPLICATION NUMBER: US/09/827,948
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/013,896
; PRIOR FILING DATE: 1998-01-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Human
US-09-827-948-4

Query Match          5.3%; Score 7; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
Db 28 EFIYGGC 34

RESULT 44
US-09-741-106-1
; Sequence 1, Application US/09741106
; Patent No. 6783960
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; Creasey, Abba
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/741,106
; FILING DATE: 12-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,521
; FILING DATE: 1994-08-05
; ATTORNEY/AGENT INFORMATION:
; NAME: Saveriede, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
PCT-US95-09464-1

Query Match          5.3%; Score 7; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
Db 28 EFIYGGC 34

RESULT 45
PCT-US95-09464-1
; Sequence 1, Application PC/TUS9509464
; GENERAL INFORMATION:
; APPLICANT: CHIRON CORPORATION
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09464
; FILING DATE: 25-JULY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saveriede, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
PCT-US95-09464-1

Query Match          5.3%; Score 7; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
Db 28 EFIYGGC 34

RESULT 46
US-07-791-213D-16
; Sequence 16, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
```


;; APPLICANT: KANAMORI, Toshinori
;; APPLICANT: NOBUHARA, Masahiro
;; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
;; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
;; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
;; TITLE OF INVENTION: TREATING USING THE SAME
;; NUMBER OF SEQUENCES: 108
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/791,213D
;; FILING DATE: 13-NOV-1991
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 2-306745
;; FILING DATE: 13-NOV-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meuth, Donna M
;; REGISTRATION NUMBER: 36,607
;; REFERENCE/DOCKET NUMBER: 029650-032
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 54 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-07-791-213D-16

Query Match 5.3%; Score 7; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 35 YGGCQGN 41
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RESULT 47
US-08-293-150A-16
; Sequence 16, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/293,150A
;; FILING DATE: 19-AUG-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/791,213
;; FILING DATE: 13-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 2-306745
;; FILING DATE: 13-NOV-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meuth, Donna M.
;; REGISTRATION NUMBER: 36,607
;; REFERENCE/DOCKET NUMBER: 029650-049
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 54 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-293-150A-16

Query Match 5.3%; Score 7; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 35 YGGCQGN 41
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RESULT 48
US-08-358-160-19
; Sequence 19, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-19

Query Match 5.3%; Score 7; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 33 YGGCQGN 39

RESULT 49
US-08-358-160-20
; Sequence 20, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-20

Query Match 5.3%; Score 7; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 33 YGGCQGN 39

RESULT 50
US-08-358-160-87
; Sequence 87, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063


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; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver F.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEV=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-87

Query Match 5.3%; Score 7; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGN 113
Db 33 YGGCQGN 39

Search completed: September 21, 2005, 16:51:21
Job time : 33 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:46:12 ; Search time 109 Seconds
(without alignments)
489.161 Million cell updates/sec

Title: US-10-807-204-1

Perfect score: 131

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Word size : 0

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :

Published Applications AA:*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	106	80.9	106	16	US-10-807-204-2
4	64	48.9	86	17	US-10-480-988-21
5	64	48.9	98	16	US-10-807-204-9
6	64	48.9	101	15	US-10-276-774-2606
7	64	48.9	131	16	US-10-807-204-15
8	43	32.8	43	16	US-10-807-204-5
9	30	22.9	30	16	US-10-807-204-4
10	24	18.3	24	16	US-10-807-204-6
11	21	16.0	33	16	US-10-807-204-7

12	21	16.0	33	16	US-10-807-204-10
13	14	10.7	134	16	US-10-807-204-14
14	12	9.2	51	15	US-10-58-993-118
15	12	9.2	58	16	US-10-361-997-5
16	12	9.2	58	17	US-10-931-153-21
17	12	9.2	102	9	US-09-852-659A-120
18	12	9.2	102	15	US-10-058-993-121
19	12	9.2	117	9	US-09-852-659A-119
20	12	9.2	117	15	US-10-058-993-120
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23	12	9.2	133	9	US-09-852-797-75
24	12	9.2	133	15	US-10-058-993-75
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26	11	8.4	67	10	US-09-896-095-147
27	11	8.4	67	14	US-10-038-722-90
28	11	8.4	67	15	US-10-115-134-4
29	10	7.6	63	14	US-09-896-095-176
30	10	7.6	63	14	US-10-038-722-119
31	10	7.6	63	15	US-10-115-134-33
32	10	7.6	136	16	US-10-807-204-16
33	9	6.9	58	14	US-10-167-351-13
34	9	6.9	58	20	US-11-083-742-13
35	8	6.1	166	9	US-09-864-761-47670
36	8	6.1	324	18	US-10-213-974-24
37	8	6.1	449	17	US-10-732-923-22254
38	8	6.1	746	14	US-10-205-823-66
39	8	6.1	746	20	US-11-051-454-66
40	8	6.1	816	15	US-10-094-749-2643
41	8	6.1	1203	18	US-10-450-763-35830
42	8	6.1	1597	18	US-10-450-763-34348
43	8	6.1	1597	18	US-10-450-763-41171
44	8	6.1	1597	18	US-10-450-763-50261
45	8	6.1	1599	18	US-10-450-763-38243
46	8	6.1	1599	18	US-10-450-763-44809
47	8	6.1	1784	18	US-10-450-763-39507
48	8	5.3	18	17	US-10-753-078A-23
49	7	5.3	30	16	US-10-425-115-263879
50	7	5.3	30	16	US-10-425-115-263879

ALIGNMENTS

RESULT 1
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:
; NAME/KEY: SIGNAL

Sequence 10, Appl
Sequence 14, Appl
Sequence 118, Appl
Sequence 5, Appl
Sequence 21, Appl
Sequence 120, Appl
Sequence 121, Appl
Sequence 119, Appl
Sequence 120, Appl
Sequence 75, Appl
Sequence 75, Appl
Sequence 75, Appl
Sequence 75, Appl
Sequence 13, Appl
Sequence 147, Appl
Sequence 90, Appl
Sequence 4, Appl
Sequence 176, Appl
Sequence 119, Appl
Sequence 33, Appl
Sequence 16, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 47670, A
Sequence 24, Appl
Sequence 2254, A
Sequence 66, Appl
Sequence 2643, Ap
Sequence 35830, A
Sequence 34348, A
Sequence 40612, A
Sequence 41171, A
Sequence 50261, A
Sequence 38243, A
Sequence 44809, A
Sequence 39507, A
Sequence 23, Appl
Sequence 263879,


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; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
; US-10-807-204-2

Query Match      80.9%; Score 106; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKKKCLDFRKDICSMPQEAGP 85
Db 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKKKCLDFRKDICSMPQEAGP 60

Qy 86 CLASIPHWYKTKICSEFYGGCGNNNFQTEAICLVTKCKYH 131
Db 61 CLASIPHWYKTKICSEFYGGCGNNNFQTEAICLVTKCKYH 106

RESULT 4
US-10-480-988-21
; Sequence 21, Application US/10480988
; Publication No. US20050069877A1
; GENERAL INFORMATION:
; APPLICANT: GANDHI, Ameena R.; KABLE, Amy E.;
; APPLICANT: SWARNAKAR, Anita; HAPALATA, April J.A.;
; APPLICANT: TRAN, Bao; DUGGAN, Brendan M.;
; APPLICANT: WARREN, Bridget A.; ISON, Craig H.;
; APPLICANT: HONCHELL, Cynthia D.; NGUYEN, Damiel B.;
; APPLICANT: LU, Dying Aina M.; LEE, Ernestine A.;
; APPLICANT: YUE, Henry; FORSYTHE, Ian J.;
; APPLICANT: BARROSO, Ines; RAMKUMAR, Javalaxmi;
; APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
; APPLICANT: YANG, Junming; THANGAVELU, Kavitha;
; APPLICANT: GIETZEN, Kimberly J.; DING, Li;
; APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
; APPLICANT: YAO, Monique G.; CHAWLA, Narinder K.;
; APPLICANT: MASON, Patricia M.; GURURAJAN, Rajagopal;
; APPLICANT: LEE, Sally; BECHA, Shanya D.;
; APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
; APPLICANT: ELLIOTT, Vicki S.; LEO, Wen;
; APPLICANT: SPRAGUE, William W.; TANG, Y. Tom;
; APPLICANT: LU, Yan; ZEBARJADIAN, Yeganeh
; TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
; FILE REFERENCE: PF-1040 USN
; CURRENT APPLICATION NUMBER: US/10/480,988
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: PCT/US02/19360
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/300,508
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/303,445
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/305,405
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/311,442
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: US 60/314,821
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/315,992
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/378,205
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
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; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7675588CD1
; US-10-480-988-21

Query Match      48.9%; Score 64; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 1e-55;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQSPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQSPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Qy 61 CPFS 64
Db 61 CPFS 64

RESULT 5
US-10-807-204-9
; Sequence 9, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-807-204-9

Query Match      48.9%; Score 64; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.1e-55;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQSPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQSPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Qy 61 CPFS 64
Db 61 CPFS 64

RESULT 6
US-10-276-774-2606
; Sequence 2606, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
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; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2606
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2606

Query Match      48.9%; Score 64; DB 15; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-55;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 16 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 75
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CPFS 64
    ||||
Db 76 CPFS 79

RESULT 7
US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-15

Query Match      48.9%; Score 64; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.4e-55;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CPFS 64
    ||||
Db 61 CPFS 64

RESULT 8
US-10-807-204-5
; Sequence 5, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
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; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-5

Query Match      32.8%; Score 43; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.7e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 PCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 74
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 PCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 43
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9
US-10-807-204-4
; Sequence 4, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-4

Query Match      22.9%; Score 30; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILG 30
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILG 30
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10
US-10-807-204-6
; Sequence 6, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-6

Query Match 18.3%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 DCSMPQEGAGPCLASIPHWYNNK 98
Db 1 DCSMPQEGAGPCLASIPHWYNNK 24

RESULT 11
US-10-807-204-7
; Sequence 7, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Anos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-7

Query Match 16.0%; Score 21; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 QGNNNFQTEAICLVTCCKYH 131
Db 13 QGNNNFQTEAICLVTCCKYH 33

RESULT 12
US-10-807-204-10
; Sequence 10, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Anos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-807-204-10

Query Match 16.0%; Score 21; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 QGNNNFQTEAICLVTCCKYH 131
Db 13 QGNNNFQTEAICLVTCCKYH 33

RESULT 13
US-10-807-204-14
; Sequence 14, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Anos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-14

Query Match 10.7%; Score 14; DB 16; Length 134;
Best Local Similarity 100.0%; Pred. No. 9.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGCQCGNNNFQ 118
Db 105 FIYGCQCGNNNFQ 118

RESULT 14
US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970

; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-118

Query Match 9.2%; Score 12; DB 15; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNFQ 118
Db 31 YGGCGGNNNFQ 42

RESULT 15
US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Lev, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5

Query Match 9.2%; Score 12; DB 16; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNFQ 118
Db 35 YGGCGGNNNFQ 46

RESULT 16
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-PEGYLATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30

; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match 9.2%; Score 12; DB 17; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNFQ 118
Db 35 YGGCGGNNNFQ 46

RESULT 17
US-09-852-659A-120
; Sequence 120, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120

Query Match 9.2%; Score 12; DB 9; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNFQ 118
Db 76 YGGCGGNNNFQ 87

RESULT 18


```

US-10-058-993-121
; Sequence 121, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-121

Query Match          9.2%; Score 12; DB 15; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNFQ 118
DB 76 YGCGCGNNNFQ 87

RESULT 19
US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762

```

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; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-119

Query Match          9.2%; Score 12; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNFQ 118
DB 91 YGCGCGNNNFQ 102

RESULT 20
US-10-058-993-120
; Sequence 120, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762

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; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-120

Query Match 9.2%; Score 12; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNFQ 118
Db 91 YGGCQGNNNFQ 102
|||||

RESULT 21

US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-75

Query Match 9.2%; Score 12; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNFQ 118
Db 107 YGGCQGNNNFQ 118
|||||

RESULT 22

US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US20020077287A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-75

Query Match 9.2%; Score 12; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNFQ 118
Db 107 YGGCQGNNNFQ 118
|||||

RESULT 23

US-09-852-797-75
; Sequence 75, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-852-797-75

Query Match 9.2%; Score 12; DB 9; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.00097;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNFQ 118
 Db 107 YGGCGGNNNFQ 118

RESULT 24
 US-10-058-993-75
 ; Sequence 75, Application US/10058993
 ; Publication No. US2003022509A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: P2003P5
 ; CURRENT APPLICATION NUMBER: US/10/058,993
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: 09/852,659
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/852,797
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/853,161
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/265,583
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/152,060
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/04858
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-05
 ; PRIOR APPLICATION NUMBER: 60/050,934
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,100
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,357
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/040,710
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/040,762
 ; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-058-993-75

Query Match 9.2%; Score 12; DB 15; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.00097;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNFQ 118
 Db 107 YGGCGGNNNFQ 118

RESULT 25
 US-10-807-204-13
 ; Sequence 13, Application US/10807204
 ; Publication No. US20040229312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Bairoch, Amos
 ; APPLICANT: Niknejad, Anne
 ; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
 ; TITLE OF INVENTION: Inhibitor
 ; FILE REFERENCE: 54720-8015.US00
 ; CURRENT APPLICATION NUMBER: US/10/807,204
 ; CURRENT FILING DATE: 2004-03-22
 ; PRIOR APPLICATION NUMBER: PCT/EP03/01629
 ; PRIOR FILING DATE: 2003-02-18
 ; PRIOR APPLICATION NUMBER: US 60/358,683
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-807-204-13

Query Match 9.2%; Score 12; DB 16; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.00097;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNFQ 118
 Db 107 YGGCGGNNNFQ 118

RESULT 26
 US-08-896-095-147
 ; Sequence 147, Application US/09896095
 ; Publication No. US20030219886A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LADNER, Charles C.
 ; APPLICANT: GUTERMAN, Sonia K.
 ; APPLICANT: ROBERTS, Bruce L.
 ; APPLICANT: MARKLAND, William
 ; APPLICANT: LEY, Arthur C.
 ; APPLICANT: KENT, Rachel B.
 ; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
 ; FILE REFERENCE: LADNER=7L
 ; CURRENT APPLICATION NUMBER: US/09/896,095
 ; CURRENT FILING DATE: 2001-05-29
 ; PRIOR APPLICATION NUMBER: 08/415,922
 ; PRIOR FILING DATE: 1995-03-04
 ; PRIOR APPLICATION NUMBER: 08/009,319
 ; PRIOR FILING DATE: 1993-01-26
 ; PRIOR APPLICATION NUMBER: 07/664,989
 ; PRIOR FILING DATE: 1991-03-01
 ; PRIOR APPLICATION NUMBER: 08/993,776
 ; PRIOR FILING DATE: 1997-12-18
 ; NUMBER OF SEQ ID NOS: 274
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 147
 ; LENGTH: 67
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 US-09-896-095-147

Query Match 8.4%; Score 11; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNF 117
| | | | | | | | | |
Db 38 YGGCGGNNNF 48

RESULT 27
US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038.722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Query Match 8.4%; Score 11; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNF 117
| | | | | | | | | |
Db 38 YGGCGGNNNF 48

RESULT 28
US-10-115-134-4
; Sequence 4, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-115-134-4

Query Match 8.4%; Score 11; DB 15; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNF 117
| | | | | | | | | |
Db 38 YGGCGGNNNF 48

RESULT 29
US-09-896-095-176
; Sequence 176, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER=7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 176
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Bombyx mori
US-09-896-095-176

Query Match 7.6%; Score 10; DB 10; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFYGGCGGN 113
| | | | | | | | | |
Db 38 EFYGGCGGN 47

RESULT 30
US-10-038-722-119
; Sequence 119, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 119

Thu Sep 22 07:16:41 2005

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; LENGTH: 63
; TYPE: PRT
; ORGANISM: Bombyx mori
US-10-038-722-119

Query Match          7.6%; Score 10; DB 14; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGCQGN 113
Db 38 EFIYGGCQGN 47

RESULT 31
US-10-115-134-33
; Sequence 33, Application US/10115134
; Publication No. US2003022397A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Bombyx mori
US-10-115-134-33

Query Match          7.6%; Score 10; DB 15; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGCQGN 113
Db 38 EFIYGGCQGN 47

RESULT 32
US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairejad, Anne
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-16

Query Match          7.6%; Score 10; DB 16; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGCQGN 113
Db 104 EFIYGGCQGN 113

RESULT 33
US-10-167-351-13
; Sequence 13, Application US/10167351
; Publication No. US20030165896A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Markland, William
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
; FILE REFERENCE: DYX-007.2P US-4
; CURRENT APPLICATION NUMBER: US/10/167,351
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 09/638,770
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/414,878
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 09/240,136
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/676,124
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: PCT/US95/00298
; PRIOR FILING DATE: 1995-01-11
; PRIOR APPLICATION NUMBER: 08/208,265
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/179,658
; PRIOR FILING DATE: 1994-01-11
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant Kunitz domain selectants
US-10-167-351-13

Query Match          6.9%; Score 9; DB 14; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGCQGN 113
Db 33 FIYGGCQGN 41

RESULT 34
US-11-083-742-13
; Sequence 13, Application US/11083742
; Publication No. US20050186649A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Markland, William
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
; FILE REFERENCE: DYX-007.2P US-4
; CURRENT APPLICATION NUMBER: US/11/083,742
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/167,351
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 09/638,770
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/414,878
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 09/240,136
```


; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/676,124
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: PCT/US95/00298
; PRIOR FILING DATE: 1995-01-11
; PRIOR APPLICATION NUMBER: 08/208,265
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/179,658
; PRIOR FILING DATE: 1994-01-11
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant Kunitz domain selectants
US-11-083-742-13

Query Match 6.9%; Score 9; DB 20; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGCGN 113
Db 33 FIYGGCGN 41
|||||

RESULT 35
US-09-864-761-47670
; Sequence 47670, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47670
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AJ239323.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9
; OTHER INFORMATION: EST HUMAN HIT: AUI33286.1, EVALUATE 1.00e-60
; OTHER INFORMATION: SWISSPROT HIT: P51795, EVALUATE 5.00e-82
US-09-864-761-47670

Query Match 6.1%; Score 8; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 36 LVPFILLG 43
|||||

RESULT 36
US-10-213-974-24
; Sequence 24, Application US/10213974
; Publication No. US20050125159A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Joshua C
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Methods for Analyzing Biological Elements
; FILE REFERENCE: 38-10(52045)B
; CURRENT APPLICATION NUMBER: US/10/213,974
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US 60/325,537
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-213-974-24

Query Match 6.1%; Score 8; DB 18; Length 324;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 221 LVPFILLG 228
|||||

RESULT 37
US-10-732-923-22254
; Sequence 22254, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 22254
; LENGTH: 449


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; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-732-923-22254

Query Match      6.1%; Score 8; DB 17; Length 449;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GLLPILVP 12
        |||||
Db      391 GLLPILVP 398

RESULT 38
US-10-205-823-66
; Sequence 66, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-454-66

Query Match      6.1%; Score 8; DB 20; Length 746;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 LVPPILLG 17
        |||||
Db      319 LVPPILLG 326

RESULT 40
US-10-094-749-2643
; Sequence 2643, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 2643
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2643

Query Match          6.1%; Score 8; DB 15; Length 816;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 389 LVPFILLG 396

RESULT 41
US-10-450-763-35830
; Sequence 35830, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 35830
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (675)..(693)
; OTHER INFORMATION: CHLORIDE CHANNEL SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00762A, p-value=4.000e-22, raw score of 14.22
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (663)..(1029)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1203)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-35830

Query Match          6.1%; Score 8; DB 18; Length 1203;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 836 LVPFILLG 843

RESULT 42
US-10-450-763-34348
; Sequence 34348, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450.763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
```

```
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 34348
; LENGTH: 1597
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1057)..(1423)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-34348

Query Match          6.1%; Score 8; DB 18; Length 1597;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 1230 LVPFILLG 1237

RESULT 43
US-10-450-763-40612
; Sequence 40612, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 40612
; LENGTH: 1597
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1058)..(1424)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-40612

Query Match          6.1%; Score 8; DB 18; Length 1597;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
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Db      1230 LVFPILLG 1237
|||||
RESULT 44
US-10-450-763-41171
; Sequence 41171, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 41171
; LENGTH: 1597
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1057)..(1423)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-41171

Query Match      6.1%; Score 8; DB 18; Length 1597;
Best Local Similarity 100.0%; Pred. No. 78;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      10 LVFPILLG 17
|||||
Db      1230 LVFPILLG 1237

RESULT 45
US-10-450-763-50261
; Sequence 50261, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 50261
; LENGTH: 1597
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)

Query Match      6.1%; Score 8; DB 18; Length 1597;
Best Local Similarity 100.0%; Pred. No. 78;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      10 LVFPILLG 17
|||||
Db      1230 LVFPILLG 1237

RESULT 46
US-10-450-763-38243
; Sequence 38243, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 38243
; LENGTH: 1599
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1061)..(1427)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-38243

Query Match      6.1%; Score 8; DB 18; Length 1599;
Best Local Similarity 100.0%; Pred. No. 78;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      10 LVFPILLG 17
|||||
Db      1232 LVFPILLG 1239

RESULT 47
US-10-450-763-44809
; Sequence 44809, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
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; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44809
; LENGTH: 1599
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1599)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-44809

Query Match          6.1%; Score 8; DB 18; Length 1599;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
Db      1232 LVPFILLG 1239

RESULT 48
US-10-450-763-39507
; Sequence 39507, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39507
; LENGTH: 1784
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (297)..(338)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354I, p-value=1.000e-40, raw score
; OTHER INFORMATION: 15.55
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1246)..(1612)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by PFam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.3
US-10-450-763-39507

Query Match          6.1%; Score 8; DB 18; Length 1784;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
```

```
Db      1417 LVPFILLG 1424

RESULT 49
US-10-753-078A-23
; Sequence 23, Application US/10753078A
; Publication No. US20050037475A1
; GENERAL INFORMATION:
; APPLICANT: Reifsnnyder, David
; APPLICANT: Inlow, Duane
; APPLICANT: Dorin, Glenn
; APPLICANT: Riquelme, Patricio
; APPLICANT: Cowgill, Cynthia
; APPLICANT: Bolesch, Doug
; APPLICANT: Gustafson, Mark
; TITLE OF INVENTION: Improved Method of Purifying TFPI and
; TITLE OF INVENTION: TFPI Analogs
; FILE REFERENCE: 012441.00050
; CURRENT APPLICATION NUMBER: US/10/753,078A
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/494,546
; PRIOR FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: US 60/509,277
; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/512,199
; PRIOR FILING DATE: 2003-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-753-078A-23

Query Match          5.3%; Score 7; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      104 EFYGGC 110
Db       5 EFYGGC 11

RESULT 50
US-10-425-115-263879
; Sequence 263879, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 263879
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172271C.1.pep
US-10-425-115-263879

Query Match          5.3%; Score 7; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy       4 SGLLPIL 10
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Thu Sep 22 07:16:41 2005

Db 15 SGLLPIL 21

Search completed: September 21, 2005, 16:53:19
Job time : 112 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 16:41:20 / Search time 31 Seconds
(without alignments)
406.593 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 131
Sequence: 1 MGLSGLPILVPFILLGDIQ.....GNNNNFQTEAICLVTCCKYH 131

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : PIR 79:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	7.6	62	2 S01802	chymotrypsin inhib
2	10	7.6	63	1 TIMTC3	chymotrypsin inhib
3	8	6.1	67	1 TIBOC	trypsin inhibitor,
4	8	6.1	126	2 S54159	probable sodium po
5	8	6.1	324	2 B96738	probable ABC trans
6	8	6.1	449	2 G95876	probable permease
7	8	6.1	1515	2 T52081	MRP-like ABC trans
8	7	5.3	53	2 B29235	hemolymph trypsin
9	7	5.3	57	1 TIMJVC	venom basic protei
10	7	5.3	62	2 S01803	chymotrypsin inhib
11	7	5.3	211	2 F95851	probable nitrateni
12	7	5.3	215	2 D84382	hypothetical prote
13	7	5.3	272	2 AC0140	probable membrane
14	7	5.3	299	2 I46937	tissue factor path
15	7	5.3	300	2 S12143	lipoprotein-associ
16	7	5.3	302	1 TIRTKG	tissue factor path
17	7	5.3	304	1 JC2264	tissue factor path
18	7	5.3	304	1 TIHUGK	tissue factor path
19	7	5.3	337	2 F83839	hypothetical prote
20	7	5.3	337	2 A72042	conserved hypothet
21	7	5.3	337	2 H86582	CT 368 hypothetical
22	7	5.3	337	2 T19885	hypothetical prote
23	7	5.3	348	2 T19885	alpha-1-microglobu
24	7	5.3	352	1 HCHU	myb-related protei
25	7	5.3	374	2 T05891	myb-related trans
26	7	5.3	376	2 T51673	tissue factor path
27	7	5.3	396	2 S53325	tissue factor path
28	7	5.3	497	2 F83634	hypothetical prote
29	7	5.3	564	2 F72268	ABC transporter, A

30	7	5.3	602	2 D90557	hypothetical prote
31	7	5.3	615	2 S74277	probable membrane
32	7	5.3	615	2 S40624	probable membrane
33	7	5.3	988	2 B96621	hypothetical prote
34	7	5.3	1030	2 T37868	probable helicase
35	7	5.3	1073	1 S56822	SK12 protein homol
36	7	5.3	1117	2 T11667	probable RNA helic
37	6	4.6	43	2 C47447	calcium channel pr
38	6	4.6	53	2 C90850	fimbrial minor pil
39	6	4.6	55	2 S30332	proteinase inhibit
40	6	4.6	56	2 JN0380	trypsin inhibitor
41	6	4.6	57	1 TIRIV2	venom basic protei
42	6	4.6	57	2 S13846	venom animal Kunit
43	6	4.6	58	1 TIHABK	isoinhibitor K (BP
44	6	4.6	61	1 TIVIT1	venom basic protei
45	6	4.6	62	2 S07451	proteinase inhibit
46	6	4.6	62	2 A44180	taicatoxin serine
47	6	4.6	62	2 S19327	venom basic protei
48	6	4.6	63	2 T34799	probable transcrip
49	6	4.6	65	1 TIVIVC	venom basic protei
50	6	4.6	71	2 D42506	F-ORF-E protein -

ALIGNMENTS

RESULT 1

S01802
chymotrypsin inhibitor I - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01802
R:Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3072972
A:Accession: S01802
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:Cross-references: UNIPROT:P10831
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 7.6%; Score 10; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EPIYGGCQGN 113

Db 37 EPIYGGCQGN 46

RESULT 2

TIMTC3
chymotrypsin inhibitor III - silkworm
N:Alternate names: SCI-III
C:Species: Bombyx mori (silkworm)
C:Date: 22-Jul-1987 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C:Accession: A25740
R:Sasaki, T.
FEBS Lett. 168, 227-230, 1984
A:Title: Amino acid sequence of a novel Kunitz-type chymotrypsin inhibitor from hemolymph
A:Reference number: A25740
A:Accession: A25740
A:Molecule type: protein
A:Residues: 1-63 <SAS>
A:Cross-references: UNIPROT:P07481
A:Experimental source: larval hemolymph
C:Comment: In contrast to chymotrypsin inhibitors I and II, which are basic, this inhibi
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:10-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;10-61.20-44.36-57/disulfide bonds: #status predicted
F;21/Inhibitory site: Phe (chymotrypsin) #status predicted

Query Match 7.6%; Score 10; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGCGNN 113
|||||
Db 38 EFIYGGCGNN 47

RESULT 3

TIBOC

trypsin inhibitor, colostrum (BPI type) - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A01207

R;Cechova, D.; Jonakova, V.; Sorm, F.

Collect. Czech. Chem. Commun. 36, 3342-3357, 1971

A;Title: Primary structure of trypsin inhibitor from cow colostrum (component B2).

A;Reference number: A90928

A;Accession: A01207

A;Molecule type: protein

A;Residues: 1-26, 'B', 28-67 <CEC>

A;Cross-references: UNIPROT:P00976

A;Note: the residue identified as Asx is bound to carbohydrate; therefore, we have shown

R;Cechova, D.; Ber, E.

Collect. Czech. Chem. Commun. 39, 680-688, 1974

A;Title: Disulfide bonds of trypsin inhibitor from cow colostrum.

A;Reference number: A90929

A;Contents: annotation; disulfide bonds

R;Cechova, D.; Muszynska, G.

FEBS Lett. 8, 84-86, 1970

A;Title: Role of lysine 18 in active center of cow colostrum trypsin inhibitor.

A;Reference number: A91440

A;Contents: annotation

A;Note: the inhibitory site was determined

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C;Keywords: colostrum; glycoprotein; serine proteinase inhibitor

F;8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;8-58,17-41,33-54/disulfide bonds: #status experimental

F;18/Inhibitory site: Lys (trypsin) #status experimental

F;27/Binding site: carbohydrate (Asn) (covalent) #status experimental

Qy 107 YGGCGQNN 114
|||||
Db 38 YGGCGQNN 45

RESULT 4

S54159

probable sodium potassium ATPase gamma chain - human

C;Species: Homo sapiens (man)

C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S54159

R;Austrey, E.; Belley, L.; Millasot, P.; Junten, C.; Jeanpierre, C.

submitted to the EMBL Data Library, April 1995

A;Description: Characterization of the human cDNA for L-arginine:glycine amidinotransfer

A;Reference number: S54159

A;Accession: S54159

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-126 <AUS>

A;Cross-references: UNIPROT:Q15332; EMBL:X86400; NID:g791046; PIDN:CAA60152.1; PID:g7910

Query Match 6.1%; Score 8; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 EAGPCLAS 89
|||||
Db 35 EAGPCLAS 42

RESULT 5

B96738

Probable ABC transporter F3117.2 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: B96738

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: B96738

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-324 <STO>

A;Cross-references: UNIPROT:Q9FVU9; GB:AE005173; NID:g6714334; PIDN:AAF26026.1; GSPDB:GN

C;Genetics:

A;Gene: F3117.2

A;Map position: 1

Query Match 6.1%; Score 8; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVFFILIG 17
|||||
Db 221 LVFFILIG 228

RESULT 6

G95876

probable permease protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: G95876

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: G95876

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-449 <KUR>

A;Cross-references: UNIPROT:Q92WQ0; GB:AL591985; PIDN:CAC48679.1; PID:g15140151; GSPDB:G

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: SMD20289

A;Genome: plasmid

Query Match 6.1%; Score 8; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GLLPILVP 12
|||||
Db 391 GLLPILVP 398

RESULT 7
T52081
MRP-like ABC transporter [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52081
R:Tommasini, R.; Vogt, E.; Schmid, J.; Fromentau, M.; Amrhein, N.; Martinoia, E.
FEBS Lett. 411, 206-210, 1997
A:Title: Differential expression of genes coding for ABC transporters after treatment of
A:Reference number: Z25942; MUID:97415407; PMID:9271206
A:Accession: T52081
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1515 <TOM>
A:Cross-references: UNIPROT:Q24510; EMBL:U92650; PIDN:AAC49791.1
A:Experimental source: cultivar Columbia
C:Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 6.1%; Score 8; DB 2; Length 1515;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LVPFILLG 17
|||||
Db 949 LVPFILLG 956

RESULT 8
B29235
hemolymph trypsin inhibitor B (BPI type) - tobacco hornworm (fragment)
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: B29235
R:Ramesh, N.; Sugumaran, M.; Mole, J.E.
J. Biol. Chem. 263, 11523-11527, 1988
A:Title: Purification and characterization of two trypsin inhibitors from the hemolymph
A:Reference number: A92663; MUID:88298810; PMID:3165377
A:Accession: B29235
A:Molecule type: protein
A:Residues: 1-53 <RAM>
A:Cross-references: UNIPROT:P26227
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:4-53/Domain: animal Kunitz-type proteinase inhibitor homology (fragment) <BPI>

Query Match 5.3%; Score 7; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGQGN 113
|||||
Db 34 YGCGQGN 40

RESULT 9
TINJVC
venom basic proteinase inhibitor II - Cape cobra
C:Species: Naja nivea (Cape cobra)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C:Accession: A01217
R:Hokama, Y.; Iwanaga, S.; Tateuchi, T.; Suzuki, T.
J. Biochem. 79, 559-578, 1976
A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitor
o acid sequences of two of them.
A:Reference number: A91942; MUID:76237547; PMID:950337
A:Accession: A01217
A:Molecule type: protein

A:Residues: 1-57 <HOK>
A:Cross-references: UNIPROT:P00986
C:Comment: The activity of this inhibitor is probably similar to that of bovine basic pr
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor; venom
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 5.3%; Score 7; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGC 110
|||||
Db 32 EFIYGGC 38

RESULT 10
S01803
chymotrypsin inhibitor II - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01803
R:Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3072972
A:Accession: S01803
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:Cross-references: UNIPROT:P10832
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 5.3%; Score 7; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGC 110
|||||
Db 37 EFIYGGC 43

RESULT 11
F95851
probable nitrate/nitrite response regulator protein [imported] - Sinorhizobium meliloti (C
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: F95851
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: F95851
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <KUR>
A:Cross-references: UNIPROT:Q92X84; GB:AL591985; PIDN:CAC48478.1; PID:G15139950; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.,
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welle, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb20078
A:Genome: plasmid
C:Superfamily: response regulator with HTH DNA-binding domain, NarL type; response regul

Query Match 5.3%; Score 7; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MGLSGLL 7
 | | | | |
 Db 96 MGLSGLL 102

RESULT 12
 D84382
 hypothetical protein Vng3314h [imported] - Halobacterium sp. NRC-1
 C;Species: Halobacterium sp. NRC-1
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: D84382
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
 ; Leitthausser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950
 A;Accession: D84382
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-215 <STO>
 A;Cross-references: UNIPROT:Q9HMZ7; GB:AE004437; NID:gl0581728; PIDN:AAG20424.1; GSPDB:G
 C;Genetics:
 A;Gene: VNG2314H

Query Match 5.3%; Score 7; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GLLPILV 11
 | | | | |
 Db 92 GLLPILV 98

RESULT 13
 AC0140
 probable membrane protein YP01140 [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AC0140
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AC0140
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-272 <KUR>
 A;Cross-references: UNIPROT:Q8ZGY1; GB:AL590842; PIDN:CAC89982.1; PID:g15979204; GSPDB:G
 C;Genetics:
 A;Gene: YP01140

Query Match 5.3%; Score 7; DB 2; Length 272;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILL 16
 | | | | |
 Db 114 LVPFILL 120

RESULT 14
 I46937
 tissue factor pathway inhibitor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
 C;Accession: I46937
 R;Belaouaj, A.; Kuppusewamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
 Thromb. Res. 69, 547-553, 1993
 A;Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
 A;Reference number: I46937; MUID:93276427; PMID:8503123
 A;Accession: I46937
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-299 <BEL>
 A;Cross-references: UNIPROT:PI9761; GB:S61902; NID:g386015; PIDN:AAB26836.1; PID:g386016
 C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 F;45-99/Domain: animal Kunitz-type proteinase inhibitor homology <BP11>
 F;120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>

Query Match 5.3%; Score 7; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFYGGC 110
 | | | | |
 Db 76 EFYGGC 82

RESULT 15
 S12143
 lipoprotein-associated coagulation inhibitor precursor - rabbit
 N;Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
 C;Accession: S12143; A61373
 R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
 Nucleic Acids Res. 18, 6440, 1990
 A;Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
 A;Reference number: S12143; MUID:91057146; PMID:2136251
 A;Accession: S12143
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-300 <WES>
 A;Cross-references: EMBL:X54708; NID:gl612; PIDN:CAA38515.1; PID:g1613
 R;Colburn, P.; Crabb, J.W.; Buonassisi, V.
 J. Cell. Physiol. 148, 320-326, 1991
 A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell
 A;Reference number: A61373; MUID:91349227; PMID:1880157
 A;Accession: A61373
 A;Molecule type: protein
 A;Residues: 25-33,'X',35-46 <COL>
 C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 C;Keywords: anticoagulant; glycoprotein
 F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F;121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match 5.3%; Score 7; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFYGGC 110
 | | | | |
 Db 77 EFYGGC 83

RESULT 16
 TIRYTK
 tissue factor pathway inhibitor precursor - rat
 N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibi
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: JX0213
 R;Enryoji, K.; Emi, M.; Mukai, T.; Kato, H.
 J. Biochem. 111, 681-687, 1992
 A;Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).

A;Reference number: JX0213; MUID:92348361; PMID:1639767
A;Accession: JX0213
A;Molecule type: mRNA
A;Residues: 1-302 <ENJ>
A;Cross-references: UNIPROT:Q02445; DDBJ:D10926; NID:g220916; PIDN:BA01724.1; PID:g2209
A;Experimental source: liver
C;Comment: This serine proteinase inhibitor regulates clotting by factor Xa-dependent in
C;Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-302/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;124-174/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;222-272/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;288-291/Region: heparin binding #status predicted
F;53/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted
F;134/Inhibitory site: Arg (coagulation factor X) #status predicted
F;144,251,261/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;232/Inhibitory site: Lys (unidentified proteinase) #status predicted

Query Match 5.3%; Score 7; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGC 110
|||||
Db 80 EPIYGGC 86

RESULT 17
JC2264
tissue factor pathway inhibitor precursor - rhesus macaque
N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC2264
R;Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Yonemura, H.; Miyamoto
J. Biochem. 115, 708-714, 1994
A;Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path
A;Reference number: JC2264; MUID:94375417; PMID:8089087
A;Accession: JC2264
A;Molecule type: mRNA
A;Residues: 1-304 <KMS>
A;Cross-references: UNIPROT:Q28864; GB:S73337; NID:g685016; PIDN:AAB31955.1; PID:g685017
A;Experimental source: liver
C;Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VI
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Diulfide bonds: #
F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted
F;135/Inhibitory site: Arg (coagulation factor X) #status predicted
F;145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 5.3%; Score 7; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGC 110
|||||
Db 81 EPIYGGC 87

RESULT 18
TIHUGK
tissue factor pathway inhibitor precursor [validated] - human

N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A23712; A39176; A28650; A60433; B60433; S13034; A34315; A38294; S03903
R;Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; MacPhail, L.A.; Likert, K.M.; Byers, M.G.
J. Biol. Chem. 266, 5036-5041, 1991
A;Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. Intro
A;Reference number: A23712; MUID:91161593; PMID:2002045
A;Accession: A23712
A;Molecule type: DNA
A;Residues: 1-304 <GR>
A;Cross-references: UNIPROT:P10646; GB:M59493; GB:M59499; NID:g187204; PIDN:AAA59526.1;
R;van der Logt, C.P.E.; Reitsma, P.H.; Bertina, R.M.
Biochemistry 30, 1571-1577, 1991
A;Title: Intron-exon organization of the human gene coding for the lipoprotein-associated
A;Reference number: A39176; MUID:91129227; PMID:1993173
A;Accession: A39176
A;Molecule type: DNA
A;Residues: 1-304 <VAN>
A;Cross-references: GB:M58650; GB:J05312; NID:g186827; PIDN:AAA59480.1; PID:g186829
R;Wun, T.C.; Kretzmer, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 263, 6001-6004, 1988
A;Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated co
A;Reference number: A28650; MUID:88198127; PMID:2452157
A;Accession: A28650
A;Molecule type: mRNA
A;Residues: 1-304 <WUN>
A;Cross-references: GB:J03225; NID:g180545; PIDN:AAA52022.1; PID:g180546
A;Note: part of this sequence, including the amino end of the mature protein, was confil
R;Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G.J.
Thromb. Res. 55, 37-50, 1989
A;Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associated
A;Reference number: A60433; MUID:89388722; PMID:2781520
A;Accession: A60433
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-304 <GI2>
A;Experimental source: endothelial cells
A;Accession: B60433
A;Molecule type: protein
A;Residues: 'XX', 31-53, 'X', 55-56 <GI3>
A;Experimental source: recombinant material from mouse C137 cells
R;Girard, T.J.; McCourt, D.; Novotny, W.F.; MacPhail, L.A.; Likert, K.M.; Broze Jr., G.J.
Biochem. J. 270, 621-625, 1990
A;Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibitor
A;Reference number: S13034; MUID:91054349; PMID:2122883
A;Accession: S13034
A;Molecule type: protein
A;Residues: 29-35 <GI4>
R;Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 264, 18832-18837, 1989
A;Title: Purification and characterization of the lipoprotein-associated coagulation inh
A;Reference number: A34315; MUID:90036996; PMID:2553722
A;Accession: A34315
A;Molecule type: protein
A;Residues: 'XX', 31-33, 'L', 35-50 <NOV>
A;Experimental source: plasma
R;Pedersen, A.H.; Nordfang, O.; Norris, F.; Wiberg, F.C.; Christensen, P.M.; Mosler, K.
J. Biol. Chem. 265, 16786-16793, 1990
A;Title: Recombinant human extrinsic pathway inhibitor. Production, isolation, and chara
A;Reference number: A38294; MUID:91009092; PMID:2211593
A;Accession: A38294
A;Molecule type: protein
A;Residues: 29-41 <PED>
R;Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.;
Nature 338, 518-520, 1989
A;Title: Functional significance of the Kunitz-type inhibitory domains of lipoprotein-as
A;Reference number: S03903; MUID:89181950; PMID:2927510
A;Contents: annotation; site-directed mutagenesis
C;Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
C;Genetics:
A;Gene: GDB:TFPI
A;Cross-references: GDB:127364; OMIM:152310

A;Map position: 2q32-2q32
A;Intons: 41/1; 107/1; 120/1; 179/1; 210/1; 270/1
C;Function:
A;Description: regulates clotting by factor Xa-dependent inhibition of the coagulation f
A;Pathway: blood coagulation
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-304/Product: tissue factor pathway inhibitor #status experimental <MAT>
F;54-104/Domain: animal Kunitz-type proteinase inhibitor #status experimental
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;284-289/Region: heparin binding #status predicted
F;30/Binding site: phosphate (Ser) (covalent) #status experimental
F;54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds: #
F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status experim
F;135/Inhibitory site: Arg (coagulation factor X) #status experimental
F;145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 5.3%; Score 7; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFVGGC 110
|||||
Db 81 EFVGGC 87
|||||

RESULT 19
TIQB1
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
N;Alternate names: bikunin; ITI; PI-14 (inhibitory fragment of ITI)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: S11066; S13493; A01208
R;Gebhard, W.; Schreitmüller, T.; Vetr, H.; Wachter, E.; Hochstrasser, K.
FEBS Lett. 269, 32-36, 1990

A;Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microglobu
A;Reference number: S11066; MUID:90353595; PMID:1696914
A;Accession: S11066
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-337 <GB>
A;Cross-references: UNIPROT:P04366; EMBL:X53685; NID:g1877; PIDN:CAA37725.1; PID:g1878
R;Tavakkoli, A.
Biochim. Biophys. Acta 1088, 47-56, 1991

A;Title: Molecular cloning of porcine alpha(1)-microglobulin/HI-30 reveals developmental
A;Reference number: S13493; MUID:91113729; PMID:1703444
A;Accession: S13493
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'M', '3-48', 'M', '50-337' <TAV>
A;Cross-references: GB:X52087; NID:g1881; PIDN:CAA36306.1; PID:g1882
A;Note: the authors translated the codon GTG for residue 2 as a Met initiation codon
R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985

A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A;Reference number: A90685; MUID:85225967; PMID:2408637
A;Accession: A01208
A;Molecule type: protein
A;Residues: 212-258,'Q',260-269,'S',271-277,'Q',279-282,'A',284,'IR',287-292,'A',294-310
C;Comment: This inhibitory fragment, released from native ITI after limited proteolysis
First domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
C;Comment: The amino acid at position P2' (228-Met) appears to determine the specificity
nd elastase; those with leucine interact strongly.

C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;20-173/Domain: lipocalin homology <lip>
F;216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;216-266,225-249,241-262,272-322,281-305,297-318/Disulfide bonds: #status predicted
F;226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted

F;235/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;282/Inhibitory site: Arg (trypsin) #status predicted

Query Match 5.3%; Score 7; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGQN 113
|||||
Db 302 YGCGQN 308
|||||

RESULT 20

F83839

hypothetical protein BHI518 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: F83839

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: F83839

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-337 <STO>

A;Cross-references: UNIPROT:Q9KCQ1; GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA8052;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BHI518

Query Match

5.3%; Score 7; DB 2; Length 337;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VPFILG 17
|||||

Db 56 VPFILG 62
|||||

RESULT 21

A72042

conserved hypothetical protein CP0006 [imported] - Chlamydophila pneumoniae (strains CWL0

N;Alternate names: ct 368 hypothetical protein

C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: A72042; B81624

R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: A72042

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-337 <ARN>

A;Cross-references: UNIPROT:Q9Z7G6; GB:AE001655; GB:AE001363; NID:94377039; PIDN:AAD18874

A;Experimental source: strain CWL029

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.;

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: B81624

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-337 <REA>

A;Cross-references: GB:AE002164; GB:AE002161; NID:g7188939; PIDN:AAF37902.1; PID:g718894

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CPn0739; CP0006

Query Match

5.3%; Score 7; DB 2; Length 337;

Best Local Similarity 100.0%; Pred. No. 16;

Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	96	NKTKIC 102							
Db	7	NKTKIC 13							
RESULT 22									
H86582									
CT 368 hypothetical protein [imported] - Chlamydomonada pneumoniae (strain J138)									
C:Species: Chlamydomonada pneumoniae, Chlamydia pneumoniae									
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004									
C:Accession: H86582									
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie									
Nucleic Acids Res. 28, 2311-2314, 2000									
A>Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.									
A:Reference number: A86491; MUID:20330349; PMID:10871362									
A:Accession: H86582									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-337 <STO>									
A:Cross-references: UNIPROT:Q9JSS0; GB:BA000008; NID:G8979111; PIDN:BAA98946.1; GSPDB:GN									
A:Experimental source: strain J138									
C:Genetics:									
A:Gene: CPJ0739									
Query Match									
Best Local Similarity 5.3%; Score 7; DB 2; Length 337;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	96	NKTKIC 102							
Db	7	NKTKIC 13							
RESULT 23									
T19885									
hypothetical protein C41G6.6 - Caenorhabditis elegans									
C:Species: Caenorhabditis elegans									
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004									
C:Accession: T19885									
R:Cummings, P.									
A:Reference number: Z19191									
A:Accession: T19885									
A:Status: preliminary; translated from GB/EMBL/DBJ									
A:Molecule type: DNA									
A:Residues: 1-348 <WIL>									
A:Cross-references: UNIPROT:O17659; EMBL:Z81047; PIDN:CAB02831.1; GSPDB:GN00023; CESP:C4									
A:Experimental source: clone C41G6									
C:Genetics:									
A:Gene: CESP:C41G6.6									
A:Map position: 5									
A:Introns: 131/1; 321/1									
Query Match									
Best Local Similarity 5.3%; Score 7; DB 2; Length 348;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	113	NNNNFQT 119							
Db	189	NNNNFQT 195							
RESULT 24									
HCHU									
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human									
N:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) pr									
rich protein									
N:Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor									
C:Species: Homo sapiens (man)									
C>Date: 15-Oct-1982 #sequence_revision 30-Jun-1987 #text change 09-Jul-2004									
C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; PNO450; B39079; A61580; B25									

3217
R:Vetr, H.; Gebhard, W.
Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
A>Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
A:Reference number: S13433; MUID:91214554; PMID:1708673
A:Accession: S13433
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <VET1>
A:Cross-references: UNIPROT:P02760; EMBL:X54816; NID:G24475; PIDN:CAA38585.1; PID:982561
R:Diarra-Mehrpor, M.; Bourguignon, J.; Seabouee, R.; Salier, J.P.; Leveillard, T.; Mart
Eur. J. Biochem. 191, 131-139, 1990
A>Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene
A:Reference number: S10778; MUID:90336621; PMID:1696200
A:Accession: S10778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <DIA>
R:Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
Nucleic Acids Res. 14, 7839-7850, 1986
A>Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-
A:Reference number: A93642; MUID:87040757; PMID:2430261
A:Accession: A93642
A:Molecule type: mRNA
A:Residues: 1-352 <KAU>
A:Cross-references: GB:X04494; NID:G24478; PIDN:CAA28182.1; PID:924479
R:Lopez Otin, C.; Grubb, A.O.; Mendez, E.
Arch. Biochem. Biophys. 228, 544-554, 1984
A>Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge
A:Reference number: A90074; MUID:84126849; PMID:6198962
A:Accession: A90074
A:Molecule type: protein
A:Residues: 20-56.58-202 <LOP>
A:Experimental source: individual with tubular proteinuria
A>Note: no evidence of sequence heterogeneity could be found, in spite of persistent het
R:Takagi, T.; Takagi, K.; Kawai, T.
Biochem. Biophys. Res. Commun. 98, 997-1001, 1981
A>Title: Complete amino acid sequence of human alpha-1-microglobulin.
A:Reference number: A90225; MUID:81184038; PMID:6164372
A:Accession: A90225
A:Molecule type: protein
A:Residues: 20-47.58-136.138-141, 'T', 143-144, 146-198 <TAK>
A:Experimental source: pooled urine of patients with tubular proteinuria
R:Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempert, K.; Salier, J.P.
Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
A>Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in
A:Reference number: A90686; MUID:85225968; PMID:2408638
A:Accession: A90686
A:Molecule type: protein
A:Residues: 206-290, 'VI', 293-342, 'E', 344-350 <REI>
R:Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueke, T.; Daudon, M.
Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
A>Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of cr
A:Reference number: PNO450; MUID:93221481; PMID:8466493
A:Accession: PNO450
A:Molecule type: protein
A:Residues: 206-214, 'X' <ATM1>
R:Engel, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S.V
J. Biol. Chem. 266, 747-751, 1991
A>Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot
A:Reference number: A39079; MUID:91093267; PMID:1898736
A:Accession: B39079
A:Molecule type: protein
A:Residues: 206-225 <ENGI>
R:Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
Int. J. Biochem. 23, 1201-1203, 1991
A>Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inh
A:Reference number: A61580; MUID:92175157; PMID:1794445
A:Accession: A61580
A:Molecule type: protein
A:Residues: 214, 'X', 216-222, 'X' <CHI>
R:McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.
J. Biol. Chem. 261, 5378-5383, 1986

A;Title: Two apparent human endothelial cell growth factors from human hepatoma cells and
A;Reference number: A92583; MUID:86168278; PMID:3007499
A;Accession: B25604
A;Molecule type: protein
A;Residues: 206-214, 'X', 216-230, 'X', 232-239, 'X', 241-248, 'XX', 251-252, 'X', 254 <MCK>
R;Englhard, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A;Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha
A;Reference number: A92736; MUID:89380192; PMID:2476436
A;Accession: C34245
A;Molecule type: protein
A;Residues: 206-225 <ENG2>
R;Traboni, C.; Cortese, R.
Nucleic Acids Res. 14, 6340, 1986
A;Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobulin
A;Reference number: A25303; MUID:86312901; PMID:2428011
A;Accession: A25303
A;Molecule type: mRNA
A;Residues: 1-218, 'HW' <TRA>
A;Note: this mRNA sequence appears to contain errors after residue 218
R;Calero, M.; Escribano, J.; Grubb, A.; Mendez, E.
J. Biol. Chem. 269, 384-389, 1994
A;Title: Location of a novel type of interpolypeptide chain linkage in the human protein
A;Reference number: A53110; MUID:94103241; PMID:7506257
A;Accession: A53110
A;Molecule type: protein
A;Residues: 45-57 <CAL2>
R;Vetri, H.; Koegler, M.; Gebhard, W.
FEBS Lett. 245, 137-140, 1989
A;Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inhibitor
A;Reference number: S03552; MUID:89171290; PMID:2466696
A;Accession: S03552
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 206-352 <VET2>
R;Malki, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fournier
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A;Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation
A;Reference number: S28928; MUID:93033735; PMID:1384548
A;Accession: S28930
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-215 <MAL>
R;Morelle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalski, C.; Fournier
Eur. J. Biochem. 221, 881-888, 1994
A;Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of inter-alpha-
A;Reference number: S43466; MUID:94229087; PMID:7513643
A;Accession: S43466
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-221 <MOR>
R;Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
Biochemistry 33, 7423-7429, 1994
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex
A;Reference number: A53642; MUID:94271799; PMID:7516184
A;Accession: A53642
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-217 <WIS>
R;Calero, M.; Mendez, E.; Garcia, E.
Biochim. Biophys. Acta 1249, 91-99, 1995
A;Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)
A;Reference number: S55688; MUID:95284116; PMID:7539295
A;Accession: S55688
A;Molecule type: protein
A;Residues: 20-24 <CAL2>
R;Bourguignon, J.; Diarra-Mehrpour, M.; Sesboue, R.; Fraim, M.; Sala-Trepat, J.M.; Marti
Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
A;Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide sequence
A;Reference number: 152208; MUID:86025577; PMID:2413856
A;Accession: 152208
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 302-352 <BOU>
A;Cross-references: GB:M11562; NID:g186587; PIDN:AAAS9194.1; PID:g307077
R;Wojcik, E.G.C.; van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Berti
Biochem. J. 311, 753-759, 1995
A;Title: Factor IX Zuthphen: a Cys(18) -> Arg mutation results in formation of a heterodimer
A;Reference number: S59509; MUID:96067589; PMID:7487929
A;Accession: S59509
A;Molecule type: protein
A;Residues: 27-35, 'Y', 37 <WOJ>
R;Atmani, F.; Mizon, J.; Khan, S.R.
Eur. J. Biochem. 236, 984-990, 1996
A;Title: Identification of uronic-acid-rich protein as urinary bikunin, the light chain of
A;Reference number: S66434; MUID:96270753; PMID:8665922
A;Accession: S66434
A;Molecule type: protein
A;Residues: 206-214, 'X', 216-230 <ATM2>
R;Akerstroem, B.; Bratt, T.; Enghild, J.J.
FEBS Lett. 362, 50-54, 1995
A;Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect cells
A;Reference number: S68728; MUID:95212582; PMID:7535251
A;Accession: S68728
A;Molecule type: protein
A;Residues: 89-100 <AKE>
R;Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A;Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a novel
A;Reference number: S02431; MUID:88167187; PMID:2450785
A;Accession: S02431
A;Molecule type: protein
A;Residues: 206-214, 'X', 216-217 <JES>
R;Lopez, C.; Grubb, A.; Mendez, E.
FEBS Lett. 144, 349-353, 1982
A;Title: Human protein HC displays variability in its carboxyl-terminal amino acid sequence
A;Reference number: A91304
A;Contents: annotation; variant of alpha-1-microglobulin
A;Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys and
R;Hoppe-Seyler, K.; Schonberger, O.L.; Rossmannith, I.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-
A;Note: affinity chromatography.
A;Reference number: A91698; MUID:82074265; PMID:6171497
A;Contents: annotation; carbohydrate binding sites
R;Morii, M.; Travis, J.
Biol. Chem. Hoppe-Seyler 366, 19-21, 1985
A;Title: The reactive site of human inter-alpha-trypsin inhibitor is in the amino-terminal
A;Reference number: A90882; MUID:8525940; PMID:3690890
A;Contents: annotation; inhibitory site
A;Note: in vitro, the first twelve residues of the amino end of the inhibitor appear to
C;Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolytically pro-
C;Comment: Alpha-1-microglobulin occurs in many physiological fluids including plasma, u-
. It contains at least one brown-yellow chromophore.

Query Match	Best Local Similarity	Score	DB	Length
Matches	7;	Conservative	0;	Mismatches
Indels	0;	Gaps	0;	

Qy	107	YGCCQGN	113
Db	317	YGCCQGN	323

RESULT 25
T05891
myb-related protein homolog F6H1.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Aug-2004
C;Accession: T05891
R;Bavan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mewer
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15456
A;Accession: T05891
A;Molecule type: DNA

A;Residues: 1-374 <BEV>
 A;Cross-references: UNIPROT:O49538; EMBL:AL021684; GSPDB:GN00063; ATSP:F6H11.100
 A;Experimental source: cultivar Columbia; BAC clone F6H11
 C;Genetics:
 A;Gene: ATSP:F6H11.100
 A;Map position: 5
 A;Introns: 46/1; 89/2
 C;Superfamily: myb DNA-binding repeat homology
 F;9-62/Domain: myb DNA-binding repeat homology <MYB>

A;Map position: 5

A;Introns: 46/1; 89/2

C;Superfamily: myb DNA-binding repeat homology

F;9-62/Domain: myb DNA-binding repeat homology <MYB>

Query Match 5.3%; Score 7; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 NFQTEAI 122

|||||

Db 294 NFQTEAI 300

RESULT 26

TS1673

myb-related transcription factor MYB68 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C;Accession: TS1673

R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J

; Paz-Ares, J.; Weisshaar, B.

Plant J. 16, 263-276, 1998

A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from A

A;Reference number: Z14349; MUID:9839469; PMID:9839469

A;Accession: TS1673

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-376 <KRA>

A;Cross-references: UNIPROT:Q9SBF7; EMBL:AF062901; PIDN:AAC83623.1

A;Experimental source: cultivar Columbia

C;Genetics:

A;Map position: V

C;Superfamily: Arabidopsis myb-related protein M4; myb DNA-binding repeat homology

C;Keywords: transcription factor

Query Match 5.3%; Score 7; DB 2; Length 376;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 NFQTEAI 122

|||||

Db 294 NFQTEAI 300

RESULT 27

S53325

tissue factor pathway inhibitor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-2003

C;Accession: S53325

R;Girard, T.J.; Gallani, D.; Broze Jr., G.J.

Biochem. J. 303, 923-928, 1994

A;Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor reveals

A;Reference number: S53325; MUID:95071310; PMID:7980463

A;Accession: S53325

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-396 <GIR>

C;Superfamily: tissue factor pathway inhibitor

F;53-103/Domain: animal Kunitz-type proteinase inhibitor

F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

F;309-359/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Score

Pred. No.

Length

396;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFYGGC 110

|||||

Db 80 EFYGGC 86

RESULT 28

F83634

hypothetical protein PA0081 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: F83634

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: F83634

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-497 <STO>

A;Cross-references: UNIPROT:Q9I751; GB:AE004447; GB:AE004091; NID:g9945902; PIDN:AAG0347

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA0081

Query Match 5.3%; Score 7; DB 2; Length 497;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GLSGLLP 8

|||||

Db 443 GLSGLLP 449

RESULT 29

F72268

ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 16-Aug-2004

C;Accession: F72268

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72268

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-564 <ARN>

A;Cross-references: UNIPROT:Q9X144; GB:AE001786; GB:AE000512; NID:g4981873; PIDN:AAD3639

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1319

C;Superfamily: ATP-binding cassette homology

Query Match 5.3%; Score 7; DB 2; Length 564;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GLLPILV 11

|||||

Db 250 GLLPILV 256

RESULT 30

DP0557

hypothetical protein MYPV_3640 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C;Species: Mycoplasma pulmonis

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: D90557
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: P90557
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-602 <KUR>
A;Cross-references: UNIPROT:Q90QJ7; GB:AL445566; PID:gl4089778; PIDN:CAC13537.1; GSPDB:G000000000
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU 3640
A;Genetic code: SGC3

Query Match 5.3%; Score 7; DB 2; Length 602;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILL 16
|||||
Db 184 LVPFILL 190

RESULT 31
S74277
Probable membrane protein YCL073c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YCL070c; hypothetical protein YCL071c
C;Species: Saccharomyces cerevisiae
C;Date: 19-Mar-1997 #sequence revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74277; S6990; S19402; S19403; S19405
R;Voet, M.; Volckaert, G.
submitted to the Protein Sequence Database, September 1996
A;Reference number: S74277
A;Accession: S74277
A;Molecule type: DNA
A;Residues: 1-615 <VOB>
A;Cross-references: UNIPROT:P25596; EMBL:X59720; NID:G1907116; PIDN:CAA42397.1; PID:gl907116
A;Note: this is a revision to the sequence from reference S19400
R;Gromadka, R.; Gora, M.; Zielenkiewicz, U.; Slonimski, P.P.; Rytka, J.
Yeast 12, 583-591, 1996
A;Title: Subtelomeric duplications in Saccharomyces cerevisiae chromosomes III and XI: b
A;Reference number: S6990; MUID:96367599; PMID:8771713
A;Accession: S6990
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-465, 'I', 467-526, 'N', 528-533, 'S', 535-615 <GRO>
A;Cross-references: EMBL:X59720
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
R;van der Aart, Q.J.M.; Steensma, H.Y.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19400
A;Accession: S19402
A;Molecule type: DNA
A;Residues: 1-214, 'G', 216-270, 'L', 272-326, 'PNLPNLLF', 335-349, 'VLL', 353, 'SI', 354, 'SP', 357-358, 'G', 360-361, 'G', 363-364, 'G', 366-367, 'G', 369-370, 'G', 372-373, 'G', 375-376, 'G', 378-379, 'G', 381-382, 'G', 384-385, 'G', 387-388, 'G', 390-391, 'G', 393-394, 'G', 396-397, 'G', 399-400, 'G', 402-403, 'G', 405-406, 'G', 408-409, 'G', 411-412, 'G', 414-415, 'G', 417-418, 'G', 420-421, 'G', 423-424, 'G', 426-427, 'G', 429-430, 'G', 432-433, 'G', 435-436, 'G', 438-439, 'G', 441-442, 'G', 444-445, 'G', 447-448, 'G', 450-451, 'G', 453-454, 'G', 456-457, 'G', 459-460, 'G', 462-463, 'G', 465-466, 'G', 468-469, 'G', 471-472, 'G', 474-475, 'G', 477-478, 'G', 480-481, 'G', 483-484, 'G', 486-487, 'G', 489-490, 'G', 492-493, 'G', 495-496, 'G', 498-499, 'G', 501-502, 'G', 504-505, 'G', 507-508, 'G', 510-511, 'G', 513-514, 'G', 516-517, 'G', 519-520, 'G', 522-523, 'G', 525-526, 'G', 528-529, 'G', 531-532, 'G', 534-535, 'G', 537-538, 'G', 540-541, 'G', 543-544, 'G', 546-547, 'G', 549-550, 'G', 552-553, 'G', 555-556, 'G', 558-559, 'G', 561-562, 'G', 564-565, 'G', 567-568, 'G', 570-571, 'G', 573-574, 'G', 576-577, 'G', 579-580, 'G', 582-583, 'G', 585-586, 'G', 588-589, 'G', 591-592, 'G', 594-595, 'G', 597-598, 'G', 600-601, 'G', 603-604, 'G', 606-607, 'G', 609-610, 'G', 612-613, 'G', 615-616, 'G', 618-619, 'G', 621-622, 'G', 624-625, 'G', 627-628, 'G', 630-631, 'G', 633-634, 'G', 636-637, 'G', 639-640, 'G', 642-643, 'G', 645-646, 'G', 648-649, 'G', 651-652, 'G', 654-655, 'G', 657-658, 'G', 660-661, 'G', 663-664, 'G', 666-667, 'G', 669-670, 'G', 672-673, 'G', 675-676, 'G', 678-679, 'G', 681-682, 'G', 684-685, 'G', 687-688, 'G', 690-691, 'G', 693-694, 'G', 696-697, 'G', 699-700, 'G', 702-703, 'G', 705-706, 'G', 708-709, 'G', 711-712, 'G', 714-715, 'G', 717-718, 'G', 720-721, 'G', 723-724, 'G', 726-727, 'G', 729-730, 'G', 732-733, 'G', 735-736, 'G', 738-739, 'G', 741-742, 'G', 744-745, 'G', 747-748, 'G', 750-751, 'G', 753-754, 'G', 756-757, 'G', 759-760, 'G', 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A;Cross-references: UNIPROT:Q9XIF2; GB:AEO05173; NID:g5080810; PIDN:AAD39319.1; GSPDB:G.C;
C;Genetics:
A;Gene: F23H11.8
A;Map position: 1
C;Superfamily: yeast probable SKI2 protein YJL050w

Query Match 5.3%; Score 7; DB 2; Length 988;
Best Local Similarity 100.0%; Pred.No.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SGLLPIL 10
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|
Db 391 SGLLPIL 397

RESULT 34
T37868
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37868
R;Kellon, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21751
A;Accession: T37868
A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: DNA
A;Residues: 1-1030 <SKE>
A;Cross-references: UNIPROT:O13799; EMBL:Z98597; PIDN:CAB11211.1; GSPDB:GN00066; SPDB:S.H.
A;Experimental source: strain 972h-; cosmid c17H9
C;Genetics:
A;Gene: SPDB:SPAC17H9.02
A;Map position: 1
C;Superfamily: yeast probable SKI2 protein YJL050w

Query Match 5.3%; Score 7; DB 2; Length 1030;
Best Local Similarity 100.0%; Pred.No.39;
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Db 441 SGLLPIL 447

RESULT 35
S56822
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N;Alternate names: protein Jll58
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S56822
R;Pohl, T.M.; Aljinovic, G.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56793
A;Accession: S56822
A;Molecule type: DNA
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A;Cross-references: SGD:S0003586; MIPS:YJL050w
A;Map position: 10L
C;Superfamily: yeast probable SKI2 protein YJL050w
C;Keywords: ATP; nucleotide binding; P-loop
F;171-178/Region: nucleotide-binding motif A (P-loop)
F;258-263/Region: nucleotide-binding motif B
F;262-265/Region: DEXH motif

Query Match 5.3%; Score 7; DB 1; Length 1073;
Best Local Similarity 100.0%; Pred.No.40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SGLLPIL 10

A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs1771

Query Match 4.6%; Score 6; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 GHAEGI 28
Db 20 GHAEGI 25

RESULT 39

S30332
proteinase inhibitor (Kunitz-type) - sea anemone (Stichodactyla helianthus)
C:Species: Stichodactyla helianthus, Stichodactyla helianthus (Caribbean sea anemone)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
A:Accession: S30332
R:Antuch, W.; Berndt, K.D.; Chavez, M.A.; Delfin, J.; Wuethrich, K.
Eur. J. Biochem. 212, 675-684, 1993
A:Title: The NMR solution structure of a Kunitz-type proteinase inhibitor from the sea anemone Stichodactyla helianthus
A:Reference number: S30332; MUID:93215644; PMID:8462542
A:Accession: S30332
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-55 <ANT>
A:Cross-references: UNIPROT:P31713
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology <BPI>
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 31 FIYGGC 36

RESULT 40

JN0380
trypsin inhibitor IV - sea anemone (Radianthus macrodactylus)
C:Species: Radianthus macrodactylus
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004
A:Accession: JN0380
R:Zykova, T.A.; Vinokurov, L.M.; Markova, L.F.; Kozlovskaya, E.P.; Elyakov, G.B.
Bioorg. Khim. 11, 293-301, 1985
A:Title: Amino-acid sequence of trypsin inhibitor IV from Radiantis macrodactylus.
A:Reference number: JN0380
A:Accession: JN0380
A:Molecule type: protein
A:Residues: 1-56 <ZYK>
A:Cross-references: UNIPROT:P16344
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology <BPI>
F:4-54/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:4-54,13-37,29-50/Disulfide bonds: #status predicted

Query Match 4.6%; Score 6; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 32 FIYGGC 37

RESULT 41

TIKIV2
venom basic proteinase inhibitor II - ringhals
C:Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004

C:Accession: A01216
R:Hokama, Y.; Iwanaga, S.; Tateuchi, T.; Suzuki, T.
J. Biochem. 79, 559-578, 1976
A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitors of acid sequences of two of them.
A:Reference number: A91942; MUID:76237547; PMID:950337
A:Accession: A01216
A:Molecule type: protein
A:Residues: 1-57 <HOK>
A:Cross-references: UNIPROT:P00985
C:Comment: The activity of this inhibitor is similar to that of bovine basic protease inhibitor
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology <BPI>
C:Keywords: serine proteinase inhibitor; venom
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 4.6%; Score 6; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 33 FIYGGC 38

RESULT 42

S13846
venom animal Kunitz-type trypsin inhibitor - Indian cobra
C:Species: Naja naja naja (Indian cobra)
C:Date: 18-Feb-1994 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
A:Accession: S13846
R:Shafqat, J.; Beg, O.U.; Yin, S.J.; Zaidi, Z.H.; Joernvall, H.
Eur. J. Biochem. 194, 337-341, 1990
A:Title: Primary structure and functional properties of cobra (Naja naja naja) venom Kunitz-type proteinase inhibitor
A:Reference number: S13846; MUID:91099304; PMID:1702708
A:Accession: S13846
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-57 <SHA>
A:Cross-references: UNIPROT:P20229
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology <BPI>
C:Keywords: serine proteinase inhibitor; venom
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 33 FIYGGC 38

RESULT 43

TIHABK
isoinhibitor K (BPI type) - Roman snail
C:Species: Helix pomatia (Roman snail)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
A:Accession: A91232; A01225
R:Tschesche, H.; Dietl, T.
Eur. J. Biochem. 58, 439-451, 1975
A:Title: The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A sequence of isoinhibitor K from snails (Helix pomatia).
A:Reference number: A91232; MUID:76043680; PMID:1183446
A:Accession: A91232
A:Molecule type: protein
A:Residues: 1-58 <TSC>
A:Cross-references: UNIPROT:P00994
R:Dietl, T.; Tschesche, H.
Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976
A:Title: Die Disulfidbrücken des Trypsin-Kallikrein-Inhibitors K aus Weinbergsschnecken
A:Reference number: A91666; MUID:76141310; PMID:3462
A:Contents: annotation; disulfide bonds
C:Comment: This is one of several isoinhibitors of broad specificity that are secreted in

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: pyroglutamic acid; serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 4.6%; Score 6; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 35 FIYGGC 40
|||||

RESULT 44

venom basic proteinase inhibitor I - western sand viper
N;Alternate names: venom trypsin inhibitor I
C;Species: Vipera ammodytes ammodytes (western sand viper)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C;Accession: A01222
R;Rittonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 748, 429-435, 1983
A;Title: The primary structure of Vipera ammodytes venom trypsin inhibitor I.
A;Reference number: A01222; MUID:84053385; PMID:6639951
A;Accession: A01222
A;Molecule type: protein
A;Residues: 1-61 <RIT>
A;Cross-references: UNIPROT:P00991
C;Comment: This protein inhibits trypsin and kallikrein.
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: pyroglutamic acid; serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;7-57,16-40,32-53/Disulfide bonds: #status predicted
F;17/Inhibitory site: Lys (trypsin) #status predicted

Query Match 4.6%; Score 6; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 35 FIYGGC 40
|||||

RESULT 45

S07451
proteinase inhibitor 5.II - snake-locks sea anemone
C;Species: Anemonia sulcata (snake-locks sea anemone)
C;Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: S07451; B27222
R;Wunderer, G.; Machleidt, W.; Fritz, H.
Meth. Enzymol. 80, 816-820, 1981
A;Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia s
A;Reference number: S07451
A;Accession: S07451
A;Molecule type: protein
A;Residues: 1-59 <WUN>
A;Cross-references: UNIPROT:P10280
A;Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R;Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A;Title: Isolierung und Strukturauflaerung eines haemolytisch aktiven peptids aus der s
A;Reference number: A94700
A;Accession: B27222
A;Molecule type: protein
A;Residues: 1-38, 'R', 40, 'B', 42, 'BB', 45-48, 'ZZ', 51, 'Z', 53-62 <KRE>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 33 FIYGGC 38
|||||

RESULT 46

A44180
taicetoxin serine proteinase inhibitor component - Australian taipan
C;Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44180
R;Possani, L.D.; Martin, B.M.; Yatani, A.; Mochca-Morales, J.; Zamudio, F.Z.; Gurrola, G
Toxicon 30, 1343-1364, 1992
A;Title: Isolation and physiological characterization of taicetoxin, a complex toxin wit
A;Reference number: A44180; MUID:93134601; PMID:1485334
A;Accession: A44180
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-62 <POS>
A;Cross-references: UNIPROT:Q7LZE4
A;Experimental source: subsp. scutellatus, venom
A;Note: sequence extracted from NCBI backbone (NCBIP:122482)
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 35 FIYGGC 40
|||||

RESULT 47

S19327
venom basic proteinase inhibitor - leaf-nosed viper
N;Alternate names: trypsin inhibitor (Kunitz-type)
C;Species: Eristocophis macmahoni (leaf-nosed viper)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S19327
R;Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A;Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf-
A;Reference number: S19327; MUID:92077130; PMID:1743283
A;Accession: S19327
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-82 <SID>
A;Cross-references: UNIPROT:P24541
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor; venom
F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 30 FIYGGC 35
|||||

RESULT 48

T34799
probable transcription regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T34799
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z21557
A;Accession: T34799
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-63 <MUR>
A;Cross-references: UNIPROT:O69902; EMBL:AL023797; PIDN:CAA19406.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE:SC2E1.31

Query Match 4.6%; Score 6; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 53; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 1 MGLSGL 6
|||
Db 25 MGLSGL 30

RESULT 49
TIVIVC
venom basic proteinase inhibitor III - sand viper
N;Alternate names: venom chymotrypsin inhibitor
C;Species: Vipera ammodytes (sand viper)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A01223
R;Ritonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 746, 138-145, 1983
A;Title: The primary structure Of Vipera ammodytes venom chymotrypsin inhibitor.
A;Reference number: A01223
A;Accession: A01223
A;Molecule type: protein
A;Residues: 1-65 <RIT>
A;Cross-references: UNIPROT:P00992
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;7-57,16-40,32-53/Disulfide bonds: #status predicted
F;17/Inhibitory site: Leu (chymotrypsin) #status predicted

Query Match 4.6%; Score 6; DB 1; Length 65;
Best Local Similarity 100.0%; Pred. No. 54; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 105 FIYGGC 110
|||
Db 35 FIYGGC 40

RESULT 50
D42506
F-ORF-E protein - vaccinia virus (strain Copenhagen)
C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: D42506
R;Johnson, G.P.
submitted to GenBank, June 1990
A;Reference number: A33172
A;Accession: D42506
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <JOH>
A;Cross-references: UNIPROT:P20563

Query Match 4.6%; Score 6; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 58; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 3 LSGLLP 8

Db |||||
65 LSGLLP 70

Search completed: September 21, 2005, 16:50:44
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:40:19 ; Search time 133 Seconds
(without alignments)
504.379 Million cell updates/sec

Title: US-10-807-204-1

Perfect score: 131

Sequence: 1 MGSLGLPILVPFILLGDIQ.....GNNNFQTEAICLVTKCKYH 131

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	48.9	131	1 WFD6 HUMAN	Q9bqy6 homo sapien
2	14	10.7	134	1 EPI MOUSE	Q9da01 mus musculus
3	14	10.7	137	2 Q9BDL0	Q9bd10 oryctolagus
4	12	9.2	133	1 EPI HUMAN	Q95925 homo sapien
5	12	9.2	133	2 Q8HZ45	Q8hz45 papio papio
6	12	9.2	143	2 Q86TP9	Q86tp9 homo sapien
7	11	8.4	133	1 EPI MACMU	Q9bd11 macaca mula
8	10	7.6	62	1 IC51_BOMMO	P10831 bombyx mori
9	10	7.6	63	1 IC53_BOMMO	P07481 bombyx mori
10	10	7.6	69	1 CRPT_BOOMI	P81162 boophilus m
11	10	7.6	83	2 Q6ITB9	Q6itb9 pseudechis
12	10	7.6	85	2 Q8WP15	Q8wp15 bombyx mori
13	10	7.6	86	2 Q8GQT1	Q86gt1 bombyx mori
14	9	6.9	77	2 Q8HZ44	Q8hz44 papio hamad
15	9	6.9	107	2 Q8IQ07	Q8iq07 drosophila
16	9	6.9	151	2 Q6T269	Q6t269 bitis gabon
17	9	6.9	182	2 Q6IE19	Q6ie19 rattus norv
18	8	6.1	55	1 CST1_BOMMO	P81902 bombyx mori
19	8	6.1	67	1 IBPC_BOVIN	P00976 bos taurus
20	8	6.1	76	2 Q87L9	Q87l19 bombyx mori
21	8	6.1	126	1 CL1X_HUMAN	Q15332 homo sapien
22	8	6.1	186	2 Q68V31	Q68v31 bos taurus
23	8	6.1	310	2 Q9WUG1	Q9wu1 cavia porce
24	8	6.1	324	2 Q9FV9	Q9fv9 arabidopsis
25	8	6.1	449	2 Q92WQ0	Q92wq0 rhizobium m
26	8	6.1	746	1 CLC5_HUMAN	P51795 homo sapien
27	8	6.1	746	2 Q9GK7	Q9gk7 sus scrofa
28	8	6.1	746	2 Q9TTU3	Q9ttu3 oryctolagus
29	8	6.1	746	2 Q99P66	Q99p66 cavia porce
30	8	6.1	893	2 Q7QH49	Q7qh49 anopheles g
31	8	6.1	900	2 Q8K206	Q8k206 mus musculus

ALIGNMENTS

RESULT 1

ID	WFD6 HUMAN	STANDARD;	PRT;	131 AA.
AC	Q9BQY6; Q8NFV6;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	05-JUN-2004 (Rel. 44, Last annotation update)			
DE	WAP four-disulfide core domain protein 6 precursor (Putative protease inhibitor WAP6).			
DE	Name=WFD6; Synonyms=C20orf171, WAP6;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=22306454; PubMed=12206714; DOI=10.1042/BJ20020865;			
RA	Clauss A., Lilja H., Lundwall A.			
RT	"A locus on human chromosome 20 contains several genes expressing protease inhibitor domains with homology to whey acidic protein."			
RL	Biochem. J. 368:233-242(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA	Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.,			
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,			
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,			
RA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA	Swann R.M., Sycamore A.C., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA	Tracey A., Tomams A.C., Vaudin M., Wall M., Wallis J.M.,			
RA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,			
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			
RA	Rogers J.;			

32	8	6.1	1233	2	Q69Z28
33	8	6.1	1514	2	Q9LK64
34	8	6.1	1515	2	Q24510
35	7	5.3	51	2	P78492
36	7	5.3	53	1	PTIB MANSE
37	7	5.3	57	1	IVB2_NAJNI
38	7	5.3	62	1	ISC2_BOMMO
39	7	5.3	76	2	Q96858
40	7	5.3	77	1	CVP2_FIMHY
41	7	5.3	80	2	Q8T357
42	7	5.3	80	2	Q9VCM3
43	7	5.3	83	2	Q9W96
44	7	5.3	83	2	Q9W97
45	7	5.3	83	2	Q9WAO
46	7	5.3	83	2	Q9WAI
47	7	5.3	83	2	Q6ITB0
48	7	5.3	83	2	Q6ITB1
49	7	5.3	83	2	Q6ITB2
50	7	5.3	83	2	Q6ITB3

Q69Z28	mus musculus
Q9LK64	arabidopsis
Q24510	arabidopsis
P78492	homo sapien
P26227	manduca sex
P00986	naja nivea
P10832	bombyx mori
Q96888	galleria me
Q8t0w4	pimpla hypo
Q8t387	araneus ven
Q9vcn3	drosophila
Q90w96	pseudonaja
Q90w97	pseudonaja
Q90wao	pseudonaja
Q90wai	pseudonaja
Q6itb0	tropidechis
Q6itb1	pseudechis
Q6itb2	notechis sc
Q6itb3	notechis sc


```
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC isoid=Q9BQV6-1; Sequence=Displayed;
CC Name=2;
CC isoid=Q9BQV6-2; Sequence=VSP_007550, VSP_007551;
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels
CC are found in epididymis, testis and trachea.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC -----
DR EMBL; AF411861; AA003684.1; -
DR EMBL; AL031663; CAC36264.1; -
DR HSSP; P02760; 1BIK.
DR Genew; HGNC:16164; WFD06.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; FALSE_NEG.
DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 25
FT CHAIN 26 131
FT DOMAIN 31 69
FT DOMAIN 70 128
FT DISULFID 33 61
FT DISULFID 48 60
FT DISULFID 54 69
FT VARSPPLIC 75 86
FT FTId=VSP_007550.
FT Missing (In isoform 2).
FT FTId=VSP_007551.
SQ SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;
Query Match 48.9%; Score 64; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.2e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGLSLPILVPFLLGDIQPGHAGILGKPCPKIKVCEVSEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFLLGDIQPGHAGILGKPCPKIKVCEVSEIDQCTKPRDCPENMKC 60
Qy 61 CPFS 64
Db 61 CPFS 64
RESULT 2
ID -EPPI MOUSE STANDARD; PRT; 134 AA.
AC Q9DA01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
```

```
DE inhibitor-like with Kunitz and WAP domains 1).
GN NamesSpinlwl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.W.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yahagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusica K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in epididymis and testis.
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CC CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC CC -----
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CC CC or send an email to license@isb-sib.ch)
CC CC -----
DR EMBL; AF346413; AAK31335.1; -
DR EMBL; AK006296; BAB24514.1; -
DR EMBL; BC048637; AAH48637.1; -
DR HSSP; P31713; 1SHP.
DR MGD; MGI:1922776; Spinlwl.
DR GO; GO:0001669; C:cytosome; IDA.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD00222; Prot_Inh_Kunz-m; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 134 WAP.
FT DOMAIN 29 73 BPTI/Kunitz inhibitor.
FT DOMAIN 77 127 WAP.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
FT SEQUENCE 134 AA; 15470 MW; DFEB63DD4C427F CRC64;

Query Match 10.7%; Score 14; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FYIYGCQGNNNFQ 118
Db 105 FYIYGCQGNNNFQ 118
|||||

RESULT 3
ID Q9BDL0 PRELIMINARY; PRT; 137 AA.
AC Q9BDL0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RA Levesha M.H., Levesha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McMay K., McMurray A.A.,
RT "Characterization of mouse Eppin and a gene cluster of similar
RL Gene 312:125-134(2003).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
```

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DR EMBL; AF346415; AAK31337.1; -
DR HSSP; Q16019; IAAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD00222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;

Query Match 10.7%; Score 14; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GNNNNFQTEAICLV 125
Db 112 GNNNNFQTEAICLV 125
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RESULT 4
ID EPPI_HUMAN STANDARD; PRT; 133 AA.
AC Q95925; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
DE domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINW1; Synonyms=WAP7, WFDC7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epididymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French F.S., O'Rand M.G.;
RA "Cloning and sequencing of human Eppin: a novel family of protease
RA inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stavrides G.S., Huckle E.J., Deloukas P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguely C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clegg S.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.R., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.L., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levesha M.H., Levesha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McMay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
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RESULT 6
Q86TP9 PRELIMINARY; PRT; 143 AA.
AC Q86TP9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SPINLMI protein (Fragment).
GN Name=SPINLMI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fanev J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH44829.1; -.
DR HSSP; P00974; 1UUA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR NON_TER
SQ SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;

Query Match 9.2%; Score 12; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNNFQ 118
DB 117 YGCGCGNNNNFQ 128
|||||

RESULT 7
EPPI_MACMU
ID EPPI_MACMU STANDARD; PRT; 133 AA.

AC Q9BDL1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=SPINLMI;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (potential).
CC -1- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC
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CC
CC EMBL; AF346414; AAK31336.1; -.
DR HSSP; P00974; 1BPI.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 133 AA; 15279 MW; 433AE946E39A35E9 CRC64;

Query Match 8.4%; Score 11; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GGCQGNNNNFQ 118
DB 108 GGCQGNNNNFQ 118
|||||

RESULT 8
ISCL_BOMMO
ID ISCL_BOMMO STANDARD; PRT; 62 AA.
AC P10831;
DT 01-JUL-1989 (Rel. 11, Created)

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DT	01-JUL-1989 (Rel. 11, Last sequence update)
DE	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Chymotrypsin inhibitor SCI-I.
OS	Bombyx mori (Silk moth).
OC	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC	Bombycidae; Bombyx.
NCBI_OX	NCBI_TaxID=7091;
RP	[1]
RP	SEQUENCE.
RC	TISSUE=Larval hemolymph;
RC	MEDLINE=89228538; PubMed=3072972;
RA	Sasaki T.;
RT	"Amino-acid sequences of two basic chymotrypsin inhibitors from
RT	silkworm larval hemolymph.";
RL	Biol. Chem. Hoppe-Seyler 369:1235-1241(1988).
CC	-1- FUNCTION: Inhibits chymotrypsin and thus avoids the accidental
CC	chymotrypsin-mediated activation of prophenoloxidase. This enzyme
CC	is required by the insect immune system to produce melanin which
CC	is used to engulf foreign objects.
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC	PIR: S01802; S01802.
DR	HSSP; P10646; 1ADZ.
DR	InterPro: IPR002223; Prot Inh_Kunz-m.
DR	Pfam: PF00014; Kunitz BPTI; 1.
DR	PRINTS; PR00759; BASICPTASE.
DR	ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR	SMART; SM00131; KU; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW	Direct protein sequencing; Serine protease inhibitor.
FT	SITE 20 21 Reactive bond (By similarity).
FT	DISULFID 9 60 By similarity.
FT	DISULFID 19 43 By similarity.
FT	DISULFID 35 56 By similarity.
SQ	SEQUENCE 62 AA; 7065 MW; 7E7C11E9B95AC6DA CRC64;
Query Match 7.6%; Score 10; DB 1; Length 62;	
Best Local Similarity 100.0%; Pred. No. 0.03;	
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps	
Oy	104 EFTYGGCQGN 113
Db	37 EFTYGGCQGN 46
RESULT 9	
ID	ICS3_BOMMO ICS3_BOMMO STANDARD; PRT; 63 AA.
AC	P07481;
DT	01-APR-1988 (Rel. 07, Created)
DT	01-APR-1988 (Rel. 07, Last sequence update)
DE	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Chymotrypsin inhibitor SCI-III.
OS	Bombyx mori (Silk moth).
OC	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC	Bombycidae; Bombyx.
NCBI_OX	NCBI_TaxID=7091;
RP	[1]
RP	SEQUENCE.
RC	TISSUE=Larval hemolymph;
RA	Sasaki T.;
RT	"Amino acid sequence of a novel Kunitz-type chymotrypsin inhibitor
RT	from hemolymph of silkworm larvae, Bombyx mori.";
RL	FEBS Lett. 168:227-230(1984).
CC	-1- FUNCTION: Inhibits chymotrypsin and thus avoids the accidental
CC	chymotrypsin-mediated activation of prophenoloxidase. This enzyme
CC	is required by the insect immune system to produce melanin which
CC	is used to engulf foreign objects.
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC	PIR; A25740; TIMTC3.
DR	HSSP; P10646; 1ADZ.


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RESULT 13
ID Q86QTI PRELIMINARY; PRT; 86 AA.
AC Q86QTI;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Chymotrypsin inhibitor C113.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
[1]
RP SEQUENCE FROM N.A.
RL He N., Fujii H., Banno Y.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DE EMBL; AY167664; AA017293.1; -.
DR HSSP; P10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 86 AA; 9611 MW; E4F22676B8F30B8 CRC64;
SQ

Query Match 7.6%; Score 10; DB 2; Length 86;
Best Local Similarity 100.0%; Pred.No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 104 EFYGGCGGN 113
DB 61 EFYGGCGGN 70

RESULT 14
Q8HZ44 PRELIMINARY; PRT; 77 AA.
AC Q8HZ44;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Epididymal protease inhibitor 2.
GN Name=Epplin;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
[1]
RP SEQUENCE FROM N.A.
RL TISSUE=Testis;
RA Sivaahamugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DE EMBL; AY141975; AA08509.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
KW Protease.
SQ SEQUENCE 77 AA; 8787 MW; B6E5E868C57CEBD0 CRC64;

Query Match 6.9%; Score 9; DB 2; Length 77;
Best Local Similarity 100.0%; Pred.No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

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Qy 63 FSCGKKCLD 71
Db 63 FSCGKKCLD 71

RESULT 15
ID Q81Q07 PRELIMINARY; PRT; 107 AA.
AC Q81Q07;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG31779-PA.
GN ORFNames=CG31779;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Fiankocch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bock J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleitschmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hradek N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RL melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]

SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., M.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AE003579; AAN10377.2; -.
DR HSP; P12111; IKNT.
DR FlyBase; FBgn0051779; CG31779.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
SQ SEQUENCE 107 AA; 12029 MW; 98F3423A59C9E744 CRC64;

Query Match 6.9%; Score 9; DB 2; Length 107;
Best Local Similarity 100.0%; Pred No. 0.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FYGGCGQN 113
Db 35 FYGGCGQN 43

RESULT 16
Q6T269 PRELIMINARY; PRT; 151 AA.
ID Q6T269
AC Q6T269;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Two-Kunitz protease inhibitor (Fragment).
OS Bitis gabonica (Gaboon adder) (Gaboon viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OX NCBI_TaxID=8694;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15276202; DOI=10.1016/j.gene.2004.03.024;
RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
RA Ribeiro J.M.;
RA "Bitis gabonica (Gaboon viper) snake venom gland: toward a catalog for
RT the full-length transcripts (cDNA) and proteins."
RL Gene 337:55-69(2004).

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RN  [2]
RP  SEQUENCE FROM N.A.
RA  Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
RL  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR  EMBL; AY442289; AAR19275.1; -.
DR  HSSP; Q16019; 1AAP.
DR  GO; GO:0008233; F:peptidase activity; IEA.
DR  GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR  InterPro; IPR002223; F:serine-type endopeptidase inhibitor (CSTI).
DR  Pfam; PF00014; Kunitz_BPTI_2.
DR  PRINTS; PR00759; BASICPTASE.
DR  ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR  SMART; SM00131; KU; 2.
DR  PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR  PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW  Protease.
FT  NON_TER 1.
SQ  SEQUENCE 151 AA; 16976 MW; 13E34ACE8DE591ED CRC64;

Query Match 6.9%; Score 9; DB 2; Length 151;
Best Local Similarity 100.0%; Pred.No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FIYGGCQGN 113
DB 100 FIYGGCQGN 108
|||||

RESULT 17
Q6IE19 PRELIMINARY; PRT; 182 AA.
AC Q6IE19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WAP four-disulfide core 6-like 1.
GN Name=wfd611;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RX PubMed=15060002; DOI=10.1101/gr.1946304;
RA Puente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000374; CAE51900.1; -.
DR HSSP; P00974; 1K6U.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EB12D7BFF756707E CRC64;

Query Match 6.9%; Score 9; DB 2; Length 182;
Best Local Similarity 100.0%; Pred.No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FIYGGCQGN 113
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DB 105 FIYGGCQGN 113

RESULT 18
CSTI_BOMMO STANDARD; PRT; 55 AA.
AC P81902;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC STRAIN=Asahi;
RX MEDLINE=99115431; PubMed=9914483;
RA Kurioka A., Yamazaki M., Hirano H.;
RT "Primary structure and possible functions of a trypsin inhibitor of
Bombyx mori.";
RL Eur. J. Biochem. 259:120-126(1999).
CC -1- FUNCTION: This cocoon shell-associated protein inhibits trypsin
Activity by forming a low-dissociation complex with trypsin. May
play an important part in regulating proteolytic activity in the
silk gland or protecting silk proteins from degradation during
histolysis.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
gland.
CC -1- DEVELOPMENTAL STAGE: Expression differentially regulated in the
middle silk glands during the final stage of larval growth with
highest expression before the onset of spinning.
CC -1- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray; RANGE=1-55;
NOTE=Ref.1.
CC -1- MISCELLANEOUS: Has an isoelectric point of 4.3.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP; P31713; 1SHP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Developmental protein; Direct protein sequencing;
Serine protease inhibitor.
KX Serine protease inhibitor.
FT SITE 14 15 Reactive bond for trypsin (By
similarity).
FT DISULFID 4 54 By similarity.
FT DISULFID 13 37 By similarity.
FT DISULFID 29 50 By similarity.
SQ SEQUENCE 55 AA; 6027 MW; C2739BB8F2BB6E59 CRC64;

Query Match 6.1%; Score 8; DB 1; Length 55;
Best Local Similarity 100.0%; Pred.No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EPIYGGCQ 111
DB 31 EPIYGGCQ 38
|||||

RESULT 19
IBPC_BOVIN STANDARD; PRT; 67 AA.
AC P00976;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Colostrum trypsin inhibitor (Colostrum BPI).

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OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE.
RA Cechova D., Jonakova V., Sorm F.;
RP "Primary structure of trypsin inhibitor from cow colostrum (component B2).";
RT Disulfide bonds of trypsin inhibitor from cow colostrum.";
RL Collect. Czech. Chem. Commun. 36:3342-3357(1971).
RN [2]
RN DISULFIDE BONDS.
RA Cechova D., Ber E.;
RP "Disulfide bonds of trypsin inhibitor from cow colostrum.";
RT Collect. Czech. Chem. Commun. 39:680-688(1974).
RN [3]
RN CHARACTERIZATION.
RA Cechova D., Muszyńska G.;
RP "Role of lysine 18 in active center of cow colostrum trypsin inhibitor.";
RT FEBS Lett. 8:84-86(1970).
RN [4]
RN -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR: A01207; TIBOC.
DR HSP: P02760; IBIK.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Glycoprotein; Serine protease inhibitor.
FT SITE 18 19
FT DISULFID 8 58
FT DISULFID 17 41
FT DISULFID 33 54
FT CARBOHYD 27 27 N-linked (GlcNAc...).
SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;

Query Match 6.1%; Score 8; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNN 114
Db 38 YGGCGGNN 45
|||||

RESULT 20
Q8T7L9 PRELIMINARY; PRT; 76 AA.
AC Q8T7L9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Kazal-type serine proteinase inhibitor 1.
GN Name=SP11;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21873253; PubMed=11881808;
RA Nimala X., Mita K., Vanisree V., Zurovec M., Sehnal F.;
RT "Identification of four small molecular mass proteins in the silk of Bombyx mori.";
RL Insect Mol. Biol. 10:437-445(2001).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR EMBL; AF352583; AAL83944.1; -.
DR HSP: P31713; 1SHP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 76 AA; 8445 MW; AA3F97D37353A3B CRC64;

Query Match 6.1%; Score 8; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFTYGGCQ 111
Db 52 EFTYGGCQ 59
|||||

RESULT 21
C1IX_HUMAN STANDARD; PRT; 126 AA.
ID C1IX_HUMAN
AC Q15332;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 13.2 kDa protein in chromosome 11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Austruy E., Belley L., Millasot P., Junien C., Jeanpierre C.;
RT "Characterization of the human cDNA with partial homology with the gamma subunit of sodium potassium ATPase of rat, mouse, rabbit and sheep.";
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; X86400; CAA60152.1; -.
DR PIR; S54159; S54159.
SQ SEQUENCE 126 AA; 13206 MW; F159A1BD0B64F11E CRC64;

Query Match 6.1%; Score 8; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 EAGPCLAS 89
Db 35 EAGPCLAS 42
|||||

RESULT 22
Q68V31 PRELIMINARY; PRT; 186 AA.
ID Q68V31
AC Q68V31;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chloride channel protein 5 (Fragment).
GN Name=cicn5;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Bovinae; Bos.	OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OX	NCBI_TaxID=9913;	OX	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	TISSUE=eye endothelium;	RA	Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA	Mitra R., Srinivas S.P.;	RA	Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uterback T.R., Fraser C.M.;
RT	"Expression of chloride channels in the bovine eye endothelial	RA	Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT	cells.";	RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.	RN	[2]
DR	EMBL; AJ810447; CAH17905.1; -	RP	SEQUENCE FROM N.A.
DR	InterPro; IPR001807; Cl-channel_volt.	RA	Town C.D., Kaul S.;
DR	Pfam; PF00654; Voltage_CLC; 1.	RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
FT	NON_TER 1	CC	-1- SIMILARITY: Belongs to the ABC transporter family.
FT	NON_TER 186	DR	EMBL; AC016162; AAG51884.1; -
SQ	SEQUENCE 186 AA; 20749 MW; 4264DC7DB8C7C773 CRC64;	DR	PIR; B96738; B96738.
		DR	HSSP; P26361; 1R0W.
		DR	GO; GO:0016021; C:integral to membrane; IEA.
		DR	GO; GO:0005524; F:ATP binding; IEA.
		DR	GO; GO:0042626; F:ATPase activity; IEA.
		DR	GO; GO:0006810; P:transport; IEA.
		DR	InterPro; IPR011527; ABC membrane 1.
		DR	InterPro; IPR003439; ABC_transporter.
		DR	Pfam; PF00005; ABC_tran; 1.
		DR	ProDom; PD000006; ABC transporter; 1.
		DR	PROSITE; PS00929; ABC_TM1F; 1.
		KW	ATP-binding.
		SQ	SEQUENCE 324 AA; 35810 MW; 1FA9AAE27A276D21 CRC64;
Query Match	6.1%; Score 8; DB 2; Length 186;	Query Match	6.1%; Score 8; DB 2; Length 324;
Best Local Similarity	100.0%; Pred. No. 8.3;	Best Local Similarity	100.0%; Pred. No. 12;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	10 LVPFILLG 17	Qy	10 LVPFILLG 17
Db	105 LVPFILLG 112	Db	221 LVPFILLG 228
RESULT 23		RESULT 25	
Q9WUG1	PRELIMINARY; PRT; 310 AA.	Q92WQ0	PRELIMINARY; PRT; 449 AA.
ID	Q9WUG1	ID	Q92WQ0
AC	Q9WUG1;	AC	Q92WQ0;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)	DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)	DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Chloride channel Clc-5 (Fragment).	DE	Putative permease protein.
OS	Cavia porcellus (Guinea pig).	GN	ORFNames=SMb20289;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OS	Rhizobium meliloti (Sinorhizobium meliloti).
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.	OG	Plasmid pSymb.
OX	NCBI_TaxID=10141;	OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
RN	[1]	OC	Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
RP	SEQUENCE FROM N.A.	OX	NCBI_TaxID=382;
RC	TISSUE=Small intestine epithelium;	RN	[1]
RA	Cid L.P., Salinas O., Sepulveda F.V.;	RP	SEQUENCE FROM N.A.
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	RC	STRAIN=1021;
DR	EMBL; AF133215; AAD33600.1; -	RX	MEDLINE=21395508; PubMed=11481431; DOI=10.1073/pnas.161294698;
DR	GO; GO:0016020; C:membrane; IEA.	RA	Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
DR	GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.	RA	Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie J.,
DR	GO; GO:0008821; F:chloride transport; IEA.	RA	Golding B., Puehler A.;
DR	InterPro; IPR001807; Cl-channel_volt.	RA	"The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
DR	Pfam; PF00654; Voltage_CLC; 1.	RT	fixing endosymbiont Sinorhizobium meliloti.";
DR	PRINTS; PR00762; CLCHANNEL.	RL	Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
FT	NON_TER 1	DR	EMBL; AL591985; CAC48679.1; -
FT	NON_TER 310	DR	PIR; G95876; G95876.
SQ	SEQUENCE 310 AA; 34691 MW; 15419E709DB531EF CRC64;	DR	GO; GO:0016020; C:membrane; IEA.
		DR	GO; GO:0005215; F:transporter activity; IEA.
		DR	GO; GO:0006810; P:transport; IEA.
		DR	InterPro; IPR005829; Sug transporter.
		DR	InterPro; IPR006043; Xant/urac/vitC.
		DR	InterPro; IPR006042; Xan_ur_permease.
		DR	Pfam; PF00860; Xan_ur_permease; 1.
		DR	PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
Query Match	6.1%; Score 8; DB 2; Length 310;	Query Match	6.1%; Score 8; DB 2; Length 310;
Best Local Similarity	100.0%; Pred. No. 12;	Best Local Similarity	100.0%; Pred. No. 12;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	10 LVPFILLG 17	Qy	10 LVPFILLG 17
Db	264 LVPFILLG 271	Db	264 LVPFILLG 271
RESULT 24		RESULT 24	
Q9FVV9	PRELIMINARY; PRT; 324 AA.	Q9FVV9	PRELIMINARY; PRT; 324 AA.
ID	Q9FVV9;	ID	Q9FVV9;
AC	Q9FVV9;	AC	Q9FVV9;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)	DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Putative ABC transporter; 57695-58850.	DE	Putative ABC transporter; 57695-58850.
GN	Names=F3117.2;	GN	Names=F3117.2;
OS	Arabidopsis thaliana (Mouse-ear cress).	OS	Arabidopsis thaliana (Mouse-ear cress).

DR PROSITE; PS01116; XANTH URACIL_PEMASE; UNKNOWN 1.
KW Complete proteome; Plasmid.
SQ SEQUENCE 449 AA; 46750 MW; 33E2705E52580D7D CRC64;

Query Match 6.1%; Score 8; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GLLPILVP 12
|||||||
Db 391 GLLPILVP 398

RESULT 26
CLC5 HUMAN
ID _CLC5_HUMAN STANDARD; PRT; 746 AA.

AC PS1795;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chloride channel protein 5 (CLC-5).
GN Name=CLC5; Synonyms=CLCK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96121370; PubMed=8575751;
RA Fisher S.E., van Bakel I., Lloyd S.E., Pearce S.H.S., Thakker R.V.,
RA Craig I.W.;
RA "Cloning and characterization of CLCN5, the human kidney chloride
channel gene implicated in Dent disease (an X-linked hereditary
nephrolithiasis).";
RL Hum. Mol. Genet. 3:2053-2059(1994).
RN [2]
RP SEQUENCE OF 487-746 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95173126; PubMed=7874126;
RA Fisher S., Black G.C.M., Lloyd S.E., Hatchwell E., Wrong O.,
RA Thakker R.V., Craig I.W.;
RA "Isolation and partial characterization of a chloride channel gene
which is expressed in kidney and is a candidate for Dent's disease (an
X-linked hereditary nephrolithiasis).";
RL Hum. Mol. Genet. 3:2053-2059(1994).
RN [3]
RP TISSUE SPECIFICITY.
RC TISSUE=Aortic endothelium, and Vascular smooth muscle;
RX MEDLINE=9222497; PubMed=10198195; DOI=10.1006/jmcc.1998.0901;
RA Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,
RA Schutte B.C.;
RA "Expression of CLCN voltage-gated chloride channel genes in human
RT blood vessels.";
RL J. Mol. Cell. Cardiol. 31:657-666(1999).
RN [4]
RP VARIANTS NPHL ARG-200; GLU-506 AND PRO-520, AND VARIANT XLRH LEU-244.
RX MEDLINE=96158876; PubMed=8559248; DOI=10.1038/379445a0;
RA Lloyd S.E., Pearce S.H.S., Fisher S.E., Steinmeyer K., Schwappach B.,
RA Scheinman S.J., Harding B., Bolino A., Devoto M., Goodyer P.,
RA Rigden S.P.A., Wrong O., Jentsch T.J., Craig I.W., Thakker R.V.;
RA "A common molecular basis for three inherited kidney stone diseases.";
RL Nature 379:445-449(1996).
RN [5]
RP VARIANTS NPHL.
RX MEDLINE=97402204; PubMed=9259268; DOI=10.1093/hmg/6.8.1233;
RA Lloyd S.E., Guenther W., Pearce S.H.S., Thomson A., Bianchi M.L.,
RA Bosio M., Craig I.W., Fisher S.E., Scheinman S.J., Wrong O.,
RA Jentsch T.J., Thakker R.V.;
RA "Characterisation of renal chloride channel, CLCN5, mutations in
RT hypercalcaemic nephrolithiasis (kidney stones) disorders.";
RL Hum. Mol. Genet. 6:1233-1239(1997).
CC -1- FUNCTION: Voltage-gated chloride channel. Chloride channels have

several functions including the regulation of cell volume;
membrane potential stabilization, signal transduction and
transepithelial transport. May play an important role in renal
tubular function.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- TISSUE SPECIFICITY: Kidney. Moderately expressed in aortic
vascular smooth muscle and endothelial cells, and at a slightly
higher level in the coronary vascular smooth muscle.

-1- DISEASE: Defects in CLCN5 are a cause of X-linked recessive
hypophosphatemic rickets (XLRH) [MIM:300008].

-1- DISEASE: Defects in CLCN5 are the cause of idiopathic low
molecular weight proteinuria of Japanese children (JILP)
[MIM:300008].

-1- DISEASE: Defects in CLCN5 are the cause of X-linked recessive
nephrolithiasis type 2 (NPHL2) [MIM:300009]; also known as Dent
disease. NPHL2 is a renal form of Fanconi syndrome, characterized
by hypercalciuria, nephrocalcinosis, renal stones and progressive
renal failure.

-1- DISEASE: Defects in CLCN5 are the cause of X-linked recessive
nephrolithiasis type 1 (NPHL1) [MIM:310468]; also designated XRN.
NPHL1 is characterized by hypercalciuria, nephrocalcinosis, renal
stones and renal insufficiency, but differs from Dent disease in
that the patients lack urinary acidification defects, rickets, and
osteomalacia.

-1- SIMILARITY: Belongs to the chloride channel (TC 1.A.11) family.

-1- SIMILARITY: Contains 2 CBS domains.

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or send an email to license@sib-sib.ch).

EMBL; X91906; CAA63000.1; -;
DR EMBL; X81836; CAA57430.1; -;
DR PIR; I37277; I37277.
DR Genew; HGNC:2023; CLCN5.
DR H-InvDB; HIX0016806; -;
DR MIM; 300008; -;
DR MIM; 300009; -;
DR MIM; 310468; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005254; F:chloride channel activity; TAS.
DR GO; GO:0007588; P:excretion; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel volt.
DR InterPro; IPR002247; Cl_channels.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR CBS domain; Chloride; Chloride channel; Disease mutation;
KW Ion transport; Ionic channel; Repeat; Transmembrane;
KW Voltage-gated channel.
FT TRANSMEM 55 75 Potential.
FT TRANSMEM 133 153 Potential.
FT TRANSMEM 189 209 Potential.
FT TRANSMEM 246 266 Potential.
FT TRANSMEM 317 337 Potential.
FT TRANSMEM 352 372 Potential.
FT TRANSMEM 428 448 Potential.
FT TRANSMEM 453 473 Potential.
FT TRANSMEM 494 514 Potential.
FT TRANSMEM 521 541 Potential.
FT TRANSMEM 585 645 CBS 1.
FT DOMAIN 682 733 CBS 2.
FT VARIANT 30 30 R -> RH (in NPHL2).
FT /FTID=VAR_001615;
FT VARIANT 57 57 G -> V (in NPHL2).
FT /FTID=VAR_001616.
FT VARIANT 200 200 L -> R (in NPHL2).
FT

FT VARIANT 244 244 /FTid=VAR_001617.
FT S -> L (in XLRH).
FT /FTid=VAR_001618.
FT R -> P (in JILP).
FT VARIANT 280 280 /FTid=VAR_001619.
FT G -> E (in NPHL1).
FT /FTid=VAR_001620.
FT G -> R (in NPHL2; abolishes the chloride
FT currentes).
FT /FTid=VAR_001621.
FT S -> P (in NPHL2).
FT /FTid=VAR_001622.
FT E -> D (in NPHL2; abolishes the chloride
FT currentes; total loss of function).
FT /FTid=VAR_001623.
SQ SEQUENCE 746 AA; 83146 MW; EF913C5BA0C85D8 CRC64;

Query Match 6.1%; Score 8; DB 1; Length 746;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 319 LVPFILLG 326

RESULT 27
Q9GKE7 PRELIMINARY; PRT; 746 AA.
AC Q9GKE7;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Outwardly rectifying chloride channel.
GN Name=CLC-5;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20545523; PubMed=10978325; DOI=10.1074/jbc.M004840200;
RA Dowland L.K., Luyckx V.A., Enck A.H., Leclercq B., Yu A.S.L.;
RT "Molecular cloning and characterization of an intracellular chloride
RT channel in the proximal tubule cell line, LLC-PK1";
RL J. Biol. Chem. 275:37765-37773 (2000).
DR EMBL; AF274055; AAG29104.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel volt.
DR InterPro; IPR002247; Cl_channel15.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR PRINTS; PR01116; CLCHANNELS.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83123 MW; 655E3ED45FC61229 CRC64;

Query Match 6.1%; Score 8; DB 2; Length 746;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 319 LVPFILLG 326

RESULT 28
Q9TTU3 PRELIMINARY; PRT; 746 AA.
AC Q9TTU3;

DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Chloride channel CLC-5.
GN Name=CLCN5;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand White; TISSUE=Cornea epithelia;
RA Rae J.L.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF195523; AAF06018.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel volt.
DR InterPro; IPR002247; Cl_channel15.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR PRINTS; PR01116; CLCHANNELS.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83206 MW; 667F2701C0BF006A CRC64;

Query Match 6.1%; Score 8; DB 2; Length 746;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 319 LVPFILLG 326

RESULT 29
Q99P66 PRELIMINARY; PRT; 746 AA.
ID Q99P66;
AC Q99P66;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Chloride channel CLCN5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Cornejo I., Cid L.P., Sepulveda F.V.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF326968; AAG49590.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel volt.
DR InterPro; IPR002247; Cl_channel15.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR PRINTS; PR01116; CLCHANNELS.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83093 MW; 92FC8AFDC7D8D4A5 CRC64;

Query Match 6.1%; Score 8; DB 2; Length 746;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 319 LVPFILLG 326


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Db      319 LVPEILLG 326

RESULT 30
Q7QH49          PRELIMINARY;      PRT;      893 AA.
AC Q7QH49;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eb1p4085 (Fragment).
GN Name=ebiG4085; ORFNames=ENSANG00000003243;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB0100817; EAA05380.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004527; F:exonuclease activity; IEA.
DR InterPro; IPR004859; Put_S3exo.
DR Pfam; PF03159; XRN_N; 1.
FT NON TER      893
SQ SEQUENCE      893 AA; 101361 MW; B14EB646182083C8 CRC64;

Query Match      6.1%; Score 8; DB 2; Length 893;
Best Local Similarity 100.0%; Pred. No. 26;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      111 QGNNNFQ 118
      |||||
Db      800 QGNNNFQ 807

RESULT 31
ID Q8K206          PRELIMINARY;      PRT;      900 AA.
AC Q8K206;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE A disintegrin-like and metalloprotease (Repolysin type) with
DE thrombospondin type 1 motif, 16.
GN Name=Adamt16;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins J., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034739; AAH34739.1; -.
DR HSP; P07996; ILSL.
DR MEROPS; M12.026; -.
DR MGD; MGI:2439637; Adants16.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP.1.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF01421; Repolysin; 1.
DR Pfam; PF00090; TSP_1; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS0215; ADAM MEPRO; 1.
DR PROSITE; PS0092; TSP1; 1.
KW Integrin; Metalloprotease; Protease.
SQ SEQUENCE      900 AA; 100679 MW; 590BE2B0E73740FF CRC64;

Query Match      6.1%; Score 8; DB 2; Length 900;
Best Local Similarity 100.0%; Pred. No. 26;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      70 LDFRKDIC 77
      |||||
Db      529 LDFRKDIC 536

RESULT 32
ID Q69Z28          PRELIMINARY;      PRT;      1233 AA.
AC Q69Z28;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKTAA2029 protein (Fragment).
GN Name=mKIAA2029;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestinal tract;
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Soga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-Fractionated Libraries.";
DNA Res. 11:205-218(2004).
DR EMBL; AK173338; BAD32616.1; -.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=24113856;
RX MEDLINE=8602577;
RA Bourguignon J., Diarra-Mehrpour M., Sesboue R., Frain M.,
RA Sala-Trepat J.M., Martin J.P., Salier J.P.;
RT "Human inter-alpha-trypsin-inhibitor: characterization and partial
RL nucleotide sequencing of a light chain-encoding cDNA.";
RL Biochem. Biophys. Res. Commun. 131:1146-1153(1985).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; M11562; AAA59194.1; -.
DR HSSP; P02760; 1BIK.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
FT NON_TER 1
SQ SEQUENCE 51 AA; 5698 MW; C13074054D45EED2 CRC64;

Query Match 5.3%; Score 7; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 16 YGGCQGN 22

RESULT 36
HTIB MANSE STANDARD; PRT; 53 AA.
AC P26227;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hemolymph trypsin inhibitor B (BPI-type) (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RC TISSUE=Larval hemolymph;
RX MEDLINE=88298810; PubMed=3165377;
RA Ramesh N., Sugumaran M., Mole J.E.;
RT "Purification and characterization of two trypsin inhibitors from the
RL hemolymph of Manduca sexta larvae.";
RL J. Biol. Chem. 263:11523-11527(1988).
CC -1- FUNCTION: Inhibits trypsin.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; B29235; B29235.
DR HSSP; P31713; 1SHP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 14 15
FT DISULFID 4 ?
FT DISULFID 13 37
FT DISULFID 29 50
FT NON_TER 53
SQ SEQUENCE 53 AA; 5880 MW; 3C34CFD98C6BB329 CRC64;

Query Match 5.3%; Score 7; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 16 YGGCQGN 22

RESULT 36
HTIB MANSE STANDARD; PRT; 53 AA.
AC P26227;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hemolymph trypsin inhibitor B (BPI-type) (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RC TISSUE=Larval hemolymph;
RX MEDLINE=88298810; PubMed=3165377;
RA Ramesh N., Sugumaran M., Mole J.E.;
RT "Purification and characterization of two trypsin inhibitors from the
RL hemolymph of Manduca sexta larvae.";
RL J. Biol. Chem. 263:11523-11527(1988).
CC -1- FUNCTION: Inhibits trypsin.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; B29235; B29235.
DR HSSP; P31713; 1SHP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 14 15
FT DISULFID 4 ?
FT DISULFID 13 37
FT DISULFID 29 50
FT NON_TER 53
SQ SEQUENCE 53 AA; 5880 MW; 3C34CFD98C6BB329 CRC64;

Query Match 5.3%; Score 7; DB 1; Length 53;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 34 YGGCQGN 40

RESULT 37
IVB2 NAJNI STANDARD; PRT; 57 AA.
AC P00986;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom basic protease inhibitor II.
OS Naja nivea (Cape cobra).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=8655;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=76237547; PubMed=950137;
RA Hokama Y., Iwanaga S., Tateuchi T., Suzuki T.;
RT "Snake venom proteinase inhibitors. III. Isolation of five polypeptide
RL inhibitors from the venoms of Hemachatus haemachatus (Ringhals
RT cobra) and Naja nivea (Cape cobra) and the complete amino acid
RL sequences of two of them.";
RL J. Biochem. 79:559-578(1976).
CC -1- FUNCTION: The activity of this inhibitor is probably similar to
CC that of bovine basic protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01217; TINJVC.
DR HSSP; P25660; 1JC6.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 15 16
FT DISULFID 5 55
FT DISULFID 14 38
FT DISULFID 30 51
FT DISULFID 30 51
SQ SEQUENCE 57 AA; 6466 MW; 7CA69230A02887D1 CRC64;

Query Match 5.3%; Score 7; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGC 110
Db 32 EPIYGGC 38

RESULT 38
ISC2_BOMMO STANDARD; PRT; 62 AA.
AC P10832;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chymotrypsin inhibitor SCI-II.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;

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Bombycidae; Bombyx.
KW NCBI_TaxID=7091;
RN SEQUENCE.
RP TISSUE=Larval hemolymph;
RC MEDLINE=89228538; PubMed=3072972;
RT Sasaki T.;
RA "Amino-acid sequences of two basic chymotrypsin inhibitors from
RT silkworm larval hemolymph.";
RL Biol. Chem. Hoppe-Seyler 369:1235-1241(1988).
CC -!- FUNCTION: Inhibits chymotrypsin and thus avoids the accidental
CC chymotrypsin-mediated activation of prophenoloxidase. This enzyme
CC is required by the insect immune system to produce melanin which
CC is used to engulf foreign objects.
CC -!- FUNCTION: Also inhibits trypsin weakly, this may be due to the
CC presence of a pseudo-reactive bond in positions 44-45 (Lys-Gly).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S01803; S01803.
DR HSSP; P10646; IADZ.
DR InterPro; IPR002223; Prot Inh Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot Inh Kunz-m; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 20 21 Reactive bond (By similarity).
FT SITE 44 45 Pseudo reactive bond for trypsin.
FT SITE 49 60 By similarity.
FT DISULFID 9 60 By similarity.
FT DISULFID 19 43 By similarity.
FT DISULFID 35 56 By similarity.
SQ SEQUENCE 62 AA; 7067 MW; 7E7C013DA05AC6DA CRC64;

Query Match 5.3%; Score 7; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 BFIYGC 110
DB 37 BFIYGC 43

RESULT 39
Q968S8 PRELIMINARY; PRT; 76 AA.
AC Q968S8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Silk protease inhibitor 1 precursor.
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Galleriinae; Galleria.
OX NCBI_TaxID=71137;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21175824; PubMed=11277929;
RA Nirmla X., Kodrik D., Zurovec M., Sehnal F.;
RT "Insect silk contains both a Kunitz-type and a unique Kazal-type
RT proteinase inhibitor."
RL Eur. J. Biochem. 268:2064-2073(2001).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF292098; AKA40037.1; -.
DR HSSP; P10646; IADZ.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot Inh Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.

KW Protease; Signal.
FT SIGNAL 1 20 Potential.
SQ SEQUENCE 76 AA; 8419 MW; 0C6ED52550632B79 CRC64;

Query Match 5.3%; Score 7; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGQN 113
DB 54 YGCGQN 60

RESULT 40
CVP2_PIMHY STANDARD; PRT; 77 AA.
AC Q8T0M4;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Protease inhibitor cvp2 precursor (Cysteine-rich venom protein 2).
GN Name=cvp2;
OS Pimpla hypochondriaca (Parasitoid wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Ichneumonidae; Pimplinae; Pimplini; Pimpla.
OX NCBI_TaxID=135724;
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 24-29.
RC TISSUE=Venom, and Venom gland;
RX PubMed=15147757; DOI=10.1016/j.ibmb.2004.03.003;
RA Parkinson N.M., Conyers C., Keen J., MacNicoll A., Smith I.,
RA Audsley N., Weaver R.;
RT "Towards a comprehensive view of the primary structure of venom
RT proteins from the parasitoid wasp Pimpla hypochondriaca.";
RL Insect Biochem. Mol. Biol. 34:565-571(2004).
CC -!- FUNCTION: Probable serine protease inhibitor (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
DR EMBL; AJ438993; CAD27738.1; -.
DR HSSP; P31713; ISHP.
DR InterPro; IPR002223; Prot Inh Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot Inh Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor; Signal.
FT SIGNAL 1 23
FT CHAIN 24 77 Protease inhibitor cvp2.
FT DOMAIN 28 76 BPTI/Kunitz inhibitor.
FT DISULFID 28 76 By similarity.
FT DISULFID 37 59 By similarity.
FT DISULFID 51 72 By similarity.
SQ SEQUENCE 77 AA; 7873 MW; FF40C07F3C7E0D75 CRC64;

Query Match 5.3%; Score 7; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 BFIYGC 110
DB 37 BFIYGC 43

OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN SEQUENCE.
RP TISSUE=Larval hemolymph;
RC MEDLINE=89228538; PubMed=3072972;
RT Sasaki T.;
RA "Amino-acid sequences of two basic chymotrypsin inhibitors from
RT silkworm larval hemolymph.";
RL Biol. Chem. Hoppe-Seyler 369:1235-1241(1988).
CC -!- FUNCTION: Inhibits chymotrypsin and thus avoids the accidental
CC chymotrypsin-mediated activation of prophenoloxidase. This enzyme
CC is required by the insect immune system to produce melanin which
CC is used to engulf foreign objects.
CC -!- FUNCTION: Also inhibits trypsin weakly, this may be due to the
CC presence of a pseudo-reactive bond in positions 44-45 (Lys-Gly).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S01803; S01803.
DR HSSP; P10646; IADZ.
DR InterPro; IPR002223; Prot Inh Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot Inh Kunz-m; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 20 21 Reactive bond (By similarity).
FT SITE 44 45 Pseudo reactive bond for trypsin.
FT SITE 49 60 By similarity.
FT DISULFID 9 60 By similarity.
FT DISULFID 19 43 By similarity.
FT DISULFID 35 56 By similarity.
SQ SEQUENCE 62 AA; 7067 MW; 7E7C013DA05AC6DA CRC64;

Query Match 5.3%; Score 7; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 BFIYGC 110
DB 37 BFIYGC 43

RESULT 39
Q968S8 PRELIMINARY; PRT; 76 AA.
AC Q968S8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Silk protease inhibitor 1 precursor.
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Galleriinae; Galleria.
OX NCBI_TaxID=71137;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21175824; PubMed=11277929;
RA Nirmla X., Kodrik D., Zurovec M., Sehnal F.;
RT "Insect silk contains both a Kunitz-type and a unique Kazal-type
RT proteinase inhibitor."
RL Eur. J. Biochem. 268:2064-2073(2001).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF292098; AKA40037.1; -.
DR HSSP; P10646; IADZ.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot Inh Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.


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Db          53 EFYGGC 59

RESULT 41
ID Q9VCM3 PRELIMINARY; PRT; 80 AA.
AC Q9T3S7
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 24, Last annotation update)
DE Toxin 1.
OS Araneus ventricosus.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Araneidae; Araneus.
OX NCBI_TaxID=182803;
RN [1]
RP SEQUENCE FROM N.A.
RA Jung E.H., Lee K.S., Han J.H., Je Y.H., Chang J.H., Roh J.Y.,
RA Sohn H.D., Jin B.R.;
RT "Molecular cloning of two cDNAs encoding an insecticidal toxin from
RT the spider, Araneus ventricosus, and construction of a recombinant
RT baculovirus expressing a spider toxin.";
RL Int. J. Ind. Entomol. 4:43-49 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Chung E.H., Lee K.S., Han J.H., Sohn H.D., Jin B.R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY091482; AAM14403.1; -.
DR HSSP; P12111; 1KTH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR02223; Prot Inh Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 80 AA; 9275 MW; D07F5F9AC6B7BC10 CRC64;

Query Match 5.3%; Score 7; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFYGGC 110
Db 54 EFYGGC 60

RESULT 42
ID Q9VCM3 PRELIMINARY; PRT; 80 AA.
AC Q9VCM3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG17380-PA.
GN ORNames=CG17380;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yeandle M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Efankoch C., Baldwin D.,
RA Ballew R.M., Baeu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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Query Match	5.3%	Score 7;	DB 2;	Length 83;
Best Local Similarity	100.0%;	Pred.No. 50;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	104	EFYGGC 110		
Db	58	EFYGGC 64		
RESULT 46				
Q90WAI		PRELIMINARY;	PRT;	83 AA.
ID	Q90WAI;			
AC	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	textilinin.			
OS	Pseudonaja textilis textilis.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Elapidae; Acanthophinae; Pseudonaja.			
OX	NCBI_TaxID=169397;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Venom gland;			
RC	Masci P.P., Lavlin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Venom gland;			
RC	Flippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,			
RA	Whitaker A.N., Gaffney P.J., Lavlin M.F.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.			
DR	EMBL; AF402324; AAK9519.1; -.			
DR	HSP; P25660; 1JC6.			
DR	GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.			
DR	Pfam: PF00014; Kunitz BPTI; 1.			
DR	PRINTS; PR00759; BASICPTASE.			
DR	ProDom; PD000222; Prot_Inh_Kunz-m; 1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS0279; BPTI_KUNITZ_2; 1.			
SQ	SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;			
Query Match				
Best Local Similarity	5.3%	Score 7;	DB 2;	Length 83;
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	104	EFYGGC 110		
Db	58	EFYGGC 64		
RESULT 47				
Q6ITB0		PRELIMINARY;	PRT;	83 AA.
ID	Q6ITB0			
AC	06ITB0;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Carinatin.			
OS	Tropidochis carinatus (Australian rough-scaled snake).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Elapidae; Netechinae; Tropidichis.			
OX	NCBI_TaxID=100989;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Venom gland;			
RC	Flippovich I.V., Sorokina N.I.;			
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.			

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Notechis.

OX NCBI_TaxID=70142;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=venom gland;

RA Filippovich I.V., Sorokina N.I.;

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR EMBL; AY626933; AAT45409.1; -

DR HSP; Q16019; IADP.

DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

SQ SEQUENCE 83 AA; 9073 MW; AE4D0E8367EED0A2 CRC64;

Query Match

Best Local Similarity 5.3%; Score 7; DB 2; Length 83;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGC 110

DB 58 EFIYGGC 64

RESULT 50

Q6ITB3

ID Q6ITB3 PRELIMINARY; PRT; 83 AA.

AC Q6ITB3;

DT 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE Tigerin-1.

OS Notechis scutatus scutatus (Mainland tiger snake) (Common tiger

OS snake)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Acanthophiinae; Notechis.

OX NCBI_TaxID=70142;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RA Filippovich I.V., Sorokina N.I.;

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR EMBL; AY626932; AAT45408.1; -

DR HSP; P10646; IADZ.

DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

SQ SEQUENCE 83 AA; 9135 MW; AE4D0E85A486F0A2 CRC64;

Query Match

Best Local Similarity 5.3%; Score 7; DB 2; Length 83;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGC 110

DB 58 EFIYGGC 64

Search completed: September 21, 2005, 16:50:12

Job time : 142 secs

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